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(54) Title: SECRETED EXPRESSED SEQUENCE TAGS (sESTs)

(57) Abstract .

Secreted expressed sequence tags (sESTs) isolated from a variety of human tissue sources are provided.

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SECRETED EXPRESSED SEQUENCE TAGS (sESTs)

5

FIELD OF THE INVENTION

The present invention provides novel polynucleotides which are expressed sequence tags (ESTs) for secreted proteins.

BACKGROUND OF THE INVENTION

10 Gargantuan efforts have been employed by various investigational projects to randomly sequence portions of naturally-occurring cDNAs. The rationale behind this approach to identification and sequencing genes is founded in two basic principles: (1) that transcribed cDNAs represent the product of the most important genes, namely those that are actually expressed *in vivo*, and (2) that efforts to sequence genes and other portions of the genome of
15 target organisms which are not actually expressed wastes substantial effort on areas not likely to yield genetic information of therapeutic importance. Thus, the high-throughput sequencing efforts focus on only those portions of the genome which are expressed. The randomly produced cDNA sequences represent "expressed sequence tags" or "ESTs", which identify and can be used as probes for the longer, full-length cDNA or genomic sequence from which they
20 were transcribed.

Although this "shortcut" approach to genomic sequencing presents savings of effort compared to sequencing of the complete genome, it still produced a vast array of ESTs which may not be directly useful as protein therapeutics. To date, the majority of protein-related drug discovery has focused on the use of secreted proteins to produce a desired therapeutic effect.
25 Since the EST approach theoretically identifies all expressed proteins, it produces an EST library which contains a mixture of secreted proteins (such as hormones, cytokines and receptors) and non-secreted proteins (such as, for example, metabolic enzymes and cellular structural proteins), without identifying which ESTs correspond to proteins falling into either category. As a result, these methods are not optimally tailored to the needs of investigators
30 searching for secreted proteins because they must separate the secreted "wheat" from the non-secreted "chaff", wasting effort and resources in the process.

Co-assigned U.S. Patent No. 5,536,637, which is incorporated herein by reference, provides methods for focusing genomic sequencing efforts on sequences encoding the secreted proteins which are of most interest for identification of protein therapeutics. The '637 patent
35 discloses a "signal sequence trap" which selectively identifies ESTs for secreted

proteins, namely "secreted expressed sequence tags" or "sESTs". It is to these sESTs that the present invention is directed.

SUMMARY OF THE INVENTION

5 The present invention provides for sESTs isolated from a variety of human RNA/cDNA sources.

In preferred embodiments, the present invention provides an isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

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or a complement of said sequence.

15 In other embodiments, the present invention provides an isolated polynucleotide
consisting of a nucleotide sequence selected from the group consisting of:

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NO:1497, SEQ ID NO:1498, SEQ ID NO:1499, and SEQ ID NO:1500;

or a complement of said sequence.

In further embodiments, the present invention provides an isolated polynucleotide consisting essentially of a nucleotide sequence selected from the group consisting of:

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30 or a complement of said sequence.

In yet other embodiments, the present invention provides an isolated polynucleotide comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of:

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NO:1453, SEQ ID NO:1454, SEQ ID NO:1455, SEQ ID NO:1456, SEQ ID
NO:1457, SEQ ID NO:1458, SEQ ID NO:1459, SEQ ID NO:1460, SEQ ID
30 NO:1461, SEQ ID NO:1462, SEQ ID NO:1463, SEQ ID NO:1464, SEQ ID
NO:1465, SEQ ID NO:1466, SEQ ID NO:1467, SEQ ID NO:1468, SEQ ID
NO:1469, SEQ ID NO:1470, SEQ ID NO:1471, SEQ ID NO:1472, SEQ ID
NO:1473, SEQ ID NO:1474, SEQ ID NO:1475, SEQ ID NO:1476, SEQ ID
NO:1477, SEQ ID NO:1478, SEQ ID NO:1479, SEQ ID NO:1480, SEQ ID

NO:1481, SEQ ID NO:1482, SEQ ID NO:1483, SEQ ID NO:1484, SEQ ID
 NO:1485, SEQ ID NO:1486, SEQ ID NO:1487, SEQ ID NO:1488, SEQ ID
 NO:1489, SEQ ID NO:1490, SEQ ID NO:1491, SEQ ID NO:1492, SEQ ID
 NO:1493, SEQ ID NO:1494, SEQ ID NO:1495, SEQ ID NO:1496, SEQ ID
 5 NO:1497, SEQ ID NO:1498, SEQ ID NO:1499, and SEQ ID NO:1500;
 or to a complement of said sequence.

The invention also provides for proteins encoded by the above-described polynucleotides.

10

DETAILED DESCRIPTION

The nucleotide sequences of the sESTs of the present invention are reported in the Sequence Listing below. Table 2 lists the "Clone ID Nos." assigned by applicants to each SEQ ID NO: in the Sequence Listing.

15 Table 2

Each pair of entries in this table consists of the SEQ ID NO (e.g., 1, 2, etc.) followed by the Clone ID No. for such sequence (e.g., B11, B18, etc.).

1	BV31	18	CB302	35	BZ83	52	CD244	
2	BV34	19	CB318	36	BZ87	53	CD265	
20	3	BV37	20	CB321	37	CB15	54	BT217
4	BV45	21	CB96	38	CB2	55	BV278	
5	BV8	22	CB98	39	CB44	56	BV280	
6	BV93	23	BZ42	40	CC11	57	BV282	
7	BV99	24	BZ53	41	CC182	58	BV285	
25	8	CB100	25	BZ56	42	CC298	59	BV286
9	CB107	26	BZ6	43	CC310	60	BV291	
10	CB110	27	BZ607	44	CC323	61	BV295	
11	CB114	28	BZ61	45	CC332	62	BW389	
12	CB118	29	BZ62	46	CC335	63	BX135	
30	13	CB123	30	BZ641	47	CC338	64	BX141
14	CB129	31	BZ644	48	CC41	65	BX148	
15	CB137	32	BZ72	49	CC52	66	BZ1	
16	CB239	33	BZ74	50	CD107	67	BZ16	
17	CB259	34	BZ82	51	CD205	68	BZ187	

	69	BZ19	103	CE159	137	CH315	171	CC194
	70	BZ205	104	CE2	138	CH325	172	CC198
	71	BZ222	105	CE347	139	BZ568	173	CC199
	72	BZ230	106	CE36	140	BZ578	174	CC205
5	73	BZ234	107	CE40	141	BZ588	175	CC215
	74	BZ244	108	CE87	142	BZ597	176	CC253
	75	BZ269	109	CG1	143	BZ598	177	CC258
	76	BZ280	110	CG44	144	CH637	178	CC259
	77	BZ288	111	CG60	145	CH644	179	CC265
10	78	BZ304	112	CG68	146	CH699	180	CC288
	79	BZ328	113	BP202	147	CI240	181	CC95
	80	BZ331	114	BP242	148	CI247	182	CC96
	81	BP646	115	BP243	149	CJ1	183	CD311
	82	BP652	116	BZ444	150	CJ19	184	CD323
15	83	BP656	117	BZ453	151	CJ24	185	CH338
	84	BP666	118	CC233	152	CJ27	186	CH355
	85	BP667	119	CC242	153	CJ3	187	CH377
	86	BP674	120	CC247	154	CJ37	188	CH421
	87	BP695	121	CC344	155	CJ42	189	CH425
20	88	BP705	122	CC346	156	CJ44	190	CH522
	89	BP713	123	CC351	157	CJ49	191	CH541
	90	BP720	124	CC359	158	CJ50	192	CH555
	91	BP750	125	CC364	159	CJ55	193	CH558
	92	BP754	126	CC365	160	CJ6	194	CH582
25	93	BW143	127	CC374	161	CJ76	195	CH595
	94	BR307	128	CE303	162	CJ77	196	CH720
	95	BR309	129	CE328	163	CJ84	197	CH723
	96	BR312	130	CG199	164	CJ86	198	CH724
	97	BR318	131	CG209	165	CJ91	199	CH735
30	98	CB187	132	CG210	166	CC111	200	CH742
	99	CB190	133	CG350	167	CC118	201	CI126
	100	CB204	134	CG354	168	CC120	202	CI129
	101	CB213	135	CG426	169	CC126	203	CI133
	102	CE120	136	CH303	170	CC130	204	CI181

	205	CI229	239	CG160	273	CI395	307	CJ397
	206	CI25	240	CG175	274	CI407	308	CJ400
	207	CI52	241	CG176	275	CI411	309	CJ404
	208	CI84	242	CG180	276	CI437	310	CJ415
5	209	CI91	243	CG279	277	CI443	311	CJ420
	210	BP163	244	CG292	278	CI444	312	CJ424
	211	BP175	245	CG300	279	CI459	313	CJ434
	212	BP199	246	CG301	280	CI480	314	CJ454
	213	BP272	247	CG314	281	CI490	315	CJ457
10	214	BP284	248	CG315	282	CI492	316	CJ481
	215	BP294	249	CG324	283	CI493	317	CJ493
	216	BP299	250	CG336	284	CI510	318	CJ501
	217	BP300	251	CG99	285	CI522	319	CJ514
	218	BP306	252	CH143	286	CI534	320	CJ539
15	219	BP311	253	CH207	287	CI542	321	CJ540
	220	BP312	254	CH224	288	CI560	322	CJ549
	221	BP327	255	CH227	289	CI561	323	CJ551
	222	BP345	256	CH245	290	CI583	324	CK126
	223	BP368	257	CH246	291	CI586	325	CK151
20	224	BP467	258	CH27	292	CJ145	326	CK181
	225	BP468	259	CH30	293	CJ149	327	CK201
	226	BR375	260	CH4	294	CJ160	328	CK213
	227	BR390	261	CH64	295	CJ164	329	CK218
	228	BR408	262	CH78	296	CJ168	330	CK234
25	229	BR418	263	CH85	297	CJ176	331	CK37
	230	BY66	264	CH87	298	CJ183	332	CK48
	231	CF118	265	CN320	299	CJ194	333	CL104
	232	CF127	266	CN343	300	CJ206	334	CL110
	233	CF22	267	CN344	301	CJ230	335	CL122
30	234	CF235	268	CN395	302	CJ237	336	CL132
	235	CG109	269	CN423	303	CJ257	337	CL147
	236	CG131	270	CI363	304	CJ265	338	CL152
	237	CG153	271	CI386	305	CJ378	339	CL181
	238	CG158	272	CI392	306	CJ389	340	CL182

	341	CL399	375	CN516	409	CO58	443	CO155
	342	CL469	376	CN532	410	CO48	444	CO153
	343	CL470	377	CN552	411	CO444	445	CO145
	344	CL481	378	CN593	412	CO431	446	CO140
5	345	CL493	379	CN619	413	CO391	447	CO139
	346	CM12	380	CN621	414	CO384	448	CO128
	347	CM178	381	CN667	415	CO36	449	CO1254
	348	CM188	382	CN703	416	CO351	450	CO1247
	349	CM194	383	CN718	417	CO337	451	CO1232
10	350	CM246	384	CN729	418	CO327	452	CO1224
	351	CM251	385	CN835	419	CO315	453	CO1223
	352	CM54	386	CN896	420	CO304	454	CO1206
	353	CM62	387	CO933	421	CO270	455	CO1198
	354	CN140	388	CO924	422	CO268	456	CO1196
15	355	CN171	389	CO908	423	CO264	457	CO1194
	356	CN173	390	CO900	424	CO261	458	CO1187
	357	CN238	391	CO889	425	CO257	459	CO1180
	358	CN29	392	CO888	426	CO253	460	CO1178
	359	CN291	393	CO874	427	CO25	461	CO1175
20	360	CN304	394	CO851	428	CO246	462	CO117
	361	CN327	395	CO83	429	CO244	463	CO1168
	362	CN49	396	CO821	430	CO240	464	CO1164
	363	CN50	397	CO806	431	CO228	465	CO1162
	364	CN54	398	CO798	432	CO223	466	CO1161
25	365	CN65	399	CO79	433	CO222	467	CO1159
	366	CJ305	400	CO71	434	CO209	468	CO1153
	367	CJ316	401	CO7	435	CO205	469	CO1151
	368	CJ317	402	CO69	436	CO204	470	CO1137
	369	CJ336	403	CO66	437	CO20	471	CO1123
30	370	CJ347	404	CO639	438	CO197	472	CO1076
	371	CJ360	405	CO638	439	CO185	473	CO1072
	372	CJ365	406	CO625	440	CO170	474	CO1026
	373	CJ366	407	CO62	441	CO17	475	CO1000
	374	CN483	408	CO602	442	CO163	476	CN755

	477	CN736	511	CR1166	545	CR632	579	CO409
	478	CN709	512	CR1186	546	CR641	580	CO474
	479	CO975	513	CR1190	547	CT729	581	CO480
	480	CO990	514	CR329	548	CN922	582	CO500
5	481	CP280	515	CR354	549	CN934	583	CO519
	482	CP283	516	CR377	550	CN951	584	CO522
	483	CP287	517	CR390	551	CN952	585	CO526
	484	CP289	518	CR392	552	CN980	586	CO559
	485	CP294	519	CR422	553	CP111	587	CO595
10	486	CP304	520	CR423	554	CP147	588	CO605
	487	CP307	521	CR466	555	CU13	589	CO618
	488	CP311	522	CR477	556	CP251	590	CO629
	489	CP313	523	CR478	557	CP258	591	CO643
	490	CP314	524	CR482	558	CP33	592	CO653
15	491	CP328	525	CR491	559	CP41	593	CO661
	492	CP352	526	CR494	560	CP91	594	CO667
	493	CQ286	527	CR502	561	CP92	595	CO695
	494	CQ294	528	CR506	562	CQ160	596	CO696
	495	CQ304	529	CR513	563	CQ165	597	CO707
20	496	CQ309	530	CR514	564	CQ268	598	CO716
	497	CQ331	531	CR515	565	CQ30	599	CO718
	498	CQ333	532	CR527	566	CR100	600	CO720
	499	CR1116	533	CR529	567	CR178	601	CO722
	500	CR1118	534	CR537	568	CR184	602	CO736
25	501	CR1121	535	CR538	569	CR263	603	CO763
	502	CR1127	536	CR540	570	CR335	604	CO767
	503	CR1135	537	CR541	571	CR4	605	CP116
	504	CR1141	538	CR545	572	CR61	606	CP151
	505	CR1142	539	CR587	573	CR93	607	CI293
30	506	CR1144	540	CR588	574	CO282	608	CI294
	507	CR1147	541	CR593	575	CO310	609	CI298
	508	CR1155	542	CR594	576	CO334	610	CU14
	509	CR1156	543	CR611	577	CO387	611	CU2
	510	CR1162	544	CR618	578	CO390	612	CU25

	613	CU32	647	CR678	681	CT748	715	CS520
	614	CU39	648	CR726	682	CT738	716	CS524
	615	CU40	649	CR733	683	CT726	717	CS534
	616	DA10	650	CR778	684	CT706	718	CT14
5	617	DA136	651	CR836	685	CT705	719	CT142
	618	DA155	652	CR839	686	CT702	720	CT143
	619	DA16	653	CR872	687	CT693	721	CT149
	620	DA165	654	CR890	688	CT677	722	CT156
	621	DA170	655	CR916	689	CT658	723	CT159
10	622	DA183	656	CR929	690	CT645	724	CT162
	623	DA223	657	CR930	691	CT636	725	CT188
	624	DA224	658	CR936	692	CT631	726	CT189
	625	DA225	659	CR974	693	CT616	727	CT190
	626	DA227	660	CT747	694	CT611	728	CT193
15	627	DA228	661	CT727	695	CT600	729	CT194
	628	DA234	662	CT690	696	CT585	730	CT2
	629	DA244	663	CT649	697	CT583	731	CT207
	630	DA246	664	CT624	698	CS224	732	CT220
	631	DA274	665	CT564	699	CS255	733	CT223
20	632	DA471	666	CT88	700	CS267	734	CT226
	633	DA490	667	CT864	701	CS271	735	CT227
	634	DA495	668	CT857	702	CS278	736	CT24
	635	DA496	669	CT852	703	CS284	737	CT254
	636	DA504	670	CT838	704	CS296	738	CT256
25	637	DA505	671	CT808	705	CS297	739	CT258
	638	DA507	672	CT807	706	CS317	740	CT271
	639	DA516	673	CT797	707	CS319	741	CT275
	640	DA529	674	CT791	708	CS322	742	CT28
	641	DA84	675	CT785	709	CS353	743	CT284
30	642	CR1003	676	CT783	710	CS366	744	CT293
	643	CR1013	677	CT780	711	CS471	745	CO1020
	644	CR1044	678	CT771	712	CS475	746	CO1043
	645	CR1056	679	CT754	713	CS485	747	CO1067
	646	CR1063	680	CT750	714	CS516	748	CO1069

	749	CO1080	783	DB257	817	CW1617	851	CT384
	750	CO1081	784	DB343	818	CW1632	852	CT392
	751	CO1094	785	DB415	819	CW1636	853	CT394
	752	CO956	786	DB53	820	CW1640	854	CT415
5	753	CO973	787	DB85	821	CW169	855	CT421
	754	CJ471	788	CW1000	822	CW172	856	CT423
	755	CJ472	789	CW1038	823	CW173	857	CT434
	756	CJ475	790	CW1087	824	CW175	858	CT440
	757	CJ483	791	CW1100	825	CV123	859	CT443
10	758	CJ484	792	CW1109	826	CV156	860	CT450
	759	CJ485	793	CW1112	827	CV160	861	CT453
	760	CJ486	794	CW1115	828	CV192	862	CT457
	761	CJ488	795	CW1150	829	CV203	863	CT466
	762	CJ496	796	CW1155	830	CV215	864	CT474
15	763	CJ497	797	CW1177	831	CV227	865	CT475
	764	CJ498	798	CW1195	832	CV263	866	CT479
	765	CJ507	799	CW1200	833	CV275	867	CT489
	766	CJ508	800	CW1201	834	CV305	868	CT51
	767	CJ519	801	CW1214	835	CV328	869	CT519
20	768	CJ520	802	CW1225	836	CV380	870	CT521
	769	CJ521	803	CW1230	837	CV394	871	CT526
	770	CJ522	804	CW1233	838	CV410	872	CT536
	771	CJ534	805	CW1272	839	CV416	873	CT541
	772	CJ536	806	CW1292	840	CV461	874	CT547
25	773	CJ543	807	CW1306	841	CV493	875	CT550
	774	CJ544	808	CW1311	842	CV501	876	CT559
	775	CJ547	809	CW1314	843	CT3	877	CT562
	776	CK53	810	CW1334	844	CT314	878	DE36
	777	CK7	811	CW1365	845	CT317	879	DE37
30	778	CK70	812	CW1372	846	CT320	880	DE4
	779	CL49	813	CW149	847	CT326	881	DE42
	780	CL63	814	CW152	848	CT340	882	DE63
	781	DB203	815	CW1574	849	CT353	883	DE70
	782	DB208	816	CW1611	850	CT358	884	DE83

	885	DE103	919	CS771	953	CW775	987	DA337
	886	DE105	920	CS773	954	CW795	988	DA348
	887	DE110	921	CS776	955	CW802	989	DA373
	888	DE114	922	CW222	956	CW823	990	DA388
5	889	DE117	923	CW224	957	CW835	991	DA389
	890	DE119	924	CW226	958	CZ115	992	DA390
	891	DE91	925	CW232	959	CZ122	993	DA391
	892	DE95	926	CW254	960	CZ186	994	DA414
	893	DE96	927	CW272	961	CZ214	995	DA428
10	894	CW420	928	CW280	962	CZ247	996	DA443
	895	CW424	929	CW313	963	CZ251	997	DA451
	896	CW457	930	CW314	964	CZ268	998	CW1458
	897	CW485	931	CW347	965	CZ270	999	CW1475
	898	CS383	932	CW354	966	CZ278	1000	CW1481
15	899	CS384	933	CW363	967	CZ291	1001	CW1506
	900	CS399	934	CW374	968	CZ320	1002	CW1510
	901	CS405	935	CW382	969	CZ326	1003	CW1543
	902	CS409	936	CW383	970	CZ362	1004	CW1550
	903	CS431	937	CW386	971	CW1414	1005	CW1552
20	904	CS438	938	CW388	972	CW1440	1006	CZ372
	905	CS454	939	CW512	973	CE209	1007	CZ374
	906	CS588	940	CW517	974	CE216	1008	CW902
	907	CS629	941	CW53	975	CE232	1009	CW922
	908	CS636	942	CW554	976	CE242	1010	CW924
25	909	CS637	943	CW585	977	CF193	1011	CW976
	910	CS638	944	CW618	978	CH776	1012	CW979
	911	CS645	945	CE197	979	CW1381	1013	CW984
	912	CS679	946	CW662	980	CW1389	1014	CW998
	913	CS682	947	CW675	981	CW1399	1015	CZ1
30	914	CS734	948	CW691	982	CZ653	1016	CW753
	915	CS743	949	CW707	983	CZ681	1017	CW759
	916	CS752	950	CW735	984	CZ711	1018	CW800
	917	CS756	951	CW762	985	CZ719	1019	CW891
	918	CS765	952	CW768	986	DA306	1020	CW960

	1021	CT80	1055	DC14	1089	DH1206	1123	DF478
	1022	DF1115	1056	CW1670	1090	DH1212	1124	DF483
	1023	DF1117	1057	CW1682	1091	DH1213	1125	DF494
	1024	DF1125	1058	DF814	1092	DH190	1126	DF499
5	1025	DF134	1059	DF821	1093	DI191	1127	DF7
	1026	DF14	1060	DF842	1094	DI207	1128	DF706
	1027	DF163	1061	DG1	1095	DI216	1129	DF713
	1028	DF174	1062	DG17	1096	DI243	1130	DF727
	1029	DF175	1063	DG174	1097	DI248	1131	DF737
10	1030	DF180	1064	DG256	1098	DI261	1132	DF756
	1031	DF185	1065	DG26	1099	DF1005	1133	DF757
	1032	DF201	1066	DG266	1100	DF1009	1134	DF762
	1033	DF202	1067	DG326	1101	DF1010	1135	DF776
	1034	DF203	1068	DG327	1102	DF102	1136	DF777
15	1035	DF206	1069	DG329	1103	DF1050	1137	DF780
	1036	DF219	1070	DG330	1104	DF1062	1138	DF783
	1037	DF230	1071	DG331	1105	DF1063	1139	DG12
	1038	DF232	1072	DG44	1106	DF1084	1140	DG121
	1039	DF239	1073	DG65	1107	DF153	1141	DG128
20	1040	DF244	1074	DG69	1108	DF218	1142	DG141
	1041	DF259	1075	DG7	1109	DF251	1143	DG149
	1042	DF266	1076	DG71	1110	DF280	1144	DH28
	1043	DF46	1077	DG76	1111	DF286	1145	DH303
	1044	DF65	1078	DG82	1112	DF316	1146	DH318
25	1045	DF69	1079	DH1086	1113	DF317	1147	DH322
	1046	DB145	1080	DH1098	1114	DF343	1148	DH340
	1047	DB150	1081	DH1135	1115	DF347	1149	DH371
	1048	DB159	1082	DH1145	1116	DF370	1150	DH40
	1049	DB174	1083	DH1153	1117	DF382	1151	DH401
30	1050	DB180	1084	DH1182	1118	DF396	1152	DH432
	1051	CY1	1085	DH1185	1119	DF428	1153	DH451
	1052	CY11	1086	DH1190	1120	DF453	1154	DH496
	1053	CY3	1087	DH1191	1121	DF457	1155	DH502
	1054	CY9	1088	DH1201	1122	DF460	1156	DH529

	1157	DH66	1191	DF915	1225	DH1357	1259	DI501
	1158	DF518	1192	DF948	1226	DH145	1260	DI504
	1159	DF521	1193	DF950	1227	DH999	1261	DK111
	1160	DF538	1194	DF956	1228	DI160	1262	DK113
5	1161	DF543	1195	DF966	1229	DI386	1263	DK120
	1162	DF545	1196	DF968	1230	DI391	1264	DK122
	1163	DF547	1197	DF971	1231	DI435	1265	DK126
	1164	DF568	1198	DF973	1232	DI448	1266	DK134
	1165	DF587	1199	DF979	1233	DI454	1267	DK136
10	1166	DF589	1200	DF984	1234	DJ109	1268	DK150
	1167	DF591	1201	DF989	1235	DJ146	1269	DK160
	1168	DF601	1202	DH1257	1236	DJ167	1270	DK170
	1169	DF606	1203	DH1308	1237	DF1065	1271	DK182
	1170	DF62	1204	DH1314	1238	DI387	1272	DK185
15	1171	DF620	1205	DI341	1239	DI393	1273	DK197
	1172	DF625	1206	DH1265	1240	DI403	1274	DK206
	1173	DF648	1207	DI349	1241	DI430	1275	DK219
	1174	DF657	1208	DI355	1242	DI438	1276	DK223
	1175	DF659	1209	DI362	1243	DJ2	1277	DK227
20	1176	DF661	1210	DI366	1244	DJ188	1278	DK229
	1177	DF662	1211	DI508	1245	DJ238	1279	DK230
	1178	DF670	1212	DI516	1246	DJ259	1280	DK243
	1179	DF674	1213	DI518	1247	DK64	1281	DK264
	1180	DF682	1214	DF1066	1248	DK70	1282	DK268
25	1181	DF688	1215	DF1069	1249	DK81	1283	DK31
	1182	DF810	1216	DG279	1250	DK84	1284	DK39
	1183	DF823	1217	DH1010	1251	DI462	1285	DK93
	1184	DF835	1218	DH1013	1252	DI466	1286	DL101
	1185	DF860	1219	DH1044	1253	DI474	1287	DL110
30	1186	DF877	1220	DH1045	1254	DI475	1288	DL116
	1187	DF883	1221	DH1073	1255	DI479	1289	DL132
	1188	DF895	1222	DH1078	1256	DI480	1290	DL63
	1189	DF909	1223	DH1340	1257	DI482	1291	DL82
	1190	DF910	1224	DH1349	1258	DI500	1292	DL95

	1293	DL99	1327	DL491	1361	DL547	1395	DO181
	1294	DJ332	1328	DL495	1362	DL550	1396	DO419
	1295	DJ362	1329	DL498	1363	DL551	1397	DO424
	1296	DK290	1330	DL504	1364	DL601	1398	DO440
5	1297	DK321	1331	DM118	1365	DL604	1399	DO447
	1298	DK324	1332	DM122	1366	DL605	1400	DO568
	1299	DK329	1333	DM126	1367	DL607	1401	DO575
	1300	DK357	1334	DM128	1368	DL608	1402	DO589
	1301	DK360	1335	DM130	1369	DL616	1403	DO610
10	1302	DL141	1336	DM147	1370	DL619	1404	DO715
	1303	DL146	1337	DM169	1371	DL620	1405	DO722
	1304	DL162	1338	DM26	1372	DL634	1406	DO737
	1305	DL163	1339	DM404	1373	DM194	1407	DO742
	1306	DL169	1340	DM406	1374	DM197	1408	DO755
15	1307	DL181	1341	DM407	1375	DM221	1409	DO765
	1308	DL185	1342	DM420	1376	DM248	1410	DO797
	1309	DL218	1343	DM425	1377	DM250	1411	DO836
	1310	DL220	1344	DM435	1378	DM262	1412	DO884
	1311	DL248	1345	DM445	1379	DM265	1413	DO896
20	1312	DL289	1346	DM449	1380	DM272	1414	CZ549
	1313	DL290	1347	DM459	1381	DM278	1415	CZ598
	1314	DL291	1348	DM462	1382	DM293	1416	DT431
	1315	DL316	1349	DM469	1383	DM303	1417	DT443
	1316	DL320	1350	DM482	1384	DM340	1418	DT446
25	1317	DL321	1351	DM6	1385	DM360	1419	DT449
	1318	DL425	1352	DM94	1386	DM365	1420	DT450
	1319	DL426	1353	DJ279	1387	DM522	1421	DT455
	1320	DL427	1354	DJ284	1388	DM533	1422	DT458
	1321	DL439	1355	DJ299	1389	DM542	1423	DN106
30	1322	DL440	1356	DJ319	1390	DM87	1424	DN153
	1323	DL444	1357	DJ323	1391	DN124	1425	DN176
	1324	DL457	1358	DL531	1392	DN144	1426	DT530
	1325	DL463	1359	DL535	1393	DN147	1427	DT534
	1326	DL466	1360	DL543	1394	DN167	1428	DT535

	1429	DT544	1463	DW1	1497	BK5
	1430	DT563	1464	DW389	1498	BK504
	1431	DT584	1465	DW398	1499	BK513
	1432	DT590	1466	DW654	1500	BK517
5	1433	DT596	1467	DW659		
	1434	DT597	1468	DW665		
	1435	DT598	1469	DW694		
	1436	DT640	1470	DW705		
	1437	DT655	1471	DW716		
10	1438	DT674	1472	DW749		
	1439	DT719	1473	DW761		
	1440	DT734	1474	DW765		
	1441	DT779	1475	DW771		
	1442	DT801	1476	DW78		
15	1443	DT802	1477	DW780		
	1444	DN696	1478	BK10		
	1445	DN697	1479	BK11		
	1446	DN704	1480	BK2		
	1447	DN710	1481	BK368		
20	1448	DN711	1482	BK373		
	1449	DN714	1483	BK374		
	1450	DN721	1484	BK375		
	1451	DN722	1485	BK384		
	1452	DN732	1486	BK402		
25	1453	DN740	1487	BK410		
	1454	DN746	1488	BK415		
	1455	DN747	1489	BK425		
	1456	DN753	1490	BK427		
	1457	DN756	1491	BK436		
30	1458	DN764	1492	BK445		
	1459	DN770	1493	BK455		
	1460	DN772	1494	BK458		
	1461	DN1120	1495	BK494		
	1462	DU372	1496	BK498		

The "Clone ID No." for a particular clone consists of one or two letters followed by a number. The letters designate the tissue source from which the sEST was isolated. Table 3 below lists the various sources which were run through applicants' signal sequence trap. Thus, the tissue source for a particular sEST sequence can be identified in Table 3 by the 5 one and two letter designations used in the relevant "Clone ID No.". For example, a clone designated as "BA312" would have been isolated from a human placenta (26 yrs.) library (i.e., selection "BA") as indicated in Table 3.

As used herein, "polynucleotide" includes single- and double-stranded RNAs, DNAs and RNA:DNA hybrids.

10 As used herein a "secreted" protein is one which, when expressed in a suitable host cell, is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins 15 which are transported across the membrane of the endoplasmic reticulum.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H.U. Saragovi, *et al.*, Bio/Technology 10, 773-778 (1992) and in R.S. 20 McDowell, *et al.*, J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites. For example, fragments of the protein may be fused through "linker" sequences to the Fc portion of an immunoglobulin. For a bivalent form of the protein, such a fusion 25 could be to the Fc portion of an IgG molecule. Other immunoglobulin isotypes may also be used to generate such fusions. For example, a protein - IgM fusion would generate a decavalent form of the protein of the invention.

The present invention also provides both full-length and mature forms of the disclosed proteins. The full-length form of the such proteins is identified in the sequence 30 listing by translation of the nucleotide sequence of each disclosed clone. The mature form of such protein may be obtained by expression of the disclosed full-length polynucleotide (preferably those deposited with ATCC) in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein may also be determinable from the amino acid sequence of the full-length form.

The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification
5 and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials.

Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention also provides for soluble forms of such protein. In such forms part or all of the intracellular and transmembrane domains of the protein are deleted such that
10 the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with known techniques for determination of such domains from sequence information.

Species homologs of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making
15 suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the
20 polynucleotides disclosed herein.

The invention also includes polynucleotides with sequences complementary to those of the polynucleotides disclosed herein.

The present invention also includes polynucleotides capable of hybridizing, preferably under reduced stringency conditions, more preferably under stringent conditions,
25 most preferably under highly stringent conditions, to polynucleotides described herein. Examples of stringency conditions are shown in Table I below: highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

Table 1

Stringency Condition	Polynucleotide Hybrid	Hybrid Length (bp) [‡]	Hybridization Temperature and Buffer [†]	Wash Temperature and Buffer [†]
5	A	DNA:DNA	≥ 50 65°C; 1xSSC -or- 42°C; 1xSSC, 50% formamide	65°C; 0.3xSSC
	B	DNA:DNA	< 50 T_B^* ; 1xSSC	T_B^* ; 1xSSC
	C	DNA:RNA	≥ 50 67°C; 1xSSC -or- 45°C; 1xSSC, 50% formamide	67°C; 0.3xSSC
	D	DNA:RNA	< 50 T_D^* ; 1xSSC	T_D^* ; 1xSSC
10	E	RNA:RNA	≥ 50 70°C; 1xSSC -or- 50°C; 1xSSC, 50% formamide	70°C; 0.3xSSC
	F	RNA:RNA	< 50 T_F^* ; 1xSSC	T_F^* ; 1xSSC
	G	DNA:DNA	≥ 50 65°C; 4xSSC -or- 42°C; 4xSSC, 50% formamide	65°C; 1xSSC
	H	DNA:DNA	< 50 T_H^* ; 4xSSC	T_H^* ; 4xSSC
15	I	DNA:RNA	≥ 50 67°C; 4xSSC -or- 45°C; 4xSSC, 50% formamide	67°C; 1xSSC
	J	DNA:RNA	< 50 T_J^* ; 4xSSC	T_J^* ; 4xSSC
	K	RNA:RNA	≥ 50 70°C; 4xSSC -or- 50°C; 4xSSC, 50% formamide	67°C; 1xSSC
	L	RNA:RNA	< 50 T_L^* ; 2xSSC	T_L^* ; 2xSSC
20	M	DNA:DNA	≥ 50 50°C; 4xSSC -or- 40°C; 6xSSC, 50% formamide	50°C; 2xSSC
	N	DNA:DNA	< 50 T_N^* ; 6xSSC	T_N^* ; 6xSSC
	O	DNA:RNA	≥ 50 55°C; 4xSSC -or- 42°C; 6xSSC, 50% formamide	55°C; 2xSSC
	P	DNA:RNA	< 50 T_P^* ; 6xSSC	T_P^* ; 6xSSC
	Q	RNA:RNA	≥ 50 60°C; 4xSSC -or- 45°C; 6xSSC, 50% formamide	60°C; 2xSSC
	R	RNA:RNA	< 50 T_R^* ; 4xSSC	T_R^* ; 4xSSC

5 ¹: The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

10 ¹: SSPE (1xSSPE is 0.15M NaCl, 10mM NaH₂PO₄, and 1.25mM EDTA, pH 7.4) can be substituted for SSC (1xSSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

15 ² $T_B - T_R$: The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (T_m) of the hybrid, where T_m is determined according to the following equations. For hybrids less than 18 base pairs in length, $T_m(^{\circ}C) = 2(\# \text{ of A + T bases}) + 4(\# \text{ of G + C bases})$. For hybrids between 18 and 49 base pairs in length, $T_m(^{\circ}C) = 81.5 + 16.6(\log [Na^+]) + 0.41(\%G+C) - (600/N)$, where N is the number of bases in the hybrid, and [Na⁺] is the concentration of sodium ions in the hybridization buffer ([Na⁺] for 1xSSC = 0.165 M).

20 Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and *Current Protocols in Molecular Biology*, 1995, F.M. Ausubel et al., eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

25 Preferably, such hybridizing polynucleotides have at least 70% sequence identity (more preferably, at least 80% identity; most preferably at least 90% or 95% identity) with the polynucleotide of the present invention to which they hybridize, where sequence identity is determined by comparing the sequences of the hybridizing polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps. The isolated polynucleotide encoding the protein of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman *et al.*, Nucleic Acids Res. 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, Methods in Enzymology 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control

sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

A number of types of cells may act as suitable host cells for expression of the 5 protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from in vitro culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells.

10 Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any 15 bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

20 The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, California, U.S.A. (the MaxBac® kit), and such methods are well known in the art, 25 as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting 30 expressed protein may then be purified from such culture (i.e., from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl® or Cibacrom blue 3GA

Sepharose®; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX). Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, MA), Pharmacia (Piscataway, NJ) and InVitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("Flag") is commercially available from Kodak (New Haven, CT).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The protein may also be produced by known conventional chemical synthesis. Methods for constructing the proteins of the present invention by synthetic means are known to those skilled in the art. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modifications are naturally provided or deliberately engineered. For example, modifications in the peptide or DNA sequences can be made by those skilled in the art using known techniques. Modifications

of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, 5 replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Patent No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and may thus be useful for screening 10 or other immunological methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are believed to be encompassed by the present invention.

USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention 5 may be provided by administration or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA).

Research Uses and Utilities

10 The polynucleotides provided by the present invention can be used by the research community for various purposes. The primary use of polynucleotides of the invention which are sESTs is as probes for the identification and isolation of full-length cDNAs and genomic DNA molecules which correspond (i.e., is a longer polynucleotide sequence of which substantially the entire sEST is a fragment in the case of a full-length cDNA, or 15 which encodes the sEST in the case of a genomic DNA molecule) to such sESTs. Techniques for use of such sequences as probes for larger cDNAs or genomic molecules are well known in the art.

15 The polynucleotides can also be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding 20 protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related 25 DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti- 30 DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify

polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

- The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.
- Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.
- Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

Nutritional Uses

- Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

Cytokine and Cell Proliferation/Differentiation Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, I23, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

10 The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for T-cell or thymocyte proliferation include without limitation those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., *J. Immunol.* 137:3494-3500, 1986; Bertagnolli et al., *J. Immunol.* 145:1706-1712, 1990; Bertagnolli et al., *Cellular Immunology* 133:327-341, 1991; Bertagnolli, et al., *J. Immunol.* 149:3778-3783, 1992; Bowman et al., *J. Immunol.* 152: 1756-1761, 1994.

20 Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A.M. and Shevach, E.M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human Interferon γ , Schreiber, R.D. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L.S. and Lipsky, P.E. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; DeVries et al., *J. Exp. Med.* 173:1205-1211, 1991; Moreau et al., *Nature* 336:690-692, 1988; Greenberger et al., *Proc. Natl. Acad. Sci. U.S.A.* 80:2931-2938, 1983; Measurement of mouse and human interleukin 6 - Nordan, R. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley

- and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11 - Bennett, F., Giannotti, J., Clark, S.C. and Turner, K. J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9 -
- 5 Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.
- Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in:
- 10 Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun.
- 15 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

Immune Stimulating or Suppressing Activity

A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases causes by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, *Leishmania* spp., malaria spp. and various fungal infections such as candidiasis. Of course, 30 in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre

syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other 5 conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune 10 response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from 15 immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing 20 high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys 25 the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (e.g., B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the 30 molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this manner prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-

blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as described in Lenschow *et al.*, Science 257:789-792 (1992) and Turka *et al.*, Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosus in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral

infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

- Alternatively, anti-viral immune responses may be enhanced in an infected patient
- 5 by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the *in vitro* activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding
- 10 a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells *in vivo*.

- In another application, up regulation or enhancement of antigen function (preferably
- 15 B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (*e.g.*, sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor
- 20 cells obtained from a patient can be transfected *ex vivo* with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection
- 25 *in vivo*.

- The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or
- 30 which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I α chain protein and β_2 microglobulin protein or an MHC class II α chain protein and an MHC class II β chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I

or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected 5 with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured 10 by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1- 15 3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa 20 et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Bowman et al., J. Virology 61:1992-1998; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnoli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching 25 (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: *In vitro* antibody production, Mond, J.J. and Brunswick, M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, 30 proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-

3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

25 Hematopoiesis Regulating Activity

A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for

example, in conjunction with chemotherapy to prevent or treat consequent myelosuppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

15 Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. *Cellular Biology* 15:141-151, 1995; Keller et al.,

20 *Molecular and Cellular Biology* 13:473-486, 1993; McClanahan et al., *Blood* 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M.G. In *Culture of Hematopoietic*

25 *Cells*. R.I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., *Proc. Natl. Acad. Sci. USA* 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I.K. and Briddell, R.A.

In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., *Experimental Hematology* 22:353-359, 1994;

30 Cobblestone area forming cell assay, Ploemacher, R.E. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, NY. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland,

H.J. In *Culture of Hematopoietic Cells*. R.I. Freshney, *et al.* eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

Tissue Growth Activity

5 A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in 10 circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. *De novo* bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma 15 induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract 20 bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the 25 protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein 30 may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. *De novo* tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic

plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or 5 progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural 10 cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized 15 neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from 20 chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

25 It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of 30 fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured
5 by the following methods:

Assays for tissue generation activity include, without limitation, those described in:
International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International
Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No.
WO91/07491 (skin, endothelium).

10 Assays for wound healing activity include, without limitation, those described in:
Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year
Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest.
Dermatol 71:382-84 (1978).

15 Activin/Inhibin Activity

A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention,
20 alone or in heterodimers with a member of the inhibin α family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin- β group, may
25 be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

30 The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in:
Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale

et al., *Nature* 321:776-779, 1986; Mason et al., *Nature* 318:659-663, 1985; Forage et al., *Proc. Natl. Acad. Sci. USA* 83:3091-3095, 1986.

Chemotactic/Chemokinetic Activity

5 A protein of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide
10 particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

15 A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

20 The activity of a protein of the invention may, among other means, be measured by the following methods:

25 Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. *J. Clin. Invest.* 95:1370-1376, 1995; Lind et al. *APMIS* 103:140-146, 1995; Muller et al *Eur. J. Immunol.* 25: 1744-1748; Gruber et al. *J. of Immunol.* 152:5860-5867, 1994; Johnston et al. *J. of Immunol.* 153: 1762-1768, 1994.

Hemostatic and Thrombolytic Activity

A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A 5 protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

10 Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

15 Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors 20 involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. 25 A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those 30 described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med.

169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

Anti-Inflammatory Activity

5 Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or
10 suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality,
15 arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

20 Tumor Inhibition Activity

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor
25 precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

30

Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting

(suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the
5 fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent
10 behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for
15 example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

ADMINISTRATION AND DOSING

A protein of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources) may be used in a pharmaceutical composition when combined with a pharmaceutically acceptable carrier. Such a 5 composition may also contain (in addition to protein and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the 10 invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or compliment its activity or 15 use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein of the invention, or to minimize side effects. Conversely, protein of the present invention may be included in formulations of the particular cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects 20 of the cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent.

A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric 25 or complexed form.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T 30 lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that

can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

5 The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides,

10 diglycerides, sulfatides, lysolecithin, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent No. 4,235,871; U.S. Patent No. 4,501,728; U.S. Patent No. 4,837,028; and U.S. Patent No. 4,737,323, all of which are incorporated herein by reference.

15 As used herein, the term "therapeutically effective amount" means the total amount of each active component of the pharmaceutical composition or method that is sufficient to show a meaningful patient benefit, i.e., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, 20 administered alone, the term refers to that ingredient alone. When applied to a combination, the term refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

25 In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein of the present invention is administered to a mammal having a condition to be treated. Protein of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein of the present invention may be administered either 30 simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

Administration of protein of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

When a therapeutically effective amount of protein of the present invention is administered orally, protein of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein of the present invention, and preferably from about 25 to 90% protein of the present invention.

When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein of the present invention, and preferably from about 1 to 50% protein of the present invention.

When a therapeutically effective amount of protein of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art.

The amount of protein of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein of the present invention with

which to treat each individual patient. Initially, the attending physician will administer low doses of protein of the present invention and observe the patient's response. Larger doses of protein of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is
5 contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 μ g to about 100 mg (preferably about 0.1ng to about 10 mg, more preferably about 0.1 μ g to about 1 mg) of protein of the present invention per kg body weight.

The duration of intravenous therapy using the pharmaceutical composition of the
10 present invention will vary, depending on the severity of the disease being treated and the condition and potential idiosyncratic response of each individual patient. It is contemplated that the duration of each application of the protein of the present invention will be in the range of 12 to 24 hours of continuous intravenous administration. Ultimately the attending physician will decide on the appropriate duration of intravenous therapy using the
15 pharmaceutical composition of the present invention.

Protein of the invention may also be used to immunize animals to obtain polyclonal and monoclonal antibodies which specifically react with the protein. Such antibodies may be obtained using either the entire protein or fragments thereof as an immunogen. The peptide immunogens additionally may contain a cysteine residue at the carboxyl terminus,
20 and are conjugated to a hapten such as keyhole limpet hemocyanin (KLH). Methods for synthesizing such peptides are known in the art, for example, as in R.P. Merrifield, J. Amer.Chem. Soc. 85, 2149-2154 (1963); J.L. Krstenansky, *et al.*, FEBS Lett. 211, 10 (1987). Monoclonal antibodies binding to the protein of the invention may be useful diagnostic agents for the immunodetection of the protein. Neutralizing monoclonal
25 antibodies binding to the protein may also be useful therapeutics for both conditions associated with the protein and also in the treatment of some forms of cancer where abnormal expression of the protein is involved. In the case of cancerous cells or leukemic cells, neutralizing monoclonal antibodies against the protein may be useful in detecting and preventing the metastatic spread of the cancerous cells, which may be mediated by the
30 protein.

For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a

pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein of the invention which may also 5 optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and 10 cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices 15 for the compositions may be biodegradable and chemically defined calcium sulfate, tricalciumphosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such 20 as sintered hydroxapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalciumphosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability.

25 Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

30 A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate,

poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt%, preferably 1-10 wt% based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of 5 the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells.

In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in 10 question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired 15 patients for such treatment with proteins of the present invention.

The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, e.g., amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type 20 of damaged tissue (e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress 25 can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other 30 known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA).

Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

Patent and literature references cited herein are incorporated by reference as if fully set forth.

Table 3

Sel.	Species	Tissue	Cell Type
AA	Human	Kidney	19-23wks., M/F pool of 5
AB	Human	Fetal Lung	Fetal Lung
AC	Human	Placenta	26yrs., 1 specimen
AD	Murine	Embryo	Fetal ES cells
AE	Murine	Spleen	Adult spleen
AF	Murine	Fetal Brain	Fetal Brain
AG	Murine	Fetal Brain	Fetal Brain
AH	Murine	Fetal Thymus	Fetal Thymus
AI	Human	Blood	Adult PBMC/TH1or2
AJ	Human	Testes	10-61yrs., pool of 11
AK	Human	Kidney	19-23wks., M/F pool of 5
AL	Human	Neural	Adult Glioblastoma line TG-1
AM	Human	Kidney	19-23wks., M/F pool of 5
AN	Murine	Bone Marrow	Adult Stromal cell line FCM-4
AO	Murine	Thymus	Adult Subtr. Adult Thymus
AP	Human	Placenta	26yrs., 1 specimen
AQ	Human	Ovary	PA-1 Teratocarcinoma
AR	Human	Retina	16-75yrs., pool of 76
AS	Human	Brain	19-23wks., M/F pool of 5
AT	Human	Blood	Adult lymphocytes+dend. cells
AU	Human	Testes	10-61yrs., pool of 11
AV	Murine	Spleen	Adult spleen
AW	Human	Ovary	PA-1 Teratocarcinoma
AX	Human	Testes	10-61yrs., pool of 11
AY	Human	Retina	16-75yrs., pool of 76
AZ	Human	Colon	Caco-2 Adenocarcinoma
B	Human	Blood	Peripheral Blood Mononuclear Cell
BA	Human	Placenta	26yrs., 1 specimen
BB	Human	Blood	Adult PBMC/TH1or2
BC	Murine	Embryo	Fetal ES cells
BD	Human	Kidney	19-23wks., M/F pool of 5
BE	Human	Blood	Adult PBMC/TH1or2
BF	Human	Brain	19-23wks., M/F pool of 5
BG	Human	Brain	N/A
BH	Human	Ovary	PA-1 Teratocarcinoma
BI	Human	Kidney	19-23wks., M/F pool of 5
BJ	Human	Ovary	PA-1 Teratocarcinoma
BK	Human	Retina	16-75yrs., pool of 76
BL	Human	Testes	10-61yrs., pool of 11
BM	Human	Muscle	N/A
BN	Human	Placenta	26yrs., 1 specimen
BO	Human	Retina	16-75yrs., pool of 76
BP	Human	Kidney	19-23wks., M/F pool of 5
BQ	Human	Colon	Caco-2 Adenocarcinoma Caco2

BR	Human	Kidney	19-23wks., M/F pool of 5
BS	Human	Pituitary	Adult Pituitary
BT	Human	Blood	Adult PBMC
BU	Human	Placenta	26yrs., 1 specimen
BV	Human	Brain	N/A
BW	Human	Blood	Adult PBMC
BX	Human	Ovary	PA-1 Teratocarcinoma
BY	Human	Blood	Adult PBMC/TH1or2
BZ	Human	Kidney	19-23wks., M/F pool of 5
C	Human	Blood	Peripheral Blood Mononuclear Cell
CA	Murine	Embryo	Fetal ES cell embryoid bodies
CB	Human	Brain	19-23wks., M/F pool of 5
CC	Human	Brain	N/A
CD	Human	Brain	19-23wks., M/F pool of 5
CE	Human	Blood	Adult lymphocytes+dend. cells
CF	Human	Placenta	26yrs., 1 specimen
CG	Human	Testes	10-61yrs., pool of 11
CH	Human	Kidney	19-23wks., M/F pool of 5
CI	Human	Brain	N/A
CJ	Human	Brain	19-23wks., M/F pool of 5
CK	Human	Testes	10-61yrs., pool of 11
CL	Human	Retina	16-75yrs., pool of 76
CM	Human	Adult Lung	Adult Lung
CN	Human	Brain	19-23wks., M/F pool of 5
CO	Human	Brain	N/A
CP	Human	Salivary Gland	N/A
CQ	Human	Heart	13-73yrs., pool of 3
CR	Human	Testes	10-61yrs., pool of 11
CS	Human	Brain	19-23wks., M/F pool of 5
CT	Human	Brain	N/A
CU	Human	Pineal Gland	N/A
CV	Human	Mammary	Adult Human Mammary
CW	Human	Brain	19-23wks., M/F pool of 5
CY	Human	Pineal Gland	N/A
CZ	Human	Testes	10-61yrs., pool of 11
D	Human	Blood	Peripheral Blood Mononuclear Cell
DA	Human	Placenta	26yrs., 1 specimen
DB	Human	Prostate	Adult Prostate
DC	Human	Pineal Gland	Adult Pineal Gland
DD	Human	Testes	10-61yrs., pool of 11
DE	Human	Testes	Adult NCCIT TeratoCA
DF	Human	Brain	N/A
DG	Human	Placenta	26yrs., 1 specimen
DH	Human	Brain	19-23wks., M/F pool of 5
DI	Human	Testes	10-61yrs., pool of 11
DJ	Human	Placenta	26yrs., 1 specimen
DK	Human	Fetal Kidney2	Fetal Kidney

DL	Human	Brain	N/A
DM	Human	Brain	N/A
DN	Human	Brain	19-23wks., M/F pool of 5
DO	Human	Testes	10-61yrs., pool of 11
DP	Murine	Embryo	Fetal ES cell embryoid bodies
DQ	Human	Placenta	26yrs., 1 specimen
DR	Human	SalivaryGland	N/A
DT	Human	Brain	N/A
DU	Human	Brain	19-23wks., M/F pool of 5
DV	Human	Pineal Gland	Adult Pineal Gland
DW	Human	Brain	N/A
DX	Human	Testes	10-61yrs., pool of 11
DY	Human	Brain	N/A
DZ	Human	Testes	Adult NCCIT TeratoCA
E	Human	Blood	PeripheralBloodMononuclearCell
EA	Human	Brain	19-23wks., M/F pool of 5
EB	Human	Melanoma	Adult Melanoma
EC	Human	Brain	N/A
ED	Human	Placenta	26yrs., 1 specimen
EE	Human	Testes	10-61yrs., pool of 11
EF	Human	Liver	Adult Liver
EG	Human	Pancreas	Adult HPC-3 Ductal AdenoCA
EH	Human	Blood	PeripheralBloodMononuclearCell
EI	Human	Brain	19-23wks., M/F pool of 5
EJ	Human	Placenta	26yrs., 1 specimen
EK	Human	Brain	19-23wks., M/F pool of 5
EL	Human	Testes	10-61yrs., pool of 11
EM	Human	Fetal Kidney2	Fetal Kidney
EN	Human	Brain	19-23wks., M/F pool of 5
EO	Human	Adrenal Gland	Adult Adrenal Gland
EP	Human	Placenta	26yrs., 1 specimen
EQ	Human	Testes	10-61yrs., pool of 11
ER	Human	Brain	19-23wks., M/F pool of 5
ES	Human	Placenta	26yrs., 1 specimen
ET	Human	Testes	10-61yrs., pool of 11
EU	Human	Kidney	Adult Kidney
EV	Human	Stomach	Adult Stomach
EW	Human	Placenta	26yrs., 1 specimen
EX	Human	Testes	10-61yrs., pool of 11
EY	Human	Brain	19-23wks., M/F pool of 5
EZ	Human	Fetal Kidney2	Fetal Kidney
FA	Human	Brain	19-23wks., M/F pool of 5
FB	Human	Placenta	26yrs., 1 specimen
FC	Human	Testes	10-61yrs., pool of 11
FD	Human	SalivaryGland	N/A
FE	Human	Brain	N/A
FF	Human	Testes	Adult NCCIT TeratoCA

FG	Human	Brain	N/A
FH	Human	Brain	19-23wks., M/F pool of 5
FI	Human	Small Intest	Adult Small Intestine
FJ	Human	Lung CA	Adult Lung CA
FK	Human	Kidney	Adult Kidney
FM	Human	Brain	N/A
FN	Human	Brain	19-23wks., M/F pool of 5
FO	Human	Brain	N/A
FP	Human	Placenta	26yrs., 1 specimen
FQ	Human	Testes	10-61yrs., pool of 11
FR	Human	Placenta	26yrs., 1 specimen
FS	Human	Testes	10-61yrs., pool of 11
FT	Chicken	Fetal Lung	Fetal Lung
FU	Chicken	Limb Bud	Fetal St. 23 Limb Bud
FV	Human	Testes	Adult NCCIT TeratoCA
FW	Human	Testes	Adult NCCIT TeratoCA
FX	Human	Brain	19-23wks., M/F pool of 5
FY	Human	Placenta	26yrs., 1 specimen
FZ	Human	Placenta	26yrs., 1 specimen
G	Human	Blood	PeripheralBloodMononuclearCell
GA	Human	Testes	10-61yrs., pool of 11
GB	Human	Placenta	26yrs., 1 specimen
GC	Human	Testes	10-61yrs., pool of 11
GD	Human	Placenta	26yrs., 1 specimen
GE	Human	Brain	N/A
GF	Human	Brain	19-23wks., M/F pool of 5
GG	Human	Fetal Kidney2	Fetal Kidney
GH	Human	Placenta	26yrs., 1 specimen
GI	Human	Retinoblastoma	Adult Retinoblastoma Y79
GJ	Murine	Spleen	Adult Spleen
GK	Human	Fetal Kidney2	Fetal Kidney
GL	Murine	Lymph Node	Adult Lymph Node
GM	Human	Uterus	N/A
GN	Human	Blood	PeripheralBloodMononuclearCell
GO	Human	Adrenal Gland	Adult Adrenal Gland
GP	Human	Ovary	PA-1 Teratocarcinoma
GQ	Human	Pineal Gland	N/A
GR	Human	Pancreas	Adult HPC-3 Ductal AdenoCA
GS	Human	Retina	16-75yrs., pool of 76
GT	Human	Brain	N/A
GU	Human	Fetal Kidney2	Fetal Kidney
GV	Rat	Retina	Newborn Retina
GW	Chicken	Limb Bud	Fetal St.26 Limb Bud
GX	Human	Brain	N/A
GY	Human	Testes	10-61yrs., pool of 11
GZ	Human	Brain	19-23wks., M/F pool of 5
H	Human	Blood	PeripheralBloodMononuclearCell

HA	Human	Testes	Adult NCCIT TeratoCA
HB	Human	Fetal Kidney2	Fetal Kidney
HC	Human	Brain	19-23wks., M/F pool of 5
HD	Human	Brain	N/A
HE	Human	Testes	10-61yrs., pool of 11
HF	Human	Brain	19-23wks., M/F pool of 5
HG	Human	Fetal Kidney2	Fetal Kidney
HH	Human	Brain	N/A
HI	Human	Testes	10-61yrs., pool of 11
HJ	Human	Brain	N/A
HK	Human	Brain	19-23wks., M/F pool of 5
HL	Human	Fetal Kidney2	Fetal Kidney
HM	Human	Testes	Adult NCCIT TeratoCA
HN	Human	Fetal Kidney2	Fetal Kidney
HO	Human	Brain	N/A
HP	Human	Brain	19-23wks., M/F pool of 5
HQ	Human	Testes	10-61yrs., pool of 11
HR	Human	Brain	N/A
HS	Human	Brain	N/A
HT	Human	Brain	19-23wks., M/F pool of 5
HU	Human	Fetal Kidney2	Fetal Kidney
HV	Human	Testes	10-61yrs., pool of 11
HW	Human	Brain	N/A
HX	Human	Brain Hippoca	Adult Brain Hippocampus
HY	Human	Trachea	Adult Trachea
HZ	Human	Brain Thalamus	Adult Brain Thalamus
I	Human	Blood	PeripheralBloodMononuclearCell
IA	Human	Thyroid	Adult Thyroid
IB	Human	Embryonal CA	Fetal NT2-D1
IC	Human	WER1-Rb1 line	Adult Retinoblastoma
ID	Human	Muscle	N/A
IE	Human	Brain	19-23wks., M/F pool of 5
IF	Human	Uterus	N/A
IG	Human	Testes	10-61yrs., pool of 11
IH	Human	Muscle	N/A
II	Human	Brain	N/A
IJ	Human	Blood	PeripheralBloodMononuclearCell
IK	Human	Retinoblastoma	Adult Retinoblastoma Y79
IL	Human	Retina	16-75yrs., pool of 76
IM	Human	Various	Various
IN	Human	Prostate	Adult Prostate
IO	Human	Brain	19-23wks., M/F pool of 5
IP	Human	Fetal Kidney2	Fetal Kidney
IQ	Human	Prostate	Adult Prostate
IR	Human	Brain Hippoca	Adult Brain Hippocampus
IS	Human	Trachea	Adult Trachea
IT	Human	Brain Thalamu	Adult Brain Thalamus

SEQUENCE LISTING

(1) GENERAL INFORMATION:

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LaVallie, Edward
Racie, Lisa
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Treacy, Maurice
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- (iii) NUMBER OF SEQUENCES: 1500
- (iv) CORRESPONDENCE ADDRESS
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 - (E) COUNTRY: U.S.A
 - (F) ZIP: 02140
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy Disk
 - (B) COMPUTER: IBM PC Compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) ATTORNEY/AGENT INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 320 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCCGCC	TTCATGGCCT	AAGTGTAA	ATTATAAGCT	GGTGAAGTGA	AATAACACAA	60
ATCAAGCTCA	CCAATTTAA	TACTCAGCTG	TTGATAAAACA	ACACTGAAGA	GTGACATTAA	120
AATTGAAATT	ATCTTCTTG	AAGTAGCATT	GCAGCACTTT	TGAATGACTT	CCAAAAGGCT	180
GATCATAAAA	ATCACATTCAA	TCATTTCAA	ATTTTACTTT	AGCAGCAATG	AAGTTATTTG	240

GTATGACTCA GATGAACCTT CTGCTCTGTC TTGGAGTTAT TATGGTCATT TCATTTCTG	300
CAACCTGGGA AACACCGAG	329

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 357 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAATTCCGCC TTCATGGCCT ACGAGTGGAT CTGGTTGAGA GGAAAGCAGC TAAAAATACA	60
GGAGATGAAA GGGATCATAA CGAACATAAT GAACCATGTT CATTATGGTT CGTGGGGAGG	120
CAGGAAAGCA CAGTATCCAG GGCATAGGCA GAAGAGCTGT CTTTCACGGG AGGAGGGGAA	180
CATATTCTAC TGCATAATAGC AAGGGCGGG TAAGTACCGA TCGGGTACTT TGGGAACTAT	240
GACGGTAGGG AGTTCAGGAA GTTGCTGCCT GAAGGCATAA AGGTTTTTTT TTTTTTTTTT	300
TTTTTTTGCC AATTGGTCCA GTACCCCTCCT TCTGTGGCCC CCATCTCCAG TCTCGAG	357

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 249 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAATTCTTTA TATAATTGGG ATACCTACTC ATTGTCAGTT GTATGCTTTG CAAATATCTT	60
TCCTGACCCCT TACTTACCTT TTCACTCTTA ATGGTATCTT TGATGAATCA AAAATTTTC	120
TTTTTTGTT GTTTTTGAG ACAGAGTCTT AACTCTGTCA CCCAGGCTGG AGTGCAGTGC	180
ATGAACATGG CTCACTGCAG CCTCAACTTC TTGGACTCAA GCAATCCTCC TGCCTCAGAA	240
CCTCTCGAG	249

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 262 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAATTCCGCC TTCACTGGCCT AGACCTGCCT CTAGCTCCTT TCCCTCTACT CTCCTGCTCA	60
GACCATTAGT AGGTACTTTG TAAATAAAA AACTAGATTA ACATCAATAT TACTCCAATT	120
TGGTATCTT TACACTATGT ATTATACCTA CTTTCTTTT ATTTCATTTA CAAATAGTT	180
AAATTACTTT ATCAACCAGC TGTATTGTTT CCCTCTGTAA AAAGTACCAT CAAGTGGGA	240
AAATGTATGT GGCAGTCTCG AG	262

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 250 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCTGGCC	TTCATGGCCT	AATAACTTAC	CCAGTCACGA	ATATTTCTTC	ATAGCAGCAT	60
CAGAGTGGAC	TAATACGATT	ATAATTATCA	TCACCTTTTG	ACTGACCAAT	TGATTACAG	120
TATTGAGTTTC	AATCTGTTTT	TTTAAAAAAAT	ATCTTCTAAA	TATCAGGTGC	TGTATTAGAT	180
GTGGGGTACA	AAAATGTATT	TTCATTACT	CACTAATTAA	CTTAAAATTT	ATTTATTGAG	240
GTACCTCGAG						250

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 276 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAATTCTGGCC	TTCATGGCCT	AGGTGCTGGA	AGTAAGCTGT	GTGAACAAAT	GAGACGATTC	60
CCCTTTCTAA	TGAGTTTATA	TGCAATGTGG	TATCTTACCC	GATACATGCT	CTGTCAGAAA	120
GAAGCAGCCC	ACTTCTGTCC	AATAGCCAAT	CCGGCTTCAG	GAGCAGCAGG	AGAGGCTTCG	180
GGAACGGGAG	AAGAGGCTTC	AGCACGCTGC	CGAGCCACAG	AGCGACTTGG	AGGAGCTGCA	240
CGAGAACAAAG	AGCGCACTGC	AGTTGGAGAG	CTCGAG			276

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 284 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAATTCTGGCC	TTCATGGCCT	ACTCATTCCA	AAATAAAAAA	AAAATTTCC	CATGATCTTA	60
TCTAGCTTCT	CTAGCACTAC	TTGTATGATT	TCACCTTTCT	TTCTTTATTTC	TTTCTTCCA	120
TATTTTTTTT	TTTGAGACA	GGGTCTCACT	CTATTGTCCA	GGCTAGAGTG	CAGTAGTTTG	180
ATCATGACTC	ACTCTAACCT	GGACCTCCGG	GGCCTAAGTA	ATCTTCCCAC	CTCAGCCTCT	240
CAAGTAGCTG	GGACTACAGG	GATGTACCAC	CATGCCTGGC	TAAG		284

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 394 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTTGAATTCT AGACCTGCCT CGAGGACGCC	AGGGAAAGTGA GTTGAAAATC	TGAAAATGCG	60
GCCATGGACT GGTTCTGGC	GTTGGATTAT GCTCATTCTT	TTTGCCTGGG	120
GTTTTATATA GGTGGTCACT	TGGTACGAGA TAATGACCAT	CCTGATCACT	180
ACTGTCCAAG ATTCTGCCAA	AGCTTGAACG CTTAAAACAG	CAGAATGAAG	240
AATGGCCGAA TCTCTCCGGA	TACCAAGG CCCTATTGAT	CAGGGGCCAG	300
AGTGCAGCGTT TTAGAAGAGC	AGCTTGTAA GCCCAAAGAA	CTATAGGAAG	360
ACAGACCAGA AATGGTCTGG	GGAGGATCT CGAG		394

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCTGTGATGA AAATGCTTCA	TGCTTCAACA CTGTTGGAGG	ACACAACTGT	60
CGGGCTATAC AGGGAAATGGA	ACGACATGCA AAGCATTTC	CAAAGATGGC	120
GAGGAGCTG TATTGCCGCT	AATGTGTGTG CCTGCCACCA	AGGCTTCACT	180
GTGAAACCGA CATTGATGAA	TGCTCTGATG GTTTGTTCA	ATGTGACAGT	240
GCATTAACCT GCCTGGATGG	TACCACTGTG AGTGCAGAGA	TGGCTACCAT	300
TGTTTCACC AAGTGGAGAA	TCGTGTGAAG ATATTGATGA	GTGTGGGACC	357

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GAATTCCGGCC TTCATGGCCT	ATTTCGATC TATGTATCTG	TACTCATACA	60
GCTAAACAGC CTTCTTTCA	GAACAGTAGA TCACTCACT	GGGTTTCAA	120
ACCTTTCAAG GCTGGCTTCA	TAGGTCTTGC CTCACTGTAT	GTGACTGTTT	180
CTATCCCAGT CAGGACTGCA	CACCTCATAT TGAAAGACAT	CCAGCAATCC	240
AAACCTTACA AATATCCAC	CCTGACTCC CGTTCTCGAG	AAACTTTACC	280

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAATTCTAGA CCTGCCTCGA GCGCCACACA	GTGACTGCCG GGTAAAGTTG	TGGAATTACG	60
TCCCTGGACT CACCCCCCTGC	CTTCCTCGCC GAGTCCTGGC	CATAAAGGGC CGGCCACCA	120
CCCTGCCCTG ACCCTCCCCA	ACTCTCCCTG TCTCCTCTT	CATTCTTCCC CTCTTCCCT	180
TTCCCTCTCT	TTCCCCACTT CGATATGAGC	TGCTTCTTAA CGGTATGAGA	240
CCTCTTCTT	CCTTCCCTT CCGTCCCTGC	CTGGCCTAGA GAGGTGCCCT	300
CCTGCACCCA CCGTCTTTT	CCAAGCATGA ACAGTGGGAC	AGGCCCCAGG AGATGGGTGC	360
CAGGGAGCAG AAGGGGGAGC	CTTCAGGCCT GGACAAAAGC	AAACACCCCC CCAAAAAAAG	420
NAAACCCACG ACTCGAG			437

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTTTCTTCTA AGTAGATCTT CCTTCCCCAT	TAAACTAGGT TTTCTACTGC	AAGATATTT	60
GTGCATTGCT GTTTTAAACC	CTTTAACAG CGAACATAG	CAGTCTAAGA AGTCTTCTGA	120
ACCATCCTGG	ACTCTGGTG TGATTTAAA	TTGTGTCTAC AAGTTCTCTG	180
CACCAAGAGG	TAGAGTCTGT TTCCCTCTCC	TTGAACCTA GGTAGGCCTT	240
TTGATGAATA	CAATGAGACT CGAG	TGTTACTGCC	264

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GATTTTTTAC CCAAAGCTCT GGAATTGTAC ATTTATTTT	TAAAACCTAA AGAGGGAAAG		60
AGCCTTGTAT CATATGTGAA CATTGTATCA TAGGTAATGT	TGTACAGACC CTTTTATACA		120
GTGATCTGTC TTGTTCTGC AGCAAAAATC	CTCTATGGAC ATAGGAGGTG	CTGTGTCCCA	180
TGCCCTCTTG CCCTGACAGT	GTCCCATGGG CCCCTCTG	CTCCCTGCC	240
ACTGCTGATG CACTCCCCCC	CCTCGAG	CCTCCCTGCT	267

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GAATTCTGGCC	TTCATGGCCT	ATTTTTTATT	TGTTTTGTTT	TGTTTTGTGG	GGATGGGGTT	60
TTGCCGTGTT	GCCCAGGCTG	TTTCGAATT	TTGGGCTTA	TGCAATCCAC	CCACCTTGGC	120
CTCCCAAAGT	GCAGGGATTA	CAGGCATGAG	CCATCTTGCT	GGGCCACCTT	TTTCTTCTCT	180
TTTAACAAT	TCAGCAATT	TTCACTCCA	AAATCTGTA	AATACATTT	TTGTGGAAAA	240
ATACAATGGG	AATGGCATCA	AAAGATGGTT	TCTATTAGGA	ATGGGAACAG	GTAACAGTTT	300
TCCCTGCCAC	CTCAACAAATC	TCGAG				325

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGGCTGGCAG	GCGGGCCAAA	GGTAATGAAG	CAAAGAGAGA	GGGAAAAGAC	GTGTGAAAAT	60
TGCAAGGGGG	GTGACCGAGG	GAAACACGTG	AGCGTGTATAA	TGACAGAAAAA	ACCACGGAAAG	120
GACCAAACCT	GGGCAGGGGG	TGGGAAACCC	GGGCGTTTC	CAGGGAGCAC	AGGCAGACTC	180
AGAGGTAACA	CTCAAAAGCA	ACAACAGAAG	CAAGGAGGAA	GTGGGAAAAT	ATTTTTAATG	240
TGCTACAAACG	AAACAGCTGC	CTGAATTCTA	TATACCCTCT	GAAAATAATC	TGCACATAAA	300
ATGGGAAAGC	TTCACCGCAG	CAGACCCCCAC	TCGAG			335

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAATTCTGGCC	TTCATGGCCT	ATGCTTCTTC	CACGCACCAC	CACCAACCAC	ACCACCATCA	60
TGGCCATAGC	CACCGTGGCC	TGGGGGTGCT	GCCTGATGGG	CAGTCCAAGC	TCCAGGCCCT	120
GCATGCCAG	TATTGCCAAG	GACCGGGCCC	TGCCCCGCCA	CCCTACCTCC	CACCCAGCA	180
GCCCTCTCTT	CCCCCACCTC	CCCAAGCAGCC	CCCACCCCTTG	CCCCCACCTGG	GCTCCATTCC	240
ACCGCCTCCC	GCCTCAGCCC	CACCTGTGGG	GCCACATCGC	CACTTCCACG	CCCATGGCCC	300
AGTCCCAGGG	CCCCAACACT	ATACCTTGGG	CCGGCCAGGC	AGGGCACCCA	GACGGGGGGC	360
TGGAGGACAC	CCTCAGTTTG	CTCCACATGG	CCGCCACCCC	CTGCACCAGC	CCACATCCCC	420
ACTGCCCTG	TACAGTCCTG	CCCCCAGCA	CCCTCCAGCC	CACAAACAGG	GCCCTAAGCA	480
CTTCATCTTC	AGCCACCCACC	CATCTCGAG				509

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAATTCTGGCC	TTCATGGCCT	AAAGATGGCG	GAGAACAGCG	GTCGCGCCGG	CAAGAGCAGC	60
GGGAGCGGGCG	CGGGGAAGGG	GGCGGTGTCC	GCAGAGCAGG	TGATTGCTGG	CTTCAACCGC	120
CTTCGGCAGG	AACAGCGAGG	CCTGGCATCC	AAAGCAGCTG	AGTTGGAGAT	GGAGTTGAAT	180
GAGCACAGCC	TAGTGATCGA	TACACTGAAG	GAGGTAGATG	AAACTCGTAA	GTGCTACCGC	240
ATGGTTGGAG	GAGTGTGCTGGT	GGAGCGAACT	GTCAAAGAGG	TGCTGCCCGC	TTTGGAGAAC	300
ACAAAGGAGC	AGATACAGAA	GATCATTGAG	ACACTGACAC	AAGCAACTCG	AG	352

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GAATTCTGGCC	AAAGAGGCCT	AGCTAGGTTTC	TGAAGCTTCT	GAGTTCTGCA	GCCTCACCTC	60
TGAGAAAACC	TCTTTCGCCAC	CAATACCATG	AAGCTCTGCG	TGACTGTCT	GTCTCTCCTC	120
GTGCTAGTAG	CTGCCCTCTG	CTCTCTAGCA	CTCTCAGCAC	CAATGGGCTC	AGTCCCCCCC	180
CCCGTACACG	CCTCGAGGCA	GGTCGAG				207

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GAATTCTGGCC	TTCATGGCCT	AGGCGGGACT	AACACAGGGT	TGTCATCTTT	TCCTTTGCC	60
AAGAAAGAAC	ATTAATAATGT	ACTACCAAGCA	TCTGCCATCA	CTAGCATTTC	ATAAAAAGAG	120
GTTCTGTTAG	CAACAGAGTA	GAAACTGTAG	GAAAGCATCT	CAGAACAAAA	CTAAGTTGAA	180
TAAATTCAACC	TAATAAAAAT	GCCTGGGTCT	AGGATTCCTT	TTCTTCATCA	AAAGCTGCAA	240
GAGAAAGCCA	CTGCTTACCT	GATGCCGATT	TACTGGTCAT	TGGGGTGGC	AGGTTGGTT	300
CTCGAG						306

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGTCTCACTT	GTCTCATCCT	GTGCCAGG	CTGGAATGCA	GTGGTATGAT	CTCAGCTCAC	60
TGCAACCTCA	GCCTCCTGGG	TTCAAGTGT	TATCCTGCCT	CAGCCTCAA	GTANCTGGGA	120
CTATAAGCAC	ACATCACCAAC	ACCCAGCCAA	TTTTTTGAA	TTTTTAATAG	GGTTTCACTA	180
TGTTGGCCAG	GCTGGTTGAA	CTCCTATCCT	CAAGCGATCC	ACCCACCTCG	GCCTCCCCGAA	240

GTCGCTGGAT TACCTGAGCC ACCGTGCCA GCCCATTTCA CAGTACTTTT TATTTAACCC	300
TATCGTCTA GGGCACCATG CAATATAACAG CTATTCATT TTCTTTTGT CTCTGTTCT	360
TAGGTGGTCT CGAG	374

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 306 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GCAATGGCAG GAATTCGAAA TATTGGATA TGGTTCTTT GGATTAGATT ATATAAAATC	60
AGAAGAGGTA GAACCAGGCC CCAAGCACTC CTTTTTCTCT GCATGATACT TCTGCTTATT	120
GTCTTCACA CTAGCTACAT GATTATAGT CTTGCTCCCC AATATGTTAT GTATGGAAGC	180
CAAATTACT TAATAGAGAC TAATATAACT TCTGATAATC ATAAAGGCAA TTCAACCCCTT	240
TCTGTGCCAA AGAGATGTGA TGCAGAAGCT CCTGAAGATC AGTGTACTGT TACCCGGACG	300
CTCGAG	306

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GGTAGAGATA ACAAAACAGG ATACCAAAGT TGAGCTGGAG ACTTACAAGC AAACCTGGCA	60
AGGTCTGGAT GAAATGTACA GTGATGTGTG GAAGCAGCTA AAAGAGGAGA AGAAAGTCCG	120
GTTGGAACTG GAAAAGAAC TGGAGTTACA ATTGGAATC AAAACCGAAA TGGAAATTGC	180
AATGAAGTTA CTGGAAAAGG ACACCCACGA GAAGCAGGAC ACACTAGTTG CCCTCCGCCA	240
GCAGCTGGAA GAAGTCAAG CGATTAATTT ACAGATGTTT CACAAAGCTC AGAATGCAGA	300
GAGCAGTTG CAGCAGAAGA ATGAAGCCAT CACGCTCGAG	340

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 176 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GAATTCGGCC AAAGAGGCCT AGATTTAAA TTTGTTTGAT ACCTGCTGTG TATTCCTTGC	60
ATACCCAGCA CATTGTTGCC CATATTGTTG ACATGTAGTA TGTATTTATT ACAATTATAT	120
GATTAATGAA ATGTATCTA TTTTTTCTAT CTATAGCATG TACAGTCACA CTCGAG	176

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 414 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GAATTCCGCC	AAAGAGGCCT	ATTCTTGTC	TTTGCACAT	GTTCTTGAG	TCTTAGTATC	60
TGTAACGTGG	CGCTACTCTC	TCTATCATGG	GGGGGCATGT	TTTGACATTA	AATTGACTTT	120
TAAGAAAAAC	ATGTCACTAA	CCTGAAGCTC	AGCCACACAG	TGACTTTAA	GGTTTTATTT	180
AGACTTTACT	GTTGTTCTCA	TGAGAGTAGG	TACAGACTGC	ATAAGGTTTA	GAATCCCAGC	240
ATATGTCGA	AAACGACGGGA	CTTCACTGT	GATTCCACC	AGAGAAATTA	TAGCAGAGTG	300
GCTGAGGCATG	TGCTCTGAGG	CCAGGCCCCA	GCTCTGCTGC	TGACGAGCTG	TGTGGTCCTG	360
GGCAGAGTGG	TCTCCGAGTT	CCAGTCCCTC	CTCTGTAAAA	TGGGCTTACT	CGAG	414

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 497 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GAATTCCGCC	AAAGAGGCCT	AAACATATAAC	CTAGTCTATA	CTCTCTCTTA	TCTCTGAACA	60
CTTTTCATCT	GGAGCTATTAA	ATGCCCTCTA	GCCTTTATTAA	TAATTATCAC	ATATAATTAT	120
GCCTTTCTC	CTCAAAATTAA	TCTGTTGGAG	TCATCTTATA	GTAGAGTCCT	TACAGAACAC	180
AAAGCATTCA	ATCACTTTAT	TTCAGACACC	AACTCTGTTT	TTGATGAACA	TATGTTAGTC	240
TTAAGCCAT	AAAAGTAATG	CTAATGTGGG	ATCTTATGGA	AGACTACTGG	TAATACAGGA	300
AAAAAAAGTGG	CAAAGAAATC	TCGACACGTTT	GGCAATTATT	CCTGAGGCTC	TGACCTCTCA	360
ATTGTTGAGT	GTTGGAGGTC	ACAGTAACAA	AACCATAATAA	AGATCATGTT	GAAAGTCAAC	420
ATTATTAATA	TACCATACTT	GAAGGATATG	TGGTTATTGT	CTCACGTGTC	CATGTGAAGA	480
GACCACCGTC	CCTCGAG					497

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 111 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GAATTCCGCC	AAAGAGGCCT	AGTTTTGAT	GAATTTGTGT	TATTTACTTA	TAACTAGAGT	60
TTGAATGTTT	ATTGGAAAAA	CTTAATCATG	ATCATCTACT	GGTGGCTCGA	G	111

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 311 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GAATTGGGCC	AAAGAGGCCT	ATGCAATTCT	GACCAGGAAG	CTCCCTTTA	ATTGGAAATT	60
CTTAGAAAGG	TATGGACAA	AGGAGATCCC	AGCAAACATT	CCGGCATCTA	CTGCTCTTGG	120
GT	TTCTCTG	TGTTGGTTT	TTTGTTTG	TTTGTTTAT	GAGATGGAGT	180
CGCC	CAGGCT	GGACTGCAGT	GGCGAACATCT	CAGCTCACTG	CAATCTCAC	240
CAAGTGAATA	TCCTGCCTCA	GCCTCTAAA	CAGCTGGAAT	TACAGGTATA	CACCACCA	300
CCGAGCTCGA	G					311

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 597 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GAATTGGGCC	AAAGAGGCCT	AAGTGCAGTG	GTGCGATTAT	AGC1CACTGT	AGCCTCAGAA	60
TCCTGGGCTC	AAGCTGCTCT	CCCACCTAGC	CTCCCCAAAGT	GCTGGGACTA	CAGGGCTGTG	120
CCACGGGGCC	CAGCCATT	TTCGAATATT	TTCATCTGC	AGTTGTTG	ATCCACAGAT	180
GCAGAACCCA	TTCATTAATGG	AGGGCTGACT	ATACCTTCT	GATGACCTAA	ATATTGTGT	240
CCACTATTGG	GACACTCCTT	TCTTAGTGTC	AAGGTTG	AGAAATTGAG	GGCTGTTG	300
TGGGCAAAGA	TTTATTATT	TATTTACTGG	CTTATCTACA	ATTGAGACAG	GGTCTCACTA	360
TGTTTCTCAG	GCTAGTCTA	ACTCCTGGGA	TGAAGCAGTC	CTCCCATCTC	AGCCTCCCAG	420
AGTGTGGGA	TTACAGGTGT	GACACCCAT	ACCCGGCAGA	GCAAAGAGTT	AAGAGTACAA	480
GACATTGAT	CATCTTGAGG	AGTATTACT	TCAGACTGAA	ACACCCACATG	AAATTCTAGA	540
GTCCAACAGA	AAAGTGTAAATA	ATTTTTGCT	TTTCCCTTCT	TCCGCTACAT	CCTCGAG	597

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 506 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GAATTGGGCC	AAAGAGGCCT	AATTCTAGAC	ATGCTCAGCT	TTGTGGATAC	GGCGACTTTG	60
TTGCTGCTTG	CAGTAACCTT	ATGCCCTAGCA	ACATGCCAAT	CTTTACAAGA	GGAAACTGTA	120
AGAAAGGGCC	CAGCCGGAGA	TAGAGGACCA	CGTGGAGAAA	GGGGTCCACC	AGGCC	180
GGCAGAGATG	GTGAAGATGG	TCCACAGGC	CCTCCTGGTC	CACCTGGTCC	TCTGGCCCC	240
CTGGTCTCGG	TGGGAAC	TCTGCTCAGT	ATGATGGAAA	AGGAGTTGGA	CTTGGCCCTG	300
GACCAATGGG	CTTAATGGGA	CCTAGAGGCC	CACCTGGTGC	AGCTGGAGCC	CCAGGCCCTC	360
AAGGTTCCA	AGGACCTGCT	GGTGAGGCC	GTGAACCTG	TCAAAC	TGTCAGGTG	420
GTCGTGGTCC	AGCTGGCCCT	CCTGGCAAGG	CTGGTGAAGA	TGGTCAC	GGAAAACCCG	480
GACGACCTGG	TGAGAGAGGC	CTCGAG				506

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GAATTCGGCC	AAAGAGGCCT	AGTCTGTGGT	CATTTCAAC	TCTCATTTAT	AGGATTCTAA	60
AAAGGCACTA	CATTAATCCA	CTCCCTTATC	TAAAATAAAT	TTAAAATTCA	TCGGAATTG	120
TCCAGTCCTC	CATCACTGGA	AAATGTACAG	ATTCCTTCTC	TGGAAATATC	TAAAGAAAAG	180
TACAGCTAAT	GTTCCCCCAT	TTCCTGTGT	TTTGTGCTG	CTTTAACTAT	GAACTCATCT	240
GGCGGGCGC	AGTGACCAAG	CCGCCGGGAG	CTGGGGAGAG	ACGCACCGGG	GCGGCCACTG	300
GGCCAGGAGA	CCAGAACACT	CGAG				324

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GAATTCGGCC	AAAGAGGCCT	AGGAGCAGAT	TCCTCATGGT	GCTTGTTAT	TATATATATT	60
TAATCCTGCT	TGACACTTTA	CCCAAGGGAG	ATGGTCCCTT	TTATCAGTTG	AATGTTAGCA	120
GGCTTATTTC	AGAGTGTGGT	GACTGGTTAG	AGAAACTCAT	GTACTCAACC	AGCCACAGTT	180
TCAAACAAAA	TTTTATGTG	CAAAGGACAG	CAACCTCTT	GTATGTTAAA	CCACCAAGTAC	240
TCGAG						245

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GAATTCGGCC	AAAGAGGCCT	AGGTGTTTG	GTAAAAAGCTT	TTTTAGTCAT	CCCCATGAGA	60
ATAATAAACT	CCATGAGGGC	AGCAACTTGG	CTGGCCTGTG	TGCCAGTGCT	GGGGACATCA	120
CTGAGAAATG	AAGGCCATT	TGGCAGGCTA	TTTTGAGCA	AGATTCTGA	GGCCCAATCG	180
TTGGGTGATG	AGATGGACCC	GAGGTATTTG	ACTCCAGCTC	TCGAG		225

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GCCAAAGAGG CCTAGAGAGC TCTGGGGGC AACCTGGAGG TCTGAAAAGA GGACCCAGAG	60
AAGGTGGTAC CAGGCTTCCT GGTCAAGAACC GGCCTGGAGC TCCTTCCCTT CCCCTGGCC	120
TGAGAGGTG CTTTTAACGTC TTCCACCCCT TGTTCCATCT GCCTGCCAAC CCATCGGAAA	180
CGAATCCACA TCATATTGGA GTGACCCCCA TCAACCCCCAG GGCTCCAGCA CTACCAAGTT	240
GGAAATTCCAC GCCCCGGGAGT GGGGTAGAGG AAGACGAGAC AGGACGAGGC AGAAAAGCAC	300
ATTTTAAAAAA CCAGACAAGA TGGCTAGGCC ATCACCAACC AACGGACTTA CCTTACATTT	360
TTGTAGGTAA TTCCCCCCAA ATCTTGATTT TTTTTTCCT CAATTATCCT TTAAAAAAATA	420
AGAAAAACACA TTCCAAACCC ACTCGAG	447

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCGATTGAAT TCTAGACCAC GCCTGCTCTG GGGCCAGCTC TTCTCCAGGC TCTCTGGGCC	60
GGGTGGGTCC TCACCCCTCCA GCCCCCTTCCA CCAACTGCAT TCACTCCCAA TGGCACGTAT	120
CTGCAGCACCC TGGCAAGGGAA CCCCCACCTCA GGCACCCCTCT ACCTGGGGGC TACCAACTTC	180
CTGTTCCAGC TGAGCCCTGG GCTGCAGCTG GAGGCCACAG TGTCACCCGG CCCCTGTGCTA	240
GACAGCAGGG ACTGCTGCG ACCCTGTGATG CCTGATGAGT GCCCCCAGGC CCACCTTACCC	300
AACAACCCGA ATCAGCTGCT CCTGGTGAGC CCAGGGGCC CGGGAGGTATG CGGGAGCGTG	360
CACCAAGGGGG TCTGTGAACA CGGGCGCCTG GGGCAGCTCG AG	402

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GAATTCCGGCC AAAGAGGGCCT AGTGGAAAGAT TTGGGTACTG TCTTTAATAA ATCAATCAAT	60
CGACTCTTAT TTCAAGGAGA AACTTCTATG TTATATGTTG AAGGTGAACA GATCATATTT	120
AGAGGATATA ACAATTAGAA ATCTAGAAAA TAATTATCAC TTTTATAAAA TTTTTAGTCA	180
ACTGTACAAA TAATTACATA AAACATCAAT TAATTATGCT TAAATATCAC TAATGTTCAT	240
AATATATAAT CACTATTTGT AATCAAAAGT TTAATTTAT GCCAAAAAAT AAAAATGCT	300
TACTCGA	307

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GAATTCGGCC AAAGAGGCC ACTTCCATAA CCGTGCTTT GACGTTAAA ATTTAAATT	60
CAGCCTTTG GAGAACACTA AGTATCTTAG TGTGTTTTA CTTACTATAA TAATATTATT	120
GACCTAGTGT AATATTACTG CCATATGGAC CTCAGGGTA CTTTCTGAT AAATTCTGT	180
TATGGTTCA TAATTAACA AAAGGATAAT ATACAGAGTT GTGGAGTTT TTTGGTTTG	240
TTTGTGTTTG AGATAGCCTG GGCAACGACT GAAACTCTGT CACACACACA CACACACACA	300
CACAGACACA CACCAAATCT CGAG	324

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GAATTCGGCT TCATGGCCTA CAAAGAGATG AAGAAGATTG TCGATGCCGT GATCAAGTAC	60
AAGGACAGCA GTGGACGTCA GCTCAGCGAG GTCTTCATCC AGCTGCCCTC GCGAAAGGAG	120
CTGCCCGAGT ACTACCGAGCT CATCCGCAAG CCCGTGGACT TCAAGAAAGAT AAAGGAGCGC	180
ATTCGCAACC ACAAGTACCG CAGCCTCAAC GACCTAGAGA AGGACGTAT GCTCCTGTGC	240
CAGAACGCCAC AGACCTTCAA CCTGGAGGGC TCCCTGATCT ATGAAGACTC CATCGTCTTG	300
CAGTCGGTCT TCACCAGCGT GCGGCAGAAA ATCGAGAAGG AGGATGACAG TGAAGGCGAG	360
GAGAGTGAGG AGGAGGAAGA GGGCGAGGG GAAGGCTCCG AATCCGAATC TCGGTCCAGT	420
CTCGAG	426

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GAATTCGGCC TTTCATGGCCA ACACATAATC CACGCTCATC TTGCAAAGCG CTATTTCAGG	60
CACATCATTG GAATACAGGA AGTAGCCCTG CACCTGCCAG TGAGCTGCC ATTCACTGAT	120
TGGAAGAGTG ACCTGGCCTC TTGGAAATCA TTGTGTTCT TCAGGAGAAT GTGCAGTGTG	180
TTGTAACAAC TAATTATAAT GCAAATTAGG GCTACATTGT AATCTGCTT GTTAATGAAA	240
ATGATAAAAC AGAATATTGA CAAGCTAGGA CACCTGTGGT ATCTTTAATT GTATCTCCTT	300
CAGAAAGTTTG CTTCTTATGG TATAATAAG TATGAAAGAA TATTGAGTAT ATGTTTACTC	360
TGGGCCTGGG AGAACTTAAC TTTCTAGAGC AGTTTGTGTA CTTGTGTGCA ATGGGGAGAG	420
GTACCATGAT GACACTCACA GGGAGCCACT GTTCACTGAC ACTTGGAGG CCCTGCCTCG	480
AG	482

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 363 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GTGTTTGC	ACACCC	TGAATT	AAAC	TGCC	CACA	TATCG	CAGA	TGT	TTTG	TG	60
TCTGTT	TC	TTTCA	CT	AGCG	TTGCG	TTGCTT	CCTC	TGAAG	CCAGA	GGGTGAA	120
CCCTAG	CAA	GTTAG	TATC	ACTGA	TGATA	ACTGT	GATC	CTTAAA	GATGA	ATTCC	180
CAGCCTG	GAGG	TGACAC	ACAG	AGGTCAG	GACGT	CTCAG	GATCT	GTCAC	ATGTC	CATGTT	240
GCTTGGT	G	GTA	GAG	AACAA	AGTCC	ACATC	AGT	TC	AAACAG	GTCG	300
TCGATAT	GAA	ACATTG	GAGAT	TTGGC	AGAAA	CATGT	GCCTA	GTTTG	CAGCA	CAAATACTC	360
GAG											363

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 336 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GAATT	CGGCC	TTCAT	GGCCT	AAAGGG	ATAT	TC	ACTCAA	AT	CCCTA	AGTAT	TTCAGAA	ACA	60
GCCT	GAGAGC	AAGT	CCCT	GGG	CTTC	CGCT	TTTC	TAG	TTTAA	AGG	TTTAA	CTG	120
TGAGATT	CCC	CTAA	AAAG	TTTC	CAG	AAAG	CA	ACT	AAAAA	GAG	CCTAG	GT	180
TATTTTG	GCT	CGT	TTAT	AT	AA	ATAAT	TCAG	GCC	AGTTAA	TGAG	ACTAAA	CTT	240
AAGCAA	ATCA	GTCTT	GGCTT	AT	TTTGG	TA	GGA	ATGGGG	TAATGG	GAG	AGAA	ATT	300
ATGTT	CAGA	AGAA	AACT	AT	AGCA	CAC	CAA	CTCGAG	AG	AACT	AT		336

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 251 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GAATT	CGGCC	TTCAT	GGCCT	AGTGG	AAAC	ATT	TTCAA	GAC	ATTAG	GGG	ATAAG	AA	TC	60
CA	GGT	GCT	AC	TG	ATG	TTG	GT	TT	TT	CA	TT	AT	TC	120
TGTTTG	C	GCT	T	GTT	AT	TGTT	CAA	GG	TTT	AT	TT	CA	AT	180
CAAGTT	TAGA	GT	TCT	AT	TAT	TTT	TT	TT	TT	ACT	TTAG	AAA	CT	240
ACCGG	CTCGA	G	CA	GGT	AT	TTCAA	AT	TT	CT	GA	AGCT	TC	T	251

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 265 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GTTCAAACCAAG TTCAAATACT TTTCAACCT CTATTTCTTA CTTCTTGCT GCTCTCAGTT	60
TGTTCCCGAA ATGAGACTTG GTGCACTCTA TACCTACTGG GTTCCCGTGG GCTTCGTGCT	120
GGCCGTCACT GTCATCCGTG AGGCGGTGGA GGAGATCCGA TGCTACGTGC GGGACAAGGA	180
AGTCAACTCC CAGGTCTACA GCCGGCTCAC AGCACGAGGC ACAGTGAAGG TGAAGAGTTC	240
TAACATCCAA GTTGGAGCCC TCGAG	265

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 437 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GAATTCCGCC TTCATGGCCT AAGATGATTG TGCTATTATT GTTTGCCCTG CTCTGGATGG	60
TGGAAGGAGT CTTTCCCCAG CTTCACTACA CGGTACAGGA GGAGCAGGAA CATGGCACTT	120
TCGTGGGAA TATCGCTGAA GATCTGGTC TGGACATTAC AAAACTTTG GCTCGCGGT	180
TTCAGACGGT GCCCAACTCA AGGACCCCTT ACTTAGACCT CAACCTGGAG ACAGGGGTGC	240
TGTACGTGAA CGAGAAAATA GACCGCGAAC AAATCTGCAA ACAGAGCCCC TCCTGTGTCC	300
TGCACCTGGA GGTCTTCTG GAGAACCCCC TGGAGCTGTT CCAGGTGGAG ATCGAGGTGC	360
TGGACATTA TGACAAACCCC CCCTCTTCC CGGAGCCAGA CCTGACGGTG GAAATCTCTG	420
AGGGCGCCAC ACTCGAG	437

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 242 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GAATTCCGCC TTCATGGCCT AGTACCTTAA AAACCTTGGA ATAATAATA ATAATAATAA	60
ACAAAAAAATA ATCCCAACCC CGGTAAGTTT AACTTTCTAT GCTTTGGCTG TTTTTGGTTT	120
ATTTTTGTT TTTTAGAAGG GGTCTCGCTC TGTCGCCAG AATGGAGTGC AGTGGCTTAA	180
TCAGGGCTCA TTGAGCCTC GACCTCCTTG GTTCGGCGA TCCTCCTCCC TCCACACTCG	240
AG	242

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 264 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

AATTAAAATTA AATTAAAATC TTTGTTACAA ACTATGAAAA TGAATATAAG TAAATTTCAT	60
ATCATTTCTT TTCTAGATTT ATTATCTAGG ATAGATTG ATGAACTAAT GAAAAAAAGAT	120
GAACCGCCCTC TTGATTTCTC TGATACCTCTG GAAGGGATTG AAATATGCTTT TAATGAAAAG	180
GGACAGTTAA GACACATAAA AACTGGGGAA CCATTTGTTT TTAACTACCG GGAAGATTAA	240
CACAGATGGA ACCAGAAGCT CGAG	264

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GAATTTCGGCC TTCATGGCCT AACCTGGAGA AACTATTTAA GTTGGATGAA GCAAGTGCCT	60
AGCTCCTTGC TTATAAGGAA AAAGGCCATT CTCAGAGTTC ACAATTTCC TCTGATCAAG	120
AAATAGCTCA TCTGCTGCCT GAAAATGTGA GTGCGCTCCC AGCTACGGTG GCAGTTGCTT	180
CTCCACATAC CACCTCGGCT ACTCCAAAGC CGGCCACCCCT TCTACCCACC AATGCTTCAG	240
TGACACCTTC TGGGACTTCC CAGCCACAGC TGCCACCCAC AGCTCCACCT GTAACCACTG	300
TCACCTCTCA GCCTCCCACG ACCCTCATT CTACAGTTTT TACACGGGCT GCGGCTACAC	360
TCCAAGCAAT GGCTACAACA GCAGTTCTGA CTACCCACCTT TCAGGCACCA TAGTGACTCG	420
AG	422

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GAATTTCGGCC TTCATGGCCT ACCGAAGGGC ATCCCATCGG TTGGGTAGGT CATGGTTAAA	60
AAATCATCTC CTTGGTTGC ATATTTAATT ATTTTCCACT ATTTTTCTT CACACAAAT	120
GATTTGGCCC GGTACCCCTT TTGGGGGTGC ACAGTCCATG AGATGAATAT TGAATGGGA	180
GACCTGGGTT CTAGTCTCGC ATTATTACAGT CAGGTTACAA TGCGACCTTG AGCAAGTCAC	240
TTCACCTCCC AGCCGCTCAG TTTCTCATT GTAAGATAGG AAAAGCCTTG TCATTTTAA	300
AATTTTATTT TTGCAATATA CCTCATGGCG AACTCGAG	338

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GAATTCCGCC	TTCATGGCCT	ACTATGCTCT	GCACGTGGGT	CATTTCTTAC	TGGTTTCTAA	60
AAGCCTTCA	TTTTCTGCCT	GTACACAATA	GCCCCCTTC	TCCATTGTTT	TTAGGATCCT	120
TTTTCTCTT	ACCAGCTGTT	AACTGGAAG	TATTTCTTCT	TCATCCGAA	TCTCCCATGT	180
CCTCCCCACT	TCTATTGTT	TCCATCCAAT	GTGGATTAT	GATCATTAA	TGGATTTAA	240
ACTACTCTGG	GGCTACCCCTC	GAG				263

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GAATTCCGCC	TTCATGGCCT	AGAAACACAT	GTGATCTGTA	CTCATGAGAA	CCTGTAGTTA	60
ACTATACGAG	CCTTGCTGTG	CATTTGTTT	TTATCTGAGC	CTGTCTTCA	ATGTCTATC	120
CCTTGAGAGA	ACTGAGGGCT	GAGAACCAAG	CTTCCGAAG	CGGTCTGAGT	GTCAGCGGTG	180
GTAGTGGTCT	CTGGAGAAAA	GAATGGAGAC	AGGATAGGAC	TTGGAGAAGA	GTGAGTCATT	240
GTTACCCAGA	AACCCTGGAG	AACACTGGAC	TCGAG			275

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GGCGTTCTC	ACGCCGCAA	CAATTCTGA	GTAGGGCCTT	GCTTGAGTT	TTCGGAAAGT	60
CTCATCCACC	CCCACATCGC	CTCTTAGGA	AGTCACCTAA	TGTTGGGCTT	CATTATTCCC	120
ACATCCCTT	CCTTACTACT	TGCTCTGACT	TCTTGAGAAA	AAGACTGCAG	AAAGGAGAGG	180
TGGGGTTTC	AGTAGAAACA	AGCAAACCGC	AGGTCCCTGT	GGGGGGACTC	TCCAGGAAGA	240
AGGGTAATT	CTGCCTCCT	TAAATTGGCT	GCTACTGTCA	GTTATTTGC	TCCCAACCCC	300
AGAGCTTCAC	TTGCTCTTC	ACTTCCCAGT	TCCGCAAGAA	CCGTGGGGCA	CAGTTATGGA	360
GAAGCGTCTG	CAGGAGGCTC	AGCTGTACAA	GGAGGAAGGG	AACCAGCGCT	ACCGGGAAAGG	420
GAAGTACCGA	GATGCTGTGA	GTAGGTACCA	TCGAGCTCTG	CTTCAGCTGC	GGGGTCTGGA	480
TCCGAGTCTG	CCCTCTCCGT	TACCTAATCT	CGGACCTCAG	GGCCCGGGCCC	TCACGCCCTGA	540
ACGACCTGCC	TCGAG					555

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GTGAAGATGG ACTGCTCTGG GGCCCATGTG CAAGTGACCT GTGCCAAGCT CATCTCCAGG	60
ACAGGCCACC TGATGAAGCT TCTCAGTGGG CAGCAGGAAG TAAAGGCATC CAAGATAGAA	120
TGGGATACCG ACCAATGGAA GATTGAGAAC TACATTAATC AGAGCACAGA AGCCCAGAGT	180
GAACAGAAAG AGAACCTCGCT TGAGCTCAAA AAAGAAGTTC CAGGATATGG CTATACTGAC	240
AAACTCATCT TGGCATTAAT TGTTACTGGA ATACTAACGA TTTTGATTAT ACTTTCTGC	300
CTCATTGTGA TATGTTGTCA CCGAAGGTCA TTACAAGAAG ATGAAGAAGG ATCACTCGAG	360

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GAATTCCGGCC TTCATGGCCT AGCTCCTCG TAAAGGAGCA TGAGAGCGTG GGAGTTTG	60
AGTGGCCGTG GGGTTCTCG TCGCGTCTCG GTCGGCGTC GCTTCTGCA GCTCCTGTCA	120
GGGAGCGCGA GGCCTGTTAT TAACCGCGGA GCGCTTTGTC ACGAANTCCC TGTGGCGTCT	180
TGAAGAAGGC ATTCCCCACC CGCCAAATGG CGTCCATGCC CCCGACGCC GAGGCCAGG	240
AGACTCGAGG TACCTTTTC GTCCAAGTTT ATNGCTGTT TCGGTCTCTG CCTGACCCCN	300
TCCCTTGAG GAGAGTTGGG CATGCCCTTGT GTGGTAGGG TGCTCNTGAG CCCCAAATAG	360
CCCTTGACCC AAGTGTCTT CGTCCAAGA CCACACACAT AATGGTTTAC CAACTTCNTT	420
CTTTCAAGAAC TACCAACTGG GAGCAGGGAC CTGTGGAGGA ATCTCTGAGA GAGTTTCTCA	480
ATGTCTTATC TGTTTGTGTTT GTTTGTTTG GAGATAGGGT CTGGCTTGT CGCTGGAGTG	540
TTGCTTGCTC GGCTGGAGTG CAGTGCTGAT ATCATAGCTC CGTCTGGAAC TCAGGGAATC	600
CTTACGCCCTC AGCCTCTCGA G	621

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GAATTCCGGCC TTCATGGCCT ACAATTGGG GCAAGGCTTA GCAGAAGACG GCGGCATGAG	60
CAGCGTCACT CAGGAGGGCA GACAAGCCTC TATCCGGCTG TGAGGTCAC GTCTGGCCG	120
GGTGATGTAC TCCATGGCAA ACTGTCTGCT CCTGATGAAG GATTATGTGC TGGCGTGG	180
GGCGTATCAT TCGTTATCA AGTATTACCC AGAGCAAGAG CCCCAGCTGC TCAGCGGCAT	240
CGGCCGGATT TCCCTGCAGA TTGGAGACAT AAAACAGCT GAAAAGTATT TTCAAGACGT	300
TGAGAAAAGTA ACACAGAAAT TAGACGGACC TCTCGAG	337

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GAATTCCGCC	AAAGAGGCCT	ACATTA	ACTGG	GTTAGAAA	AC	AAAGAGGGAG	TGCCC	TGCAC	60
ATTTTCTTT	GTGCTTTAA	ATGTT	CCTTA	AGTTGGA	ACA	GGTTT	CCTCG	GGCCTGTTT	120
GA	ACTGATTG	TGGAGTG	CAT	TTGATAG	TTA	AAAATT	ACTA	ATTGGTTT	180
CACTCTGC	CCT	CCCCATTG	A	CCCTAAC	CT	CGAG			224

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GATTTAATGC	ATGCTAGCAA	CAGCCTTAAC	TTGGATTCA	GTTATTTGAA	ACACTTTCC	60	
GGCATCTTC	CCTTCTAA	AT	GTGTTGGGT	GGAAACCGGA	TGGCAAATCA	CTGTGAGCCG	120
GATA	ACCTCTAG	CACAGTCCAC	CTTGTGTGTG	ACTTCACAAA	TGGGGACTT	CACAAATGGG	180
GTA	ACTGAAT	GTTATTACTT	TCAAATTTG	ACATGGAGCA	TTATGATCAA	GAAATGGAG	240
CA	ACTCGAG						249

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GCTGCGCCGC	ACCCCTGAGAG	ATGGTTGGTG	CCATGTGGAA	GGTGATTGTT	TCGCTGGTCC	60
TGTTGATGCC	TGGCCCTGT	GATGGGCTGT	TTCACTCCCT	ATACAGAA	GT	120
CACCTAAGGG	AGACTCAGGA	CAGCATTAT	TTCTCACCCC	TTACATTGAA	GCTGGGAAGA	180
TCCAAAAGG	AAGAGAATTG	AGTTGGTCG	GTCCTTCCC	AGGACTGAAC	ATGAAGAGTT	240
ATGCCGGCTA	CCTCGAG					257

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GAATTCTAGA CTTTGTCTCC AGAGCATTGC CTTTATAAGC AGATGGCAC CAACAGTTCC	60
ATAGTTAAC ATCTAGTTAA GCTACAAAATA TAGTATAAGC ATTATTAGCA GCTGGTACTT	120
CTGCTAGGGG TTGTAAATTTC CAGGTGTTAC ACTGACCTCA ATCCAATTAA CATAATTAC	180
ATAAAATGCAT CTCGGTGAA AAATAATCAT TTTCTTGCA TATCTCGAG	229

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 257 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GAATTCGGCC TTCATGGCCT ACACTGCTAT GTATGTTTC TCCTTAATGA TGAAGAGTGT	60
AGATGATGCT AATAATAGTA GCTGATGTAC TGACTTTAG CTGTGTGCAA AGCCATGTTTC	120
AAAATACTTT ACAAGTGTAA ACTTGTGTA TCTTCACAAC AACCTTAAGA AGTGGATATT	180
ATTTAAAGTAG ATTTTGGAAAG ACTGATCTAT TTAATTATTA ATAGATCTGT CTCATTCCTT	240
TTTTCCCCCA ACTCGAG	257

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 223 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GAATTCCGCC TTCATGGCCT ACGCGCTCTGC TTCGGAGACC GTAAGGATAT TGATGACCAT	60
GAGATCCCTG CTCAGAACCC CCTTCCTGTG TGGCCTGCTC TGGGCCTTTT GTGCCCGAGG	120
CGCCAGGGCC TTTTGTGCC CAGGCAGGCCAG GGCTGAGGAG CCTGCAGCCA GCTTCTCCCA	180
ACCCGGCAGC ATGGGCCTGG ATAAGAACAC AGTATCACTC GAG	223

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 171 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GAATTCTAGA CCTGCATGTC CCAGTGTGAA ATTCAGCAC GGCATTTCT GCATCCTTTC	60
ATGGCCATCC AAAGGATTCC GCTGCAGAAA TTATTGATGT GCTATTTTG CTGTCTTGTG	120
ATGCAGGGCTG CTTTGGGCCCT CTTGGTCACT CTTCCAAGGC TGCAACTCGA G	171

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 336 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GAATTCCGCC	TTCATGGCCT	AAAAAGCAAA	AGAAAAGTAA	AACGAAGAAA	CAAGAACAAAG	60
AAAAAAAGATT	ATATTGATT	AAAAATCATG	AAAAAACTGC	AACTCTGTGT	TTATATTTAC	120
CTGTTTATGC	TGATTGTTGC	TGGTCCAGTG	GATCTAAATG	AGAACAGTGA	GCAAAAAGAA	180
AATGTGGAAA	AAGAGGGGCT	GTGTAATGCA	TGTACTTGGA	GACAAAACAC	TAATCTTCA	240
AGAATAGAAG	CCATTAAGAT	ACAATCCCTC	AGTAAACTTC	GTCTGGAAAC	AGCTCTAAC	300
ATCAGCAAAG	ATGTTATAAG	ACAACCTTTA	CTCGAG			336

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 212 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GAATTCCGCC	AAAGAGGCCT	AGAAGAGCAA	GCGCCATGTT	GAAGCCATCA	TTACCATTCA	60
CATCCCTCTT	ATTCCTGCAG	CTGCCCCCTGC	TGGGAGTGGG	GCTGAACACG	ACAATTCTGA	120
CGCCCAATGG	GAATGAAGAC	ACCACAGCTG	ATTTCTTCCT	GACCACTATG	CCCACGTACT	180
CCCTCAGTGT	TTCCACTCTG	CACGCTCTCG	AG			212

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 349 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GAATTCCGCC	TTCATGGTCT	ATGCTACTCA	GTTGGATCTA	GCAGAAACAA	AAGCTGAGTC	60
TGAGCAGTTG	GGCGGAGGCC	TTCTGGAAGA	ACAGTATTTT	GAATTGACGC	AAGAAAGCAA	120
GAAAGCTGCT	TCAAGAAATA	GACAAGAGAT	TACAGATAAA	GATCACACTG	TTAGTCGGCT	180
TGAAGAAGCA	AACAGCATGC	TAACCAAAGA	TATTGAAATA	TTAAGAAGAG	AGAATGAAGA	240
GCTAACAGAG	AAAATGAAGA	AGGCAGAGGA	AGAATATAAA	CTGGAGAAGG	AGGAGGGAGAT	300
CAGTAATCTT	AAGGCTGCCT	TGAAAAGAA	TATCAACACT	AAACTCGAG		349

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 391 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GC	GGGCTAGT	CATGGCGTCC	CCGTCTCGGA	GA	CTGCAGAC	TAAACCAGTC	ATTACTTGTT	60
TCA	AGAGCGT	TCTGCTAATC	TACACTTTTA	TTTCTGGATC	ACTGGCGTTA	TCCTTCTTGC		120
AGT	TGGCATT	TGGGCAAGG	TGAGCCTGGA	GA	ATTACTTT	TCTCTTTAA	ATGAGAAGGC	180
CAC	CAATGTC	CCCTTCTGTC	TCATTGCTAC	TGGTACCGTC	ATTATTCTT	TGGCACCTT		240
TGG	TTGTTTT	GCTACCTGCC	GAGCTCTGC	ATGGATGCTA	AAACTGTATG	CAATGTTCT		300
GA	CTCGTT	TTTTGGTCG	AACTGGTCGC	TGCCATCGTA	GGATTGTTT	TCAGACATGA		360
GAT	TAAGAAC	AGCTTTAAGA	ATAATCTCGA	G				391

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GA	ATTCGGCC	TTCATGGCCT	AGGGAGTCTG	AAGCAATTTC	TGAAGAAGAC	AAAAAAGAAC	60	
CAC	AAGACGA	TGAATGAAA	GGCATGGAAG	CTTGGTGC	CACAAATCCT	CTCTGCCCTA		120
AG	CTACCTGC	ACTCCTGTGA	CCCCCCCAC	ATCCATGGGA	ACCTGACCTG	TGACACCATC		180
TT	CATCCAGC	ACAACGGACT	CATCAAGATT	GGCTCTGTGG	CTCCTGACAC	TATCAACAAT		240
CAT	GTGAAGA	CTTGTGAGA	AGAGCAGAAG	AATCTACACT	TCTTGCACC	AGAGTATGGA		300
GA	AGTCACTA	ATGTGACAAC	AGCAGTGGAC	ATCTACTCCT	TTGGCATGTG	TGCACTGGAG		360
AT	GGCAGTGC	TGGAGATTCA	GGGCAATGGA	GAGTCCTCAT	ATGTGCCACA	GGAAGCCATC		420
AG	CAGTGCCA	TCCAGCTTCT	AGAAGACCA	TTACAGAGGG	AGTTCATTC	AAAGTGCCTG		480
C								481

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 583 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GA	ATTCGGCC	AAAGAGGCCT	ACGATTGAAT	TCTAGATCTG	CCCGTCTTGG	CCTCGCAAAG	60	
TG	CTGGGATT	ACAGGCGTGA	ACCACTGTGC	CTGGCATATT	TGTCTATTAA	TTTGTCTTTC		120
TT	TAGATGTA	TTCTAGAGGG	GGAAAATCA	GTAGAAGAAC	AGTTATGTAA	TTCTAACAG		180
CT	CTCCATGT	GTCTTGCAT	CTNGCTTTT	CTCATCCTAT	CAGTACTGGA	TGAGAATGTT		240
TAT	TTCACTG	AACTTGCCA	AAGAGTTCA	ACATTTTTT	GT	TTAATCAT	AGGAGAAAAA	300
TT	TTATCTT	ATTTTAAAAA	ATTTTATTT	AA	TTCTTCA	TTACAAATGA	AGTCCCAGAA	360
GT	GTATTG	TTCTTCTAGG	CTGTTCTAA	TTGTTCATG	GAACAGGAG	GGTTTGAAGG		420
AG	TGGGGATA	CTGGAAAGC	CAGGGTGATG	AGAAAATAGG	AAAGGGTCT	TGTCATTGGG		480
AG	GGCCACTAT	ACCA	GTGGCC	CTTGTACCA	GACTAATATG	GTACTTTGAA	GCTTTAAATT	540
CAT	TTTCTTAA	TTCAATAATT	TTAGGCATCC	CAGGATAC	TG			583

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 484 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GAATTCTGGCC	AAAGAGGCCT	ACCTATCCGC	TTTGCTATTG	TAGTGGCATT	ATCAAAATCA	60
CTGGAAGCAC	CTGTNGTAAT	ATGGTCGGTT	CCAAATATAA	GCTCCTCTGC	CACTCTTCCT	120
CCCATACTAA	CATCCATTG	TGCAAGCAGC	TGGGCTCTAG	TTTCATTCCA	TCTGTCTTC	180
TCAGGTAAAC	GGGACACATG	TCCAAGTGTG	GGCCCCCGTG	GCATGATTGT	AGCTTTGTTG	240
ATAGGCATTG	CATCTTTGT	CTAATATGCA	ATAATGGCAT	GACCAGATTC	ATGATATGCT	300
GTGATGGTT	TGTTTTGTT	ATCAATTTC	ACACTTCTTC	TTTCAGGCC	CATTAGAATT	360
TTGTCTTTGG	AAAACCTCCAG	CTCCCTCATG	GTAACCATTG	CTTTTCCATC	AACAGCTGCT	420
TTTAATGCAG	CCTGGTTCAC	AAGATTCTCC	AACTCTGCTC	CGGAAAAGCC	AACAGTACCT	480
CGAG						484

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 458 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GAATTCTGGCC	AAAGAGCCTA	ATTGAATTCT	AGACCGGCCT	CATCGTTCTT	TGCCTTCCTG	60
GTCACCATCT	GCTACGCTGG	AAATACATAT	TTCAGTTTA	TAGCATGGAG	ATCCAGGACC	120
ATACAGTGAT	TTACCATTTT	GATAATTAAA	AGGAAAAAAA	AAGGAAGACT	CTCACTGTAA	180
AAACAGCTGT	ACGTATAATG	TATATCCCA	GAGAATTGTA	TTTAACATAAT	TAATGTTTTT	240
TATATTCTTA	AATTGCTCA	CAAATTGTGG	TTTGTACAA	TTAAACTGGA	TACTTATTTG	300
CAAAGTGTG	TAGCTTATAA	TGAACCTTA	AGTATCTTAT	TAATGTATTA	ATGTCTTCAT	360
AGATCATATT	TTCTTAGACA	ATGTTAAAT	AGATAAATTG	CTAATATTGA	GAATGTGTCA	420
AGTTGTAAA	CCTAACCTTT	AAGATGCCAG	AACTCGAG			458

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 157 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GAATTCTGGCC	AAAGAGGCCT	ACGGCCAAAG	AGGCCTAGGT	GGTGATTGAC	CTAAGAAAAA	60
AGTGTCTTAA	ATATCTGGAT	TCTATGGAC	AAAAGGGCCA	CAGGATCTGT	GAGATTCTCC	120
TTCAGTATTG	ACAGGATGAA	AGTAAGAAC	GCTCGAG			157

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GAATTCCGGCC AAAGAGGCCT AGTGGACTGC TACTTCCCTT TAGCACTATA TACAAACATA	60
ACTGCTACTT CCCTTTAGCC CAGGATCAA ATAATGATT AGTTAAAAGT TGCTTGCCTA	120
ACAAAATTC AAAATATGGA CTTCTGTGAA TTGCTAAAC ACATCCTTTT AACTAGGCAT	180
CTTTAAGTCT ATAGTATCTT TAAAGTTAAT TTCAAAATTG AGCAGAGCCT GGAACACAAA	240
TTATTCAAGGA AATAATTCCCT GAACCTACCT CTATCTTCAT AAAACGTATT GGGGCAAGAA	300
CTATTCTATT GAATTCTAGA CCTGACTCGA G	331

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GAATTCCGGCC AAAGAGGCCT ACCATCTGTC ACTAATATCA AAGGAGGGCC AAGGACACAG	60
CCCTGGGGGA ACTTACCAAG TCAACCCACA ATGGGTGAAT TTATAGTTTG TTAGTTAGTG	120
GTCAGTTACC AACTTCTCTG TCTGTCTAAT GCTTGTACTA AAATGTCCAG ATTATTTACC	180
TAGTTAACAA ATTAAGGAA GATTCTAAGA CCAGTTAGC ATCATTTCT CTGAAGTCCA	240
TAATGAATGT CTGTAAACT CTCGTCACTC TTATTTAGGT GCTTTGGGT CATTGTTGT	300
AGGTTCAATTG TCCCCAAATCA ATGTACACATA TACGCTGTGTA ACTTGTGTTA TCAGCTTCCT	360
TCCTAGGGCT TTAACCTCTT TTCAGTCTTA TAGCAATTCTC TCCATTTCCT TTTCAGTTCA	420
CTCCAATAAA AGCTCGACAA ACTCCTGGGA GCCCCTTGGT GCTCGAG	467

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GAATTCCGGCC AAAGAGGCCT ACGATTGAAG TCTAGATGCA CACATTCAAGC TTCTGTCTCA	60
GTCCTGAGAG TGGTTGTGTT TTATTGGCTG ATGAGTTATT TCCACATATC ACATGTATAA	120
GGTATTGAA TGAAGGTGCT TTGTAGTCAT GACACACTAC TCTTTACTA ATTATTAATA	180
TCTTAAGATT ACAATTGAG AGGTAGAGAT GGTATTGTT TTAATGGGTG TGGGGGGTGG	240
TGATGATAGG TATTTTACG CTGGTAAGTG ACCTACTAGG TTTTATTAAG TGTTGCAACT	300
TGTCCAGTGT GTGGATGGGA TCTCGAG	327

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GAATTCCGCC AAAGAGGCCT ACTGGTGGTA TGTATTTGAG TTCACAGTAT TTGTTTTATA	60
GCAGTTTGC AAGCACATAC TGTGCCACGG ATTTTCCAC ATTATTTTA GACAAGGAA	120
CACAGCCATC AAAACTGATA CCATGGCCGG GCGTGGTGGT GGGTGCCTGT AGTCCCAGCT	180
ACTTGGGAAC TCGGGACATT CTCGAG	206

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GAATTCCGCC AAAGAGGCCT CCACCATGCC CGGCCCTAAC GATATTGATT CTTTGGGCTG	60
TAGTCAGTAT TGGATTATGA TCAATATTAT CACCATTAT TTTGTTGCTC CAGTTCTCC	120
AGCTGTGGCC AATCCTTCAG TTGGATTCTT GTGCCCCATC AACATTCTCC ATCCTTCTCT	180
CGAG	184

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

GAATTCCGCC AAAGAGGCCG ACTTTATTAT ACCATACATA CTATAGGTAC CTGGCACAA	60
GATAGGTAG GGGTACTGT ACCCTATTT ACATGCTTAA TCACATCATA AGCTTGCAGG	120
TGGTACTTGA AATCATCACT AATGAGACAG CAAATATGTT AGACTTGCTG GCCCAGCAAG	180
CCACAGAAAT AAGGATCACC ATCTATTAGA ATAGACTGGC TTCAAACCTCG AG	232

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GAATTGGGCC	AAAGAGCCTA	CTAAAATTCC	TGTTTTGTG	TTTTAATAT	TCCATCGTG	60
ATAGTTAATA	TTCTTTNGA	GGTTTGTGTT	TAGACAAAGT	AATGTTTTC	TGAAATGATT	120
CTAACGACAAT	TGGTCAGAAA	TAGTCTCTGC	TTGTTGGTT	TATGTTGGT	CAGTTGTGCT	180
TTGATTATAG	ATGGTTCCTC	ATCTGAGATT	AAAGTGGAC	AGAACTCAA	AAGTAAAAGG	240
GTAAATGTT	CCTGCTGATGC	TTATGTGGCA	CATGTGCTAG	TCCTTGATAG	TGGCGAGAAA	300
GATCTTAATT	GCTCAAAGGA	ACTACTCGAG				330

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GAATTGGGCC	AAAGAGGCCT	ACAGTGCATT	ATGTTATTTT	GTTATCTCTG	CAGTAAC	60
CTATCATGTT	ATTTATTTTC	TTTGCTTAT	TTAAAGCTTC	TGAGATTATG	GATTTTGTT	120
TCCTTCCCTG	AAAGTTAAC	GT	TATATAGTAC	TAAGCTGTCT	ACAGAATAGT	180
GGGAGTCTGC	CCTCTTGAGT	TGGGAAGATC	CTAGTTGAA	TCTTGGCTGT	GCGACTTTAA	240
AGTTCA	TTCTCTT	AG	CTCAGTCAC	CTGAAC	CTG CAGTGGGGAT	300
CAGAGTGTCA	TTGGGAGGAC	TCACGAA	ACGTTGTAC	TTTGAGTTCA	GTACCTAGCC	360
TGTATGAGCC	AGCATTAAAGA	GGGACAGTC	TCACGCA	CTTGACAC	AGCTCTCACG	420
CCACATCCTT	TGGCTACTGT	TTGGTAAAT	CTTTACTAGT	AAATGTTCT	TAAAAGCATT	480
TACATTCA	GACATGATTC	CCTCGAG				507

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

GAATTGGGCC	AAAGAGGCCT	AGATTGAATC	TAACCTTTT	GCCTCTCCC	AAGTAGCCTA	60
TTGAGCTAG	AAACAAACTT	TGTTAGCCAT	TTTGGAGAG	AATAGGAAT	CTAGAGAATG	120
AAGATCTGCC	CGACCTGCCT	CGAG				144

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

GAATTCCGCC AAAGAGGCCT AACGACGGTA ATCAAGTTT GCTCCAGAAG CATAAGAAA	60
CTTAGCTACT CCTTCAAAT CAGTACCGGT TTCAGTTAAG CCTTGAAATAA TACAGTCTTG	120
AAACTGAGTA GGGTCAAACC TCTCTTTTC ATCTCTTTT CTAGTTTAA AACGCTGGCC	180
TGATAGCGTT GGCTTTGCT GCTTTGATT ATTCAAAAA GACACCCGAA TTAAAGCGA	240
AGAGGAAAGA GCCAGAAATC CCCGATGTAC CGGCAACTGC GCGCTATCT CCTCGAG	297

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GAATTCCGCC AAAAGAGGCCT AGACTGCTGG TGGTGAAC TG CTTTCTGT AGGTTGTGAG	60
GGCTAAAAAA GCCAATCTTA ATAGACATGA GGCTCATGTT TGCACAGTGT GCTCTCGAG	119

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

GAATTCCGCC AAAGAGGCCT ACTCAGCTGC AAAAAAGCAT ATTTTCTGTG TTTCTGGACT	60
GCACTGTNGT CCTTGCCCTC ACATAGACAC TCAGACACCC TCACAAACAC AGTAGTCTAT	120
AGTTAGGATT AAAATAGGAT CTGAACATTG AAAAGAAAGC TTGGAAAAAA AAGAGCTGGC	180
TGGCCTAAAA ACCTAAATAT ATGATGAAGA TTGTAGGACT GTCTTCCCAA GCCCCATGTT	240
CATGGTGGGG CAATGGTTAT TTGGTTATTT TACTCAATTG GTTACTCTCA TTTGAAATGA	300
GGGAGGGACA TACAGAACTC GAG	323

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GAATTCCGCC AAAGAGGCCT AGGCAAATCA GAACCTCTAA GTTGTGTTCAT CCTTATTTA	60
TTCTTAAAT AAAGAATTTC ATTTCAAATA CGGATTAATT TTTTTCTGG GAAAAAACAC	120
ACTGTAAAAC ATAATTTCT ACCTTTAAA ACGTTTACA ATTTATCCCA TCTTCTAACAA	180
AGTTATGATA CTCATACCTG CCGAGGTTTC TCTAAATTG TCGCTGGTCT TCTTTTCCT	240

CCATTTCATA GGCTTAAAGA TTTTACCAAT GGTGGATAGT TTCCCCTTTC TTTTGAAGGG	300
AGGTGTTTGG GAACCTGCTG TGGGGCCATC TGAGTTTGCT ATAGAACCTT TGCCAGTCC	350
GTCAACTGAG CCGGAGATGT GGACCCGGAG CGGGCGGCCG CTGCTCGAG	409

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GAATTCGGCC AAAGAGGCCT ATAATATAT AATTGACTTA TTTATTAAAT TTAGGAGAAA	60
AAAAAAAGTT TCCTTGACAT TCAGCTCTAT TGGATTTATT TCCATTTAAT TGCATCATGT	120
GTTATGTCTT GTTAAACACT CCATTTCTG TCTTGGTGGG CATCCTGTCT GTGTACCTGT	180
GCAGTACACT TTAATCATCA AGACTTCAAAT GTGCTTTGA GCTATCAAAT CTTGGGAGAG	240
TCCCATCTAG CATCTTAATA ATTATTTTC CAAGTTCGTT ATAATTAACT CCTTTAACCT	300
CATCTCATTA AATCAATTGT GTATTATCAT TCTGTTGTT TCTGAAAGC AGCCAATTGT	360
TCAGCTCTG AATCAGAATT TTCAAAGACT CACCTCTCTT ACCTGGGCTT GCACATATTG	420
GTCCTAAGTA ATTCTCTATC CCTTAAACCT CTGAGCCCTC GAG	463

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GAATTCGGCC AAAGAGGCCT AATTTGTAA AAAGGAATAT CATTCTTGA TTTTAGATCT	60
TAGACATCG GCACTGACAT AGAGCTTAGA TATGTTCTTA AGGTAGCTAA GCCATTATT	120
ATAGGATAGT CAGATAGGAT AGTTCTAGGA TTTATAGACC TTTTCAGATA CTCTTTATCC	180
AGTGAGAGAT GACCTATTTT TATTAACACT TGGCTTTGGT ATCTTGAAT TGGCTTGAAA	240
ATGATTGTT TTACATTGG ATGTGAACGG AAAGTTGTGTA TCTCAAATGT TTTACACCT	300
GAAGGGACAG CTCGAG	316

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GTGGACATGG AAGTAGGTGA GGTTGGGGGA CCTATGAAGA AAAAAGAGC CTTTCCACTG	60
GGCAGTGAAG TGTGTACACA CACACTGGGG GCAGAGCACT GTGAAAACAT TCTGCACCG	120
CACACAAATG ACTTTGGCA AATCATCTNC CTGATCTGTC GGATGTTACG TCTCTGCAGA	180

ATCTGGAGAA AACCAGAAAA CCCAGCTTGT TTGCCCTCAT TTTGGCAGTT TAATTAGGA	240
ATCACACTGG CTTTACATAA ACTCTTTTACCA AAAAAGACTG TATTCTGTAT TTTGAAGGCA	300
CAAGTTAACCA TGCCCCAACG GGAAGGAAGC ATTGTATACA ATTACATAAT AGCTACTCTA	360
TTACTTTAAA ACCTAATGGC AGCCTCGGGC AGAAAAGTC A AAAGGGGAGA GAAACCATTT	420
CTGTGAATT ATCTGATGCA ATCATCTCTT TGGAGACATT GTCAGTTGAC AATGGTTCTG	480
CTTTTCTCT CGAG	494

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GAATTCCGCC AAAGAGGCCT ACGGGAGCAG TTCATGCAGC ACCTCTACCC ACAGAGAAAA	60
CCTCTTGCT GTGGAAGGGAT TGATTTGGGG CCATGTACAA GCAAATGGAC AGTGGATTAC	120
CTAACGCCAAG TTGGAGGGAA GAAAGAAGTA AAGATTCTAG TTGCTGCAGT TGACAGATG	180
GACTTCATTA AACTTTACCT TTTGACCAGT TGGTCCAGAG GGCAGCTGAA GAGAACATA	240
AAGAATTCTT TGTTTCAGAG GATGAGAAAT ACTACTTACG GTCACTTGGA GAAGACCCCTA	300
GAAAGGATGT TGCAGATATC AGAAAGCAGT TTCCTTTGTT GAAAGGAGAT ATTAAGTTTC	360
CAGAATTCTT CAAAGAGGAA CAGTTCTTTT CCAGTGTGTT TCGAATTAGT TCACCAAGGAT	420
TACAACATATG GACTCATTAT GATGTAATGG ATAATTGTT AATACAAGTG ACAGGAAAAA	480
AGCGTGTGTT ACTCTTCAGT CCTCGAG	507

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GAATTCCGCC AAAGAGGCCT AGCTTATCCA GTCTAGTAAT TTTTTTTGTA TGTGTGCACA	60
GCACAAATAG TTACAAATAGT TCCCCTTTT GACATCAAAT TCAACAAATAC CTGGCATATA	120
ATTGCTAAAT ACTGTCATCA TTTCATTAT CATTATCCCC CACATAGTC AAAAAAGCA	180
CACATGCTAA TCTTCAACTC TTCTTCTATT ATTTGCTGCC TTCTTACCTG CGTTAGTGAG	240
AAAGTGCCTT CAAATAGATT GCCAACAGTT ATATGGCTCG AG	282

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GAATTCGGCC AAAGAGGCCT AGTCAGTAT TCACGTGAA CTTTTAAGTT TTCAGTACAG	60
TGCTTTATA CCTTTAATGC AATGGTGTAT TCATTTGGT ACTATTGTT AGTATTAGG	120
ATGTATGCA TTTGTTTAT ATGTAAGCTT GGTGGTGCT TTGCTTTTG TGCTACCTT	180
CTTGGATTT TGTACCAGAG ATGTCGCTAA CTGATGAAAT ACATGGAGAA AGTTCCATC	240
TTATTCCTT ATATGGACT GATCATGTGT GTTGGGGTAG ACTGCTCTG CAGAGTTGG	300
AAGAAGTCAC CAGCAAAGCC GGCCAATCTC GAG	333

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 391 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GAATTCGGCC AAAGAGGCCT AGCTTCTAG ACTGGAAGAA CAAATGAATG GCTTAAAAAC	60
ATCAAATGAA CATCTCAAA AGCATGTGGA GGATCTGTT ACCAAATTAA AAGAGGCCAA	120
GGAACAAACAG GCCAGTATGG AAGAGAAATT CCACAATGAA TTAAATGCC ACATAAAACT	180
TTCTAATTG TACAAGAGTG CCGCTGATGA CTCAGAAGCA AAGAGCAATG AACTAACCG	240
GGCAGTAGAG GAACTACACA AACTTTGAA GGAAGACAAG GAACGCNAGA AAAAAGACGA	300
AGAAAAGGTG AAGGCAGAGG AAGAATCAA GAAAAAGAA GAGGAAGAAA AAAAGAAACA	360
TCAAGAGGAA GAGAGAAAGA AGCAACTCGA G	391

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 339 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GAATTCGGCC AAAGAGGCCT AGCTTCTCTG CTTTATTTAT TCATTTATTT TTAATTTTTT	60
GAGATGAAGT CTCGCTCTGT CATCCAGGCT GGAGTGTGGT AGCGCCATCT CAGCTCACTG	120
CAACTTCCAC CTCCCAGGTT CAAGTGCATT GTCTTTTAA TGTCTATGTG AAGGATTCTG	180
AGCTGTACGA GTTCTGCCCTT AAATCTGAC TTGGGCCTCA GGATCAGGCC GCCTCCCCAT	240
CAATCTGGTG GATGCCAGTT ATAACCTTG CCCTGCACCC CATCCACACT GTAGTTAGA	300
AAAAATCAAC AGTCAGCAAT CATATCACAA GCACTCGAG	339

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 203 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GAATTCGGCC AAAGAGGCCT ACGAGTCAGC ATCTAGACTC AGCTCCTCT TCCCGCCTGC	60
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CCTCACACAT GCGTGCATTG ACTCTCCTGT CCAGGCTCAT GTCCCTGTGC CCCCTTGCTG CTTTGCCTCC TTGCTTGTCT CTGACTTGCT CACCCACTCT CTGTCATTGT CTTGCTTACT CAGGCTCACC CTATCAACTC GAG	120 180 203
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(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GAATTGGCC AAAGAGGCCT AGTTGAATTA TTGCCACATG TTAGGAATGT GGAAGGTTGC TTGGATAAAAT GAGAAAAGAA AGAAAAGAAAT GCAAGTAATG TCCTGCTGGG GTAGTGCAGT CCTCGAG	60 120 127
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(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GAATTGGCC AAAGAGGCCT AGATCCCACG AATTTAGGCT CAGAACATC GCTCCTCTCC AGCCCTGCAG CTATTCCA ATATCAGTC TCGCGGCTCT CCAGGGCTCC CTGCCCTGAC CTCTTCCCTG GGTTTCTGC CCCAGCTCC TCCTTCCCCC CCCCCCTATA TCCCTCGAG	60 120 179
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(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

GAATTGGCC AAAGAGGCCT ACTGGAATCA CTAAACTTTG TCTCATTTC TTTCTCTTCC ATCAAATATC AATTTGGAT TCAGATCCAG TTTTTCTT TCAATTATTT CTGCCTTTA AAATAACT ACCTCCTTCC TCCCACAATT CATTTCAGCT TGTTTAGTT CCTTGGGTTC TATATTTC CTTCTCTAGTA TTACAATATA TGCACAAATA TTAGGTTATA AAACCTCCAA TACAACCTT ACTGCCACTC ACAGGTTTT CAATTGTTT CATTTCATG TACATTTAAA TAATGTATAT ATTAGGGATA CTCGAG	60 120 180 240 300 326
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(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GAATTGGGCC AAAGAGGCCT AAATATGAAA AGCTGTCTAT ATCTACCCAG CCAAACCATC	60
TCCAGCTTTT ACTTTTATTG AGCAAGTATA CGTTATTAT TTAGTCATCC ATTCAATTAT	120
TTACTCATTT ATTTATTTTT TTTTCAGCTT ATTTCTGCTT TCATCTTAAT TCCTCTCTTA	180
AACTTTTGTG TATCACATTG GTTCTCCCTG ACCTCCACCA CTGTAACCTG ACTTAAGTTA	240
AAATGTTAAAT TTATTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT	300
TTTAGGTAGA GAAGATGTCT CACCATGCTG CCCACTCGAG	340

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GAATTGGGCC AAAGAGGCCT ACTTTCTTCC TTATTCTACT TCTCTTTTTT TCTTTTGTTC	60
AACATCATGT TTGTGAAAGT TTCATGCATA TCGTTGCAAG TATTGTATT TCATTCAATT	120
CTATTGTTGT ATAATGTTAC ATTGCATGAA TATGCAGCAA TTTGTTCTAC TGAAAAAGC	180
AATAAGGATT TAGTTATTC CAGGTTGGAC ACAAATAATT TTGCTATGAA GGGTCTCGAG	240

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

GAATTGGGCC AAAGAGGCCT ATAACATATAT AGCCTAGAAC TTTCCCTATT CTGTTATTAA	60
GCCTCTATCA CTATTCTTGT ATTCTAGGTT TTATAATCCA TTCTTTTTA TAACAACCTG	120
TTCTTGTGTTT ACTTTTCCCT ATTTTGTTT TATACCCATC TATTCTTTT TAGGATCTAT	180
TCTCCACTTT TAACTTTGAG GATTCTAAA TACTTACTTT AAAGTTATTT TTAACTTGTT	240
CTATTTTGTT TTTTGTCAAG AGCGAACATTG CCTTTTTAT TTGGCTGTTC TACCATGCTT	300
TTTGGAAATT TGTTTGTAG GCTTCTCGAG	330

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GAATTCTGCC	TTCATGGCCT	ACTCTACTCC	AACTAGGAAA	AGGCCAGGAG	GTCCTGTTAA	50
AGGATGCACT	CAGAGCCCGG	GCTCCCTAAC	GTATGAGAGT	GCTAACCCAGC	AGGTGTAGAC	120
TTTCAGGAG	TGAAGAATGA	CCCAGGCATT	CCAAACCTGG	ACCTTCATCA	CCTTTGTTT	180
CATCTCAAGA	CAATTCTGAG	GGACTGTTTT	GGAGCGTGTG	TGGAAGGTGA	ACGTTGAAGA	240
AGAGTGTGGG	CTTGATGTG	ACTCAGTTGA	ATACTCGAG			279

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GAATTCTCAT	GAAACTCTCA	GCGGAAAGCT	ACAAGGAAAC	ACAGATGGTG	AAGATTAAG	60
AGGAACCCAT	GGAGGTTGAC	ATCCAGGACT	CCCATGTCTC	GATATCACCC	AGCCGGAATG	120
TTGGCTACAG	CACTTTAAC	GGGGAGAGA	AAACCGAAC	CTTACAGAAG	ATCCCAGAGG	180
GCAGAGTACC	CCCAGAGAGA	AACCTCTCA	GTCAGGATAT	CTCTGTGAAA	ATGGCTTCGG	240
AGCTCCTCTT	TCAACTGTCA	AAAAAAAGTGA	GCAAAGAGCA	CAATCATACA	AAAGAAAACA	300
CCATCCGGAC	CAATCTCGAG					320

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GAATTCTGCC	TTCATGGCCT	AGAGCAACAT	AGTGAGACCT	CATCTCTACA	AAAAATAAAAG	60
AGAAAATTAG	TTGGGGGTGG	TGGCGTGCAC	CTATAGTCCC	AGCTACTCAG	GAGGTTGAGG	120
TGGGAGGATC	ACTTGAGCCC	AGGAGTTTG	GGCTGCAGTG	AGCTGTGGTC	ATGCCACTGC	180
ACTCTAGCCT	GAGTGACAGA	GCAAGATCCT	GTCTCAAAAA	ATAAAAGAAA	ATAAAATAAT	240
CAGTCACCAA	CAGTGATTTG	TCTTCAAGCT	GCCCTCCTCT	TGGCTCTCA	AGGCAGTTG	300
TGAAGTGTCT	AGGATAGGAA	TTTCCAGAA	GGGCTTGCTC	GAG		343

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GGAAGATGTG	CCAAAGTTCA	AAAAACATAA	TCTTATCTGA	TCAGATTAAA	GATCACAACT	60
CCAGTGAAGC	CAGATTTCT	TCAAAGAATA	TTAAGGATT	GCGATTAGCA	TCAGATAATG	120
TAAGCATTGA	TCAGTTTTG	AGAAAAAGAC	ATGAACTGA	ATCTGTTAGT	TCTGATGTTA	180
GGGAGCAAGG	CAGTATTCA	TTGGAACCTC	TGACTCCATC	CGAGGTACTT	GAGTATGAAG	240
CCACAGAGAT	TCTTCAGAAA	GGTAGTGCTG	ATCCTTCAGC	CAAGACTGAT	GAAGTAGTGT	300
CTGATCAAAC	AGATGACATT	CCTGGAGGAA	ATAACCCNA	CACTCTCGAG		350

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 442 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GAATTCGGCC	TTCATGGCCT	ACTCGCCGTC	TGTTAGTAGT	ATAGTGATGC	CAGCAGCTAG	60
GAATGGGAGA	GATAGGAGAA	GTAGGACTGC	TGTGATTAGG	ACGGATCAGA	CGAACAGGGG	120
CGTTTGGTAT	TGGGTTATGG	CAGGGGGTTT	TATATTGATA	ATTGTTGTGA	TGAATTGAT	180
GGCCCCTAAG	ATAGAGGAGA	CACCTGCTAG	GTGTAAGGAG	AAGATGGTTA	GGTCTACGGA	240
GGCTCCAGGG	TGGGATGAGC	GGGCCAAGAT	CGATGATCCC	ACAGACTCCA	AGCCTGAGGA	300
CTGGGACAAG	CCCGGACCAT	TCCCTGACCC	TGATGCTAAG	AAGCCCCAGG	ACTGGGATGA	360
AGAGATGGAC	GGAGAGTGGG	AACCCCCAGT	GATTCAAAAC	CCTGAGTACA	AGGGTGAGTG	420
GAAGCCCCGG	CAGCGTCTCG	AG				442

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 272 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GAATTCGGCC	TTCATGGCCT	ACAGAAAGTA	AGTTGGAAACC	ATGTAAGAAA	AAAAGACACA	60
AATAAAACTA	GGAAAGTGGC	ATGGAGCTAG	GGCTGAAGTT	GCTGCTCAGT	TTACATGTAT	120
GAAGTTCTGT	GTGGACTTAA	GCTCCTACTT	CAGTCATTAA	TTGTATGACT	TGGACAAGTT	180
GCCAAACATC	TCTAATATTC	ATTCATATT	GTAGGGTAAA	AGGATGAGTA	ATATGTATCT	240
TTAGTGATA	AAACATTTAC	AGACAACTCG	AG			272

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 290 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

GAATTCCGCC	TTCATGGCCT	AAGACACCAAG	CGAGCCCCAGG	CAGGTAATGG	AAGCAACTGT	60
AGCTGACTGG	ACCTAAGAACG	CAGTGGCAGC	GGTGCCAGGC	ACCCCAAGCTG	ACCTGCCTTG	120
GTGCTCAGAG	CAGCAGGGCT	GGCCATGGTC	AGGGAGTCTG	GGGAGGTCAT	GCTCTGTCCA	180
CAGGGTTCTA	GCCAGCTTCT	CCAAATTCT	CTCTTTTTTC	TCAAGAGAACG	CTGGGAAGGC	240
CAGTTGTGGT	GTCTCATACC	TGCAATCATA	GCACATATGGG	AGGACTCGAG		290

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GAATTCCGCC	TTCATGGCCT	ATGAAAATTT	GGAAGAACGAA	TCCAATGAAA	GTGGTAGCCC	60
TTTGACCCCT	GTTCGGAAAG	TTGAAACCTAA	TCTCTAACGA	TAACCCAGAG	GAACATGTAC	120
TGAAGGTAAT	TCCTGAGGAT	GCCTCAGAAC	CTGAGGAGAA	CCTAGACCAA	AAAGAGGATG	180
GTTCAAAATA	CGAAACTATT	CATTGACTG	AGGAACCAAC	CAAACAAATG	CACAATGCAT	240
CTGATAGTGA	GGTTGACCAA	GACGATGTTG	TTGAGTGGAA	AGACGGTGCT	TCTCCATCTG	300
AGAGTGGGCC	TGGATCCCAA	CTCGAG				326

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GAATTCCGCC	TTCATGGCCT	ATGGCAATGG	TGGCGTGGT	GCTGGTGGG	ATGNGGTCTT	60
CATCCTCTTC	CTCCAGGAAG	GATGCCCTCG	GGATATGGCT	GAAGGCTCT	GGGTGCAGCC	120
TGGCCAGTTT	CCCTTCAGC	GTCCGTATAC	GGCGGAAGAT	GATGTCAGG	TCCCGTTCA	180
TCTCTACTAG	GGTCTCGTG	TGGTCAGGA	AGCGTTCGCT	CATCTGCTGC	AGGCAGGCAT	240
TGGACAGGTT	GTGAAAGTTG	AGCAGCATCT	CATTGGTCTT	CTCAAAGCGG	TCCAGCATGT	300
TCTCTGGGA	CAGGATGATG	GGCTTGACAT	CATCTGTGTT	CACCATGCTC	AGGATGCGGC	360
CGCAGAAGAC	CCTCGAG					377

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GAATTCCGCC	TTCATGGCCT	ACATGACACC	ACCTGAACGT	CTCTTCTCTCC	CAAGGGTGTG	60
TGGCACCAACC	CTACACCTCC	TCCTTCTGGG	GCTGCTGCTG	GTTCTGCTGC	CTGGGGCCCA	120

GGGGCTCCCT	GGTGTGGCC	TGACACCTTC	AGCTGCCAG	ACTGCCGTC	AGCACCCCAA	180
GATGCATCTT	GCCCACAGCA	ACCTCAAACC	TGCTCTCAC	CTCATTGGAG	ACCCAGCAA	240
GCAGAACTCA	CTGCTCTGGA	GAGCAAACAC	GGACCGTGCC	TTCCCTCCAGG	ATGGTTCTC	300
CTTGAGCAAC	AATTCTCTCC	TGGTCCCCAC	CAGTGGCATC	TACTTCGTCT	ACTCCCAGGT	360
GGTCTTCTCT	GGGAAAGCCT	ACTCTCCAA	GGCCACCTCC	TCCCCACTCT	ACCTGGCCCA	420
TGAGGTCCAG	CTCTTCTCCT	CCCAGTACCC	CTTCCATGTG	CCTCTCCTCA	GCTCCCAGAA	480
GATGGTGTAT	CCAGGGCTGC	AGGAACCCCTG	GCTGCACTCG	ATGTACCCAG	GGGCTGCGTT	540
CCAGCTCACC	CAGGGAGACC	AGCTATCCAC	CCACACAGAT	GGCATCCCC	ACGCACTCGA	600
G						601

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GAATTCCGCC	TTCATGGCCT	ATTTTTTTTT	TTTTTATCAA	AAGTTGTTT	TATTTCAAT	60
ACAAGATAAA	TACCATGCTT	GTTA	CTAGTG	CAGTTCTCGA	G	101

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GAATTCCGCC	TTCATGGCCT	ACAGAATTGG	AGGCATGATG	AAGACTCTGC	TGCTGTTGT	60
GGGGCTGCTG	CTGACCTGGG	AGAGTGGCA	GGTCCTGGG	GACCAGACGG	TCTCAGACAA	120
TGAGCTCCAG	GAAATGTCCA	ATCAGGAAAG	TAAGTACCTC	AATAAGGAAA	TTCAAAATGC	180
TGTCAACGGG	GTGAAACAGA	TAAAGACTCT	CATAGAAAAA	ACAAACGAAG	AGCGCAAGAC	240
ACTGCTCAGC	AACCTAGAAG	AAGCCAAGAA	GAAGAAAGAG	GATGCCCTAA	ATGAGACCAG	300
GGAATCAGAG	ACAAAGCTGA	AGGAGCTCCC	AGGAGTGTC	AATGAGACCA	TGATGGCCCT	360
CTGGGAAGAG	TGTAAGCCCT	GCCTGAAACA	GACCTGCATG	AAGTTCTACG	CACCGCGTCTG	420
CAGAAGTGGC	TCAGGCCCTGG	TTGGCCGCCA	GCTTGAGGAG	TTCCTGAACC	AGAGCTCGCC	480
CTTCTACTTC	TGGATGAATG	GTGACACTCG	AG			512

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GAATTCCGCC	TTCATGGCCT	AAATTATTA	AGGTGACAGT	ACACAGGAAA	CATTACAATT	60
GAACAATGCC	TCAGCTATA	ATTACATCA	GATTATTGGG	TGCCTATTTG	TTCATCATT	120
CTCGTGTCA	AGGACAGAAT	CTGGATAGTA	TGCTTCATGG	CACTGGGATG	AAATCAGACT	180
CCGACCAGAA	AAAGTCAGAA	AATGGAGTAA	CCTTAGCACC	AGAGGATACC	TTGCCTTTT	240
TAAAGTGCTA	TTGCTCAGGG	CACTGTCCAG	ATGATGCTAT	TAATAACACA	TGCATAACTA	300
ATGGACATTG	CTTGCACATC	ATAGAAGAAG	ATGACCAGGG	AGAAACCACA	TTAGCTTCAG	360
GGTGTATGAA	ATATGAAGGA	TCTGATTTC	AGTGAAAGA	TTCTCCAAA	GCCCAGCTAC	420
GCCGGACAA	AGAATGTTGT	CGGACCAATT	TATGTAACCA	GTATTTGCAA	CCCACACCGC	480
TCGAG						485

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

GAATTCCGCC	TTCATGGCCT	ACACACATTG	TGAGCTGTAT	ACGTTAACCC	AAACTCTGCA	60
TTCAAAGTGG	AATTATAACT	GGGCAGTGAA	TGAGTTGCTC	AGTCCCATCTA	TTAACCCATAC	120
TCTTTTAGGC	TTTTTATTGC	CTCTAATTGT	TGTAATAATT	AACATTTCC	CAGGAAGTTG	180
TTTACAGAA	GAAGGGGCCT	TAGCGGCTTT	CAACTCTTTA	GAGATAAGTT	CAACTTTGTG	240
GATTGACAC	AGCACATCTT	GTTAGTAGT	GAGCGGGAGC	CATATGAATC	CTCTAGAGAC	300
ACAGCCGTGT	CTGAGATGGA	CATTGCCAAC	ACAGCTCGAG			340

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

TTCGGNCTTC	ATGGCCTACT	CTCATAAAA	TATTCAAAGA	TCAACCCAA	ACGTGCCTGC	60
ANTTGGACA	ATGTNAGCTA	AAGCTATAAA	TSGAACAGCA	GTGGTCATGG	ATGATAAAGA	120
TCAATTATT	CACCCAATT	CAGAGTCTGA	TGTGAATGCT	ACACAGGGAG	AAAATCAGCC	180
AGATCTAGAG	GATCTGAAGA	TCAAATAAT	GCTGGGAATC	TCGTTGANGA	CCCTCCCTCCT	240
CTTTGTGGTC	CNTCTGGCA	TTCTGTAGTG	CTACACTGTA	CAAACGTAGG	CATCTGAGTT	300
ATAAAAGTTG	TGAGAGTCAG	TACTCTGTCA	ACCCAGAGCT	GGCCACCGATG	TCTTACTTTTC	360
ATCCATCAGA	AGGTGTTTCA	GATACATCCT	TTTCCAAGAG	TGCAGAGAGC	AGCACATTTT	420
TGGGTACCCAC	TTCTTCAGAT	ATGAGAAGAT	CAGGCACAAG	AACATCAGAA	TCTAAGATAA	480
TGACGGATAT	CATTCCATA	GGCTCAGATA	ATGAGATGCA	TGAAACACTC	GAG	533

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

GAATTCCGGCC	AAAGAGGCCT	AGAAAATAGA	AAATCAGGTA	GCTATGTCAT	TTTATAAGCA	60
TCAGTCCTCA	CCAGATTGT	CAAGTGAAGA	AACTGAAACA	AAAAAGGAAA	TTAAAAGGAA	120
AGCTGAAGTT	AAGAAAACCA	AAGCAGGAAA	CACCAAAGAA	GCAGTGGTTC	ACCTGAGAAA	180
GAGCACAAGA	AACACAAGTA	ATATTCCAGT	GATTTTGAA	CCTGAAACTG	AAGAAAGTGA	240
AACAGAAAAG	GAAATTAAAA	GGAAAGCTGA	AGTTAAGAAA	ACCAAAGCAG	GAAACACCAA	300
AGAACGACTG	GTTCACCTGA	AAAAGAGCAC	AAGAAACACC	CTCGAG		346

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GAATTCCGCC	AAAGAGGCCT	AGGCAGGTAT	TCTTTGCTTT	GGGAAATTCT	TCTTTCTGTC	60
CTCCCTTCCC	TCACCTTTTC	CAAATTCTGG	GCACAAACAGC	AGCTCTCTCT	CTTCTGTGGC	120
AGGTGTGCAT	CCTATTGGCT	GGCTGGTATT	TCTTGTTTTT	TTTCCCCCTT	ATTCTTTTTA	180
AATGGGGGTG	GGGGTATAAA	AATATGTGA	TGGGGTACAT	GCAATAATGT	TGTAATGTTT	240
CTTGTGTTT	AATGGATAAT	TAATTGCAAA	ATAATTGTTT	TAATTATAAC	ATGTTTGAGT	300
AAATGCTAAA	TTAGTATTTT	TTTCTAATAT	AAATAATGAAT	TTGAATCTA	GCATTCCTGT	360
AACAATGTGT	CTATGTTGT	CTGCTCTGT	CTGTCTAATA	GTAATTATAA	TCTGTGGTCC	420
GCACCCACTC	GAG					433

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GAATTCCGCC	AAAGAGGCCT	AAGCAAAGCT	TAGCTTACCG	GGAAAAAAAA	AAAAAAAAAA	60
AAAGTAGAGCT	TNCCTTGAAT	CTGGAGAAAT	TAAGCACACA	GGTGTCTGC	AATATTAGTT	120
AAGAGACTAC	TGCACCCATC	ATACTGTAGC	TTAACAGACT	TTCTTCTTTT	AGTTTTTTCT	180
AAAATGTCTC	CATGTCTGTG	TTATGCCACA	AAATAACACAG	CCTTGGTTAA	CTTTGGACT	240
AAAAAAATC	AACTTATTGG	CCAAGCATGG	TGGCTTACAC	CTATGATTGT	AGCACTTTGG	300
ATAGGTCTCG	AG					312

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GAATTCCGCC AAAGAGGCCT AATTTCTAA ACTGTGTGCT GCCTTTGGG TTAATTAGAA	60
TTGTAGCATT TCGTTTGAT TATTTTTTG GCTCTTAGC TGTTCTCTCA CATTTTTAA	120
AATGCTAATG CTAGGGATTA TAATATGCTA CTTAAATGTA TCAAAGTCTG TTTTTACTAC	180
TTCGTGTAAA ATAAACGAAC CTTCATTTA TAGTTACATT TATTCCCTCTC ATCTCGAG	238

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GAATTCCGCC AAAGAGGCCT ACTCAAAAGT AGATGAGCAA TTGGTCAGAA TTGTTAGAGG	60
ATATTATTTG AGCTAAATGT TTCTCTCTC TGTTTCAGTG CTGTATGTGC AAGTGTGTGT	120
ATATGTTTT TGTTGGGAC AGTTTCAGGT AGATGGTATG AAGAGGCAGC AGGAGACTCT	180
CGAG.	184

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

GAATTCCGCC TTCATGGCCT AATTTCTAA AACCTGGAGA CAAACCACAT AAATACAAAA	60
CAAGTCTGCT TCTTCAAAAT TCTGCTGGTG AGAACTCAGA TATCAGTGAT CTTATTAGCT	120
TTTCACAAG CCAGAACATA ATGGTGACGA TGATTAATGA CAGTGAAT GTATCCGTGG	180
CTCCCCATAG TCGGCTTTA AATGTTGATGC ATTCAAGAAA GGACTATGTT TTGCAAGCTG	240
TTTTCAACAG TACTATGGTT TATTCTTAC CTATATTAGT GAATATCATT AGTAACACT	300
ATCTTTATCA TTAAATGTG ACTGAAACCA TCCAGCTCGA G	341

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

GAATTATGCT GTGCTGTTT CCTGGACACT CAGAAATCAA CAGGCCTTCC ACCCCATCCC	60
ATCATGTTGA ATTACAAAAGT ATTTTGACCA TCGTTTGTT TGTTCTTTC CACCCATACC	120
TGTGTAGGGC AGCGGTAGCA GTCTTCAACA ATGCATCCTC TTGGACAATG CATTGTAATA	180

TCTCTCTTTC AAATTCTGTT TCACATAGTC ATTTCTCATG TTCTGTTGGA GACCCCCAAA	240
AAATTCATTC CACACTGTCA TCCCTTGTC CTAACCAGAA TCTCGAG	287

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

GAATTCCGGCC TTCATGGCCT AATGTATGGT AGACAATTAA TTTTTAAGAC ACAGAGATAA	60
ACGTTTCTC GCTTGGTTA CCTTTCTTCCCCTTTAAA AGGAATTAGC TATAGAACTG	120
CTTTGTAAAG ATGCTTCTTG ATATTTACT TTTGTTCCCTT TTCCCTAATC ATTCCCTTT	180
CACCCCACTC CT CGAG	196

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

GAATTCCGGCC TTCATGGCCT AGTGATTGGG TGCAGAGGAA ACAGGAACCA GAGAAGGGTC	60
ATCTCAAGCTG CCTGTCCCAC TCCCTATGCT TGGTGTACCG TGCGCCATAG TCTCGAG	117

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GAATTCCGGCC TTCATGGCCT AGTAAGTGCT CTGAGTATAT TAGGAAAAGG AAATCTTATA	60
CATAAAAATC AAAGCTGTTG CTAATTTTC CACTAGTGAG TCAGTCTATT AACATTACTC	120
ATGGTAGGTT TTGCCATACA GAATTTTAAT TTTTTATAT TATTTTGCGC TTGTTATTA	180
TGCTTAGAAG TCCATGGGAA CCCAAAGATC AGAAAAGATT CATCTGTACT CGAG	234

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

GAATTCTGGCC	TTCATGGCCT	ACGAAACGAA	CATTGGCTCG	GCGGTGGTGA	TGCTAATTCC	60
CACTGTCATG	TTCACAGTGA	TGGCCGCTT	TTCCTTCATC	GCCCTCAGCA	TGGTTCATAA	120
ATTTTACCGG	GGAAAGTGGGG	GGAGTTTCAG	CAAAGCTAG	GAGGAGTGGGA	CCACAGGGGC	180
CTGGAAGAAT	CCACATGTGC	ACCAGCCAGC	CCAGAACGCA	GCCATGGGGG	CAGCCCAGGG	240
TGCCATGAAT	CAGCCAAGAC	TCGAG				265

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GAATTTCGCCA	CACCATGAAG	CTCTTGTGGC	AGGTAACTGT	GCACCACAC	ACCTGGAATG	60
CCATCCCTGCT	CCCGTTGTC	TACCTCACGG	CGCAAGTGTG	GATTCTGTGT	GCAGCCATCG	120
CTGCTGCCGC	CTCAGCCGGG	CCCCAGAACT	GCCCCCTCCGT	CTGCTCGTGC	AGTAACCAGT	180
TCAGCAAGGT	GGTGTCACG	CGCCGGGGCC	TCTCCGAGGT	CCCGCAGGGT	ATTCCCTCGA	240
ACACCCGGTT	CCTCGAG					257

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

GAATTCTGGCC	TTCATGGCCT	AGGAAAGATT	CGTGTGTTAC	TTTAATAAAC	CTGAAAGAAC	60
TGTCGTTTTT	CACTGCCTAT	AGGACCACTA	CAAAGCCCA	AAGAAAAATT	AGACTTGTTT	120
CATTTTATAA	CAACACAAC	TGCTACTACT	GCTACTAGTT	AGATACCGTT	TGCTCATTTA	180
TAACAATCTC	AGTTGGTAGG	ATGAAGCTTA	AACACTTGGC	ATTCATCGTC	TTTTCAAGTC	240
CTCTCGAG						248

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

GAATTCCGCC TTCATGGCCT ACTGCTTTT CATGCAGATT TCATATTGTC TTTGTCCCTT	60
TCATTGCTTC TTGACCTTCC TGGCAGGTGT CGCTCAGTTT CTTCCCTGTT CCTTCCCTGT	120
CCTCTCCACA CCTGCTATCC CGTCCCACTC CCATCTACCT CCCGGGAAGC CAGCCCTGCA	180
TGCTGAGTT GTGACCTGCT TCATTCCCAT TTCATTCTA GAGGGTTTAG AGGTGACCTG	240
GAACCGTTC CTTTCCCTCT CCTACCCCCC CCTCTGCAAC ACCAAGAGGC CTGGAGGGGC	300
AGACAGAAAG CAGCCAGCCA CGGGCGGAAG TCTCGAG	337

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 253 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GAATTCCGCC TTCATGGCCT AACTTATTTT TTTTGTTGAT TGCCTGTC TTCTTTTCTT	60
TCTTCCCTC CCTCCCTCCT TCCCTTCCT CTTCCCTCT GTAGAGATGA GGTTTCACCA	120
TGTGGCCAGG TTGGTCCCTGA GCTTAAGTGG TCCTCGCACC TCAGCCTGGC AAACGTGCTGG	180
GATTACAGGT GTGGGCCATC ACGGCTGGCC TTACAGTAAA TTCTTGATAA ACAACCCAGC	240
AACACACCTC GAG	253

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 319 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

GAATTCCGCC TTCATGGCCT AGGACGGGGG ACTCAGGTTACACTGGAA CCTGGGGTCA	60
TGTATCATGT ACCAGGTGGG GAGAAGTGTG GCAAATCTCA GTGCCATTG GAGGGGAAGC	120
CAGTCATTCC AGGAGAAGAG CTGAGGGAA AGAGCTGTTG ACTTTCATAA TGCACTTAA	180
ATTATCCAGT CACCCCTCCTG CCACATGGCA GAAGCCAGGT GGCACTGATG GTGGTGGGG	240
AAACAAAACA CACAGTCTCT GGCAAGCCCC ACCGGGAAAG GAGGGCTCAG AAGCCGTAGC	300
GGGTCCGGAT ATCCTCGAG	319

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 348 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GAATTCCGCC TTCATGGCCT ACAATAAAAG CCCATAGGGA AGAGAGAGAG GATATAGGGA	60
AACAGAACATCA GATGTGTAAT ATACTTGGCA CAGCGAAAAA ATGGATTAA AAGACAAAAAA	120
TGGAGGTCCA GGTAGATGTA ATTACACACAG ACTGAAAGTG AGTCGGGCT TGTGTAAAAC	180

ACATGAGATT GGATTGACC CCTTGGCTCT CAAGTGTCCC CTTAGATCTA GAACTGCTCC	240
TTGGTGGCCA TTAGATCGAG TCAGTTTGAG TCTGCATCAC TTAGTTATTG GGAATTTCCTT	300
TGTTGGAAAC AGGAAAATTT TTTAGATTA TTTGGCGTAC GGCTCGAG	348

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

GAATTCCGCC TTCATGGCCT AGGCACAGTG AAACCCGTGG AAATTCAAAG GTGAGCAGGA	60
CAGTGGGTCC TGTATCTTGA TCTTTACGGA TCTTTCTCTT CTTGAATCCT CACACGCC	120
ATTTTATAAGA CAGGAAGACT GAGGCCGAA AGTTCTGTCT GACTCTGAGC CTGGCCTCTT	180
TGCTGCCTCC CGTTGTCCTG TGAGGCTGTG TGGTCACAGC ACCCAGGACT TGAGAGGAGT	240
GAAGTTCTTC CTCACCCCGC AAAGGCTTCA TGAGCCCTAC TGTGTGCCAG GCCAGCCCTG	300
CTCAGTCTGG GGCGATAAAC ACAGGGCAGA TTCTGAAAGC CTGTGTGAGG GAAGTTCTAG	360
GCCTGCAGGA CCTGAGAGGA GACCCCTGGAG AGGAAGGGAG TCAGGGCCAG CTTCCCTCGAG	420

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

GAATTCCGCC TTCATGCCTA AGCTGATGGA GACTGTAAT GAACCAAGAAA CAGGTGAAGT	60
GAGCAAAGAT GCAGTCATTG TAAAGCAGGA GAAAAATAAT GAATATTGCC TTCAGGGATAT	120
TGATGATAAA TTGTCAGAAT CAGCAGAGGA TGATGGTGAAT GATGATACCA ATGATGAAGA	180
TGATGATGAA GATAGTAACC CTAAAAAGAA TACTCAGGCC CCACTAGAGT TAATGGCAGA	240
ATTTCTGAGA GCAGAAATGG CCCGAGAGTA CCAGCTGGCA AAAAATTAT GTCAGATGAT	300
CCTAACATCTAT GAACCAAGAAA ATCCTGAGGC CAAGGAGTTT TTCACACTTA TTGAAGAAAT	360
GTTGCTGATG GAGAAAATCTC AGAATCATGA GCAAGACGGT GAAAACAGTG ATGAAGACAG	420
CAGCGGGCTC GAG	433

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

GAATTCCGCC TTCATGGTCT ACAAAATCAA CTGCAAGCAG CCATCATCAG TTTGGAAGAA	60
GCTTTGGAA GCCTCTCAAAG AAAAACCTCG GTATCCACCA AGTCAGGCTC AAGCAGCTCT	120

TCAAGACACT CCCCTGAAG ACTACTCCTA TAAGAAATCA ATAAGAAACC TGTAAAAAA	180
CATTCCCTTT GTCCTCTGT TGATCACTTA TGGTATCATG ACTGCTGCCT TTTATTCAGT	240
CTCAACGTTA TAAATCAA TGATATTGAC ACAACTCGAG	280

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

GAATTCCGCC TTCATGGCCT ACGCGAGCGG CAGGTGTGCA CAGGAGGTT TCACCTTGT	60
NCTCTGAACG CGCGGTCAGG ATGGTTTCT CTGTCAGGCA GTGTGCCAT GTTGGCAGAA	120
CTGAAGAAGT TTAACTGACG TTCAAGATAT TCCTTGTAT CATTTGTCTT CATGTCGTT	180
TGGTAACATC CCTGGAAGAA GATACTGATA ATTCCAGTT GTCACCCACCA CCTGCTAAAT	240
TATCTGTTGT CAGTTTGCC CCCTCCTCCA ATGGTACTCC AGAGGTTGAA ACAACAAGCC	300
TCAATGATGT TACTTAAAGC TTACTCCCTT CAAACGAAAC AGAAAAAAACT AAAATCACTA	360
TAGTAAAAAC CTTCAATGCA TCAGCGTCA ATCTCGAG	398

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 403 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GAATTCCGCC TTCATGGCCT AGGGCGATGG TGGGCAGAGG ATCCTTAGTG CTCAGTCGGG	60
CTCCACCAGA ACCACGGACT TGAAGGAGAA GAGACTCTCG GTTCCAGGTA GCAGAAAACG	120
TGGACTTTG GACACAGATC CTCCCTGGCA GAGAAGGATG CTTGAGAACATC TGAGATTTAC	180
ACAGCTGTAT TAGGTTGTCC ACGATGACCC GGCAGTAGGT CTCTCTCTTG GGGATTTCCCT	240
CAGTGGTCTG CCAGAGACGG GCGTGAGAGA TCACATTCTAG AACGCACTCG TCTTGGTTCT	300
CTATGGTTT CCTTGGATCA TCAACAAGGC TAAGCACTTT CTCGGGAAGG CCTTCTATTAA	360
ACTTGGCTT GGTGAGCCAG AGGGCTGCT TTACACCTTC GAG	403

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

GAATTCCGCC TTCATGGCCT ACTCCATTT TCGAATGGCT TATTTAGGCC CAGCTCTTGC	60
GTTTGATTC TCCCTTCAGG CCCAGAACTT TCTCACGTCA TCGTCACCAAG GCCTAGCTTC	120
TGCATCTGGT CAGCCTTTA AGGCCCAGCT TTTGCCTCAT AAACTCAGCT CCTGTTAAT	180

GGCGGCCTCC CGGGTCCCAC TCGAG

205

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

```
GAATTCCGCC AAAGAGGCCT AGTTTATTA CTTTGGTTAA GACATCAGTT ATTTTAGTCT
TTGATAATTC ATTATCTAGA TAATGGTTAC TTTGTATTGT CTGTTCTCG AG
```

60
112

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

```
GAATTCCGCC AAAGAGGCCT ACACAGAGCC CTTCAGTACT TTTAATTCTT CTTAAATTGG
TGGTTCATGT TAATTAATT ATTATTATTT TTTTTGAGA CGGAACTCGA G
```

60
111

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

```
GAATTCCGCC AAAGAGGCCT AAAGATGTTT TCCATGAGGA TCGTCTGCCT GGTCCTAACGT
GTGGTGGCA CAGCATGGAC TGCAGATAGT GGTGAAGGTG ACTTTCTAGC TGAAGGAGGA
GGCGTGCCTG CCCCAAGGGT TGTGAAAGA CATCAATCTG CCTGCAAAGA TTCAGACTGG
CCCTTCCTGCT CTGATGAAGA CTGGAACCTAC AAATGCCCTT CTGGCTGCAG GATGAAAGGG
TTGATTGATG AAGTCAATCA AGATTTACA AACAGAATAA ATAAGCTAA AAATTCACTA
TTTGAATATC AGAAGAATCT CGAG
```

60
120
180
240
300
324

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GAATTCGGCC AAAGAGGCCT AGGTCCAGAA ACATTTAAAA AAAAAAAAAA GGGGGCTTGA	60
GAAAAGGGCT TCCAGTGCCA GGCAAGAAATA TGTTTTCTT AATAGGGC	108

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

GAATTCGGCC AAAGAGGCCT ATGAAACGT GGATTTGCTT TGTAAACTTG AGAATACATT	60
TTGTTGCCAA CAAAAAGAGA GAAGAGAAGA GGAAGATATT GAAGAGAAGA AATCGATTAA	120
GAAAAAAATT AAAGAACTTA AGTTTTAGA TTCTAAAATT GCCCAGAACCC TTTGTAAGTA	180
TCATATTCCA ATACCATTCA AAGACAGTGG AAATATTTCT TTAAATGATT TCATTTCCTT	240
TAAGACCGAT TATTCTATTAT TTGCTATTTT CATTGGTTA TTATATGCAT GATAAATTCA	300
CAGATACTCT CGAG	314

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GAATTCGGCC AAAGAGGCCT AGGGTAAGAC TAGAGTGTAAATCATCA ATAAAAAGTG	60
GAGAAAACAA AGGTATTCA CGGATTGAAT TCTAGACCTG CCTCGAGCCC TGCCCTTCCT	120
TTACTTTTAC TTTTTTTTTT TTTTTCTTTG GAAGAGAGAA GAACAGAGTG TTCGATTNTG	180
CCCTATTAT GTTTNTANTC GGGAACAAAC GTTGGTTGTG TGTGTGTGTG TTTTCTTGTG	240
TTGGTTTTAAAGAAATGG GNAGAAGAAA AAAAAAAATT CCGCCCCCTT TCCTCGATCT	300
CGCTCCCCCC TTCGGTTCTT TCGACCGGTC CCCCTCAAC CTGCCTCGAG	350

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

GAATTCGGCC AAAGAGGCCT AGAGAGTCTG GATGACAAGC AAAGCTCAAT CTCAAAACAA	60
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TAATTTTAA AGTAATGATT ATCTTAACCA TTCTTAAATC CTTCTGTCTA GTAGGAATCT 120
TATTCATGGG AGTGTCTGGA AAAGGGACAA AGAGCGGCTA TCTCGAG 167

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

GAATTCGGCC AAAGAGGCCT AGTGTTCAC AAAAGAATTG GAAACCATAG TCCTGAACTC 60
TCCCTAACTA CTATAAGCTT TAAATAGCAC TCAATCCATA TTAAGTCTTC TTAGTGTAGC 120
ATGGTTGCTC TCATGCGTCT TTCTTATGTT TAAATGGTG TAAATTTAG TCGTTGTCA 180
TTCAGAAGTG GCTTGCAAA TACAAAATAT CTCGAG 216

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

TAATCTTAC TGGTAAAAAG GATGGAAAAA TAAATCAACCA AATGCAACCA GTTTGTGAGA 60
AAAAAAAAAAA AAAAAAAANC CGAAAAAAA AAAAAAAACCA CCTGAATGCG GAAGAGCTCG 120
GCTCCCGTTT AGCATTGT ACTTAAGGAA ATAAAAAAACC AACAAAGGAT CTCACATTTT 180
CTTAAAAAGT GAAGATTGCT GTATACTATT TATTCAACTT ATAATTATG TTACTCCTTG 240
ATCTTGCTC TTTGTATGA CAAAGCATTT ATTAAATAAA GTTATGCATT CAGTTCTCGA 300
G 301

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

GAATTCGGCC AAAGAGGCCT AGTCTCTGTT AATCCTACTC TGCTTAGCC AGAATAGCCT 60
AGTATTTAT TTCTATTTA TATATTGAGA TTTCTCTAA CATTCTCTT GATAAAAATC 120
TTCTGCTTT TGAAAGTGG TATGTATCAT ATTATATGTT TTCTGGTGTG TCTCGAG 177

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GAATTCCGGC AAAGAGNCGT AGGGAAAGAT TTCAGCTATT AATCAACTGG AGGAAATTCA	60
AAGCCAGCTG GCTTCTCGG AAATGGATGT CACAAAGCTC TGTGGAGAAA TCGCTATCA	120
GCTGAATAAA ACCAACATGG AGAAGGATGA GGCAGAAAAG GAGCACAGAG AGTTCAAGAGC	180
AAAAACTAAC AGGGATNTTG AAATTAAGA TCAGGAAATA GAGAAATTGA GAATAGAACT	240
GGATGAAAGC AAACAACACT TGGAACAGGA GCAGCAGAAG GCANCCCTGG CCAGAGAGGA	300
GATTCTCGAG	310

(2) INFORMATION FOR SEQ ID NO:147:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 353 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

GGTGGCCTTG GGTCAAGATT CGCACCATGG TGGGCACAAA CCCAGGAGAA CACTTCCTG	60
TAAACGTGTT TTCATGCTGG AGCCAAGGTT TTGACTTGGG TTTGGATTTT TATTTATTTA	120
TTTATTATTA TTATTACCAAG CTTCATCTA AAGGATGTTT TCGAGGAGCA CACAGTTTGT	180
CTGGTGAGGG TAGGCTCTGG GCAGATTTT CTGTGAGTCT CCCCTGCCTG CGGCATCAGG	240
ATCATCCCTG GTGCCCTGTG GTGGCACCAG GTGGCTGCC ACCCACAGGC GTGGCCTTCA	300
CAGTGGGGGC CATCTCAGCC TGGGGTAGCG ATCTGCCTCC GACCTGCCTC GAG	353

(2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 283 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

GGCCTGCATC GCAACAGCCA GGAGGGCCAG GCCACCCAG GCAGGAGGCA GTGGGCTGGC	60
AGCCACCTG GGCACAGAAAG AGCAGACGCA GACAGTGTG GGCAACGAGG GGCTTCTTC	120
ATGGGCCCGC CTGCCCTGTC CCTCCCCCA GGTCCCCACC TTCTAGGGTT AAAGTGCAGC	180
TGGGAGGGAG GAGGCAGGCA GAATTGGGA GCTAGAGAGA GCCCAAGTGA ACCCTGACTG	240
TCCACGCAAG TCCCAGTGTCC TCCTCGTCT GGAGTTCCTC GAG	283

(2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

GAATTCCGGCC	TTCATGGCCT	AGACCTGCCT	CGAGTTCCCT	TTGTTATTT	CCTGCATCTT	60
ACAAACGTTAA	GGCCTTGGTC	CCTGCTAATA	ATAAAATAAT	AATCAACTTT	ATAAAGAGCT	120
TACAATATGC	CAGACTACTGT	ACTAAGTGCT	TTATATTTT	TTTTGGGTG	GGGGGTGGCT	180
GTTGCCAGT	GTCTCGCTCT	GTCACCCAGG	CTGGAGGCCA	GTGGCACAGT	CATGGCTCAC	240
TGCGGCCTTG	ACCTCTGGG	CTCAGGCCTC	CCGCCTCAGC	CTCCCAGGTG	GCTGGGGCTA	300
CGGGCGTGCA	ACATTCTCGA	G				321

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

GAATTCCGGCC	TTCATGGCCT	ACGTAATTCT	GGAAAAGTGA	ATACTTGTGA	AGAGTCGTCT	60
TGAATGATT	TTAATTT	GTAAAAATC	CTGTTCTTAT	ATTCAACAG	TTTCGAATCT	120
AGTATTACCA	TTAGATTGAA	AAAAAGGAA	ATAAATAATA	AACACTTTA	AAAAAAACTCC	180
CCATTCTCTT	ATTCTCACTT	TTAGGAAAG	AGACTGACTA	ATATCTCTG	CCACAAATAC	240
CGATGTTCTT	AAAAATATTT	ATGGGACTGC	TTTTGGCAAC	CAGCCCTATT	TTGTTTTCAT	300
ATCCCTTTT	GCTCCCATCT	TTCCAAACTC	ATAAACTCGA	G		341

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

GAATTCCGGCC	TTCATGGCCT	ACTCGCCTCT	ACTAAAATA	CAAAATTAG	CCAGGCACGC	60
GCCAGGTGT	GCGCACCTGT	ATCCCCAGCT	ACTAGGGAGA	CTGAGGCAGG	AGAATTGCTT	120
GAACCTGAGA	GGTAGAGGTT	GCACATAGCG	CCACTCGCCT	CCAGCCTGGG	CAACAAGAGT	180
GAGACTCTGT	CTCAAAAAAA	TATATAAATA	ATAAAATGAA	AAAAAATAAT	TGTATAACAT	240
CTATACTATA	GCCTCGTAAG	CATTAGCTAC	TTAATATTTT	TGGTATATTT	AATAATTTA	300
ATACAGCATT	TTTGATTACT	AGTGAACATG	AATATTTCC	CATATTGTT	AATTATACTT	360
TCCTCTTACA	GAATTCTGT	TTGTGTCTT	CACCCCTTCAC	TCGAG		405

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

GAATTCCGCC TTCAGGGCTC CTTCTTCCTA GGCTAGTATT TATCCCACCA CATCTGACTC	60
ATTCTCTACT ATCGCTGTT ATTCTCTT GGGTACTAAA TCTGTTGAAC ATGTTGCCAG	120
GCTTACTGCT GGTATTATGG GATAGCATTT GCCTGATGGC AGCTTCTAAA CGAGACTCCG	180
ATGGCACTAA GCAGTTCCA AAAGTTATC TTGCAAGTTC AACCCAATTC GAG	233

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

GAATTCTAGA CCTGCCTCGA GATGTTTTTG TCGTTATTTG AAATCTTTGC TCTTTTATTT	60
TTCAGCTCCC AGATCCTCTC CCTCTCTTAA GCTTCACTG TGTTTGATAT CAAGAATATG	120
AAATGTGAAT TCCACGGACT CGAG	144

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

GAATTCCGCC TTCATGGCCT AGGCAGGAAG GAGGCTGGAA TAAATAAAAAA TAAAAATAGA	60
CAAGTAAGAC AGCATAAATA ATACATTTTT AAACATGTCA ACATTGATAA TACAATGAAG	120
ATTTACCATATA AAAACTATCA TATCTAACCA AGATATGCAA AAGATGCATT CAGTAAGCTG	180
TAACGTTGAG AAATGTAACCT GTGAAATCAG CTCACCACTT CAAGTCACTA GGTTTGCCAC	240
TTGGACCGTC TTGGTTTCAG CGAGCATAGC GAGTGGCTGT AAGAAATTGT CCATGCCACC	300
AATTCCACTG CTACTGCCG AGGTGGTCTC GAG	333

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

GAATTCCGCC TTCATGGCCT AGGAAGTGG AAGGAAGCTGG GTCGCTGCTG GAAGGGAGGG	60
AGGCTGACTC TCTACCCCTC ACCTCTGCAA GGAAGCTGAGG CCTGTAGGGT TGCGGCTGTC	120
ACTGGCTACA GGCAGCATCT TTCTGTAAAA AGCTTTTCAG GCATGAAACC CATTCTGTAA	180
TGGACTGGGC TGTGTTGAAG GTGTTGCTTG GGCCTTGTTG GCCAGGCCTC TCTGGGTCCCC	240

CTCCCTGGCC TTTGCCTTCC TCTCACCTTC TCGAG

275

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GAATTCCGCC TTCATGGCCT AGAGTCATAG GTCAGACCAC	60
TTTCTAGGAG CTGTTCAAGTG	120
ATAAAATCAA TAACAGTGAC TTTTGAGTC AATAGATT TTAAAGTACT TGATTTCTC	180
TTTGATTGG AAACATCTT GTTAGCTTA ATTGAAATGA TCTAAAATAT TTGAAGGATT	240
TTATACTTTA CACAGAGGCA TGTATTTGGA TAATTAGCTT TTATTAACC CAGGCTTCCT	
CGAG	244

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

GCGGATTGAAT TCTAGACCTG CCTGAACCCC ACCCTTCACG TCCTACTTGG GCTGCCAAAG	60
TCATCTCCCC AAAACATGAC TTTTCCTCAG TCACTTTCT TATTAGATTT TATCATATT	120
CACATCCCTT CCCTGGCCCT CAAGGGTGCCT TGTAACCTAG AACCATCTTA CCTTCCACC	180
CTTGTTCACA AACCTTCCGC TTTACTTACA CATGCCTTCC CATTTCCTC CCGACCCACC	240
CCCCCTCGAG	249

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

GAATTCCGCC TTCATGGCCT AGAAAAAAC AAGTAGTTG GCAAGGAGAG CAGAAAATA	60
AAATTCCTA GTGTAGGCAT TTGGAGATT AGCAAGAGCA ACCTAGAGTC TGCCCCCAGA	120
GACACTGCCAC GTTGTCTG ACACAGAGGA TGCACATAATT CTATTCCTG TGCCACCTGA	180
AAAAATCATTA ATTGAGAAG AGAAACTGTT AGGCCATTTC TAGTGAACTA TTTTCCAAA	240
CCCTCACCGGA ACCCTGAACA GGGCGTGTCT CGAG	274

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

GAATTCCGCC	TTCATGGCCT	AAGCTTGCTC	ACTCTTCTGT	GTGTTGAAA	TAATGGTAA	60
ATACAATAAT	ATTGTCAGC	ACAGTGGATC	GGAGATTTTT	CTTCTCAGGA	CTATTCTGCT	120
TATAGGTCTA	CTTCCTATAG	CTATTTGTCA	TTGCTCTCCT	GGTCCTCTC	TTTCTCTCTC	180
TCCCTGTGCTA	GATGCTCTCT	CTTCTCTATCC	CTCCCTCTCT	TCCCACCCCC	ACCTCCCACT	240
TCTCTGTTA	TATCCTGATT	TTGGTGGAAC	ACATCCTCCA	GGCTCCCTGG	CACTCGAG	298

(2) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

ATGGCCTAAG	GTGCCCNAGC	TTGCCAATT	ATTCCAGTA	GAAATTTTTA	AATGTTAAAG	60
ACAGTAATT	AAAAAAA	AAAACCACAC	TGTTTGACA	TTTACCTCG	TGTTTGTTG	120
GTGACTAGAT	TATGCACTAG	AATTCATTC	AGTATTCTC	CAAATAAGTT	ATTTCCCAGG	180
TGTCGCTGG	TATCTAACCA	ANTANTCAAT	AAAGTATTCT	TGCTAAGTNG	GCCATGAAG	239

(2) INFORMATION FOR SEQ ID NO:161:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

GAATTCCGCC	TTCATGGCCT	AATATCATGA	TCACTGAAAT	TACATCTAGT	AAAACACACA	60
CGTGCTTATC	TGCACGTGTG	TGTAAGTTAG	AAAGAAAAAA	CAAAGCCTA	ACAGTGATTG	120
TCTTAGGTTG	ATAGGATAGT	CGGTGGGATT	TGCGAAATT	TTGTATCTGC	AGAATTTTG	180
CAAAGTGCCC	ATTAGTTTG	TAAGAAAAAA	AACCTAAATG	TATAACTTCT	AAAGAGATAA	240
TTTTTCTTT	CATGTTTTG	CTACCTATAT	CTAGGAAAAT	AACCTAGAAT	TGTAATTATT	300
TTGAAGCTCT	GGAAATTATTA	TGTTCAAAAA	TTACAGAAC	AAAAAGTCTC	GAG	353

(2) INFORMATION FOR SEQ ID NO:162:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

GAATTCCGCC	TTCATGGCCT	ACTTGCTGTG	GCTGACTCGG	TTATTGACTT	TACTTCTTT	60
CTTTTCAGGT	TTTTATGGG	CTGTTTCTAG	CCCTGATTCA	GGTGTGTATG	AAATGAAGAT	120
TGGCTCATC	ATCTTCCAGG	TGGCTTCTGG	AGATATCAAG	AAAGAAGAGG	CAGATGTGAT	180
TGTAAATCA	ACATCAAAC	CATTCAATCT	CAAAGCAGGG	GTCCTCAAAG	CAATTAGA	240
ATGTGCTGG	AAAAATGTAG	AAAGGAAATG	TTCTCAGCAA	GCTCAGCAGC	GCAAAAATGA	300
TTATATAATC	ACCGGAGGTG	GATTTTTGAG	GTGCAAGAAT	ATCATTCTATG	TAATTGGTGG	360
AAATGATGTC	AAGAGTTCA	TTTCCTCTGT	TTTGCAGGAG	TGTGAAAAAA	AAAATTACTC	420
ATCCATTGTC	CTCCCAGCCA	TTGGGACAGG	AAATGCCAA	CAACTCGAG		469

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

GATTTATTCA	TTCTTGATTA	AATGCACTGA	AAAGTAAAGG	GTCTGTTGT	GTCATGTTCA	60
TGAAAATGCG	GTTAGAGAGG	TGCTATTCAA	GTGATTCTGA	AGGCACCCCA	AGGTATATCT	120
GTAATTAA	GATTACTGCA	AATATCTTTA	CTTTACTGTG	GGTTTTAGT	ACATCTGTTA	180
ATTTAGTGT	TCTTGTGTG	TTTGTAGAC	TAGTGTCTT	CCATCCTTCA	ACTGAGCTCG	240
AG						242

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

GAATTCCGCC	TTCATGGCCT	AGCATTAAAT	TTCTTTAAAT	TATTGTATCC	ACTAGTTCTT	60
GCCAGTATAA	AGGAATAACAA	TTGACTTTTG	TGTGTTTCAT	ACGCTACAAC	CTTCTAAAT	120
TCACATTATCA	GGTCAGAAC	TCTTCTACTA	ACAATGCACT	TTTATAAAGC	CCTAACACCT	180
CTCCTGATCT	CTGTCTCACC	CTCCCCACCA	TCTCACTGTG	GGATGGGAAG	GAAGTCAATG	240
GAAAACACAG	GAGGCATTC	TAATAATAGC	CCACATGGTA	TACTCGAG		288

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

GAATTCCGCC TTCATGGCCT AGCTCGATCC AAGAAGAAAA ATTAAAATGA CAGCTTTCC	60
CATTGATATA ATCATCTTAC TTTGCTCTCT ACAAGAAATA TGCATTAGGA ACCTTCATTA	120
TAGGTCCACA GAAATAGCAG AACACAAAAG CGCCCCCCTA CCCCCCCCACCA CGGGTAACCA	180
GAAATACACA GAGGCAGAG	199

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

GAATTCCGCC TCATGGCTA GAATTAACCA ATTAAGAATT AATAAATTAC TTATAAAATT	60
AAAAATCAGG AATACCAGGC TTAATGCATT CATTTATTCT ATTTAGCAA CTTTTTTTTT	120
TTTTTGAAAT GCCCACAATG TCCTAGGTTC TGAAATACA AAATTACTTG GTACAGTAA	180
CTCGACTGTC ACCTTTCCAG CCATGGACTT GGTTAGACAA AACCCCCAGT CCACGGTTGT	240
CGTCCACTTG CAGTGCCCCGC CGACTGTGGA TATATGCTGG GGATCCAAC ACAACGCAGC	300
TACTCTCGAG	310

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

GAATTCCGCC TTCACTGGCCT AGTAAATATT TTCTTCTACT TTGTGTTTG CCTTTTTGTT	60
TTCTCAGCAT TATTTTTGA AGACAAAAAG ATTGATTTTG AAGAAGTCTA ATTTATCAGG	120
TTTTTTCTAG TAGTTTGTAG CGGATTTNTG CATGCTGCTT TTAAAAAAAT CTTTGCTAAC	180
CCTCGAG	187

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

GAATTCTAGA CCTGCCTCGA GCCTTGCCCA GAATCAGCAA GTAAACTGCA CTAATTTGTC	60
TTATATTTGA CTTCCTAACCA CTGATTTTTC TGATTTTCC CTGTTGACC CTCCAATTAA	120
TTAAAAATGTG TATAATTGTT CTGCTGCTTC TGCTTTGCC TGCTTGGCT GCTGCATATA	180

CAGGTGAAGA TCTGGAAAGA AATGATGGAT CTACAGAAAA ACCCTACTTC GAAACCCCTA	240
ACCTGCATGG AATTCTGATC AAGAAGCAAC TCGAG	275

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

GAATTCCGCC TTCATGGCCT AGTTTACAT TGTCTGTACT GTGTTGTCA GTACCAGAAG	60
TTGCTGGTAG CTACTTGGTC TTCTGGGACC TGCCATTGCA GACGTGGTGA TTGTAATCTT	120
AATCTTGTG AAACAGGATG GATTTATGAC TGGGATGGCC GGAAGCCACA CCAGACACCC	180
AGTCACCTGG TCATGGGAGA GGTAATTGT TGGCTTTCA TAGTACTTA CACTGTGAGC	240
TGCTTCCCTGA ACTGGCACTC TTAAGGCCAG GTGCCACAC CCTCGAG	287

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

GAATTCCGCC TTCATGGCCT AAGACAGACA TTTTGGCAG AGCATAGATG AAAATGGCAA	60
GTTCCCTGGC TTTCCTTCTG CTCAACTTTC ATGTCTCCCT CCTCTTGGTC CAGCTGCTCA	120
CTCCTTGCTC AGCTCAGTTT TCTGTGCTTG GACCCCTCTGG GCCCATCCTG GCCATGGTGG	180
GTGAAGACGC TGATCTGCCG TGTCACCTGT TCCCGACCAT GAGTGCAGAG ACCATGGAGC	240
TGAAGTGGGT AAGTTCCAGC CTAAGGCAGG TGGTGAATGT GTATGCAGAT GGAAAGGAAG	300
TGGAAGACCT CGAG	314

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

GAATTCCGCC TCATGGCCTA CACCAAGTTG AATCCCTATG CAGGAGGAGA CGGCCTTCAG	60
AACAAACCTGT CCCCCAAGAC AAAGGGCACT CCTGTGCACC TGGGCACCAT CGTGGGCATC	120
GTGCTGGCAG TCCTCCTCGT GGCGGCCATC ATCCTGGCTG GAATTACAT CAATGGCCAC	180
CCCACATCCCC TCGAG	195

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

GAATTCCGCC TTCATGGCCT ACACCTCTGG TCATTTGCA TTTTATCCAG CTTTTTTCA	60
TCAACCATGT TATCTGACA GACACATTAA TTGGATATT AGTTGGAAAT ACCTTATGGT	120
TGGTTGCAGT TGGCTATTAT ATCTATGTAA CTTCCTGGG ATACAGTGCA TTGCCATTT	180
TGAAAAATAC AGTAATTCTT CTGTATCCAT TTGCACCTCT GATTCTGCTC AACTCGAG	238

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

GAATTCCGCC TTCATGGCCT AGGCTAACGT AATTGAGAAA ACCAAATGAA ATATATCTTG	60
ACCAATAATT TAAAACCATA TCAGAGATTG AGTTGGTTC TGTCCTCTGC TTTACTGATT	120
TTAGGATCAG CCTCATACAA AAGGGTAATG GTGGCAGCAG CTCCAGAACT CATATCATAT	180
CCTCCCATGT TAAAGTCAAA TGAGAAAAGT CTGTCTTCGC CCCAGGATCT CGAG	234

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

GAATTCCGCC TTCATGGCCT ACTCAGTTCC ATTGTTAACG AAGGAAAAAC AAACAATACA	60
TTGAATTGAA CAACCCACTG AAGTTGAGA TAATGAGGAC TTACCATTTGT ATACCATTAT	120
TCATCTGGAC CTATATGTC CATAACATTG ACACCATCCT ATTACAAGAA AACCTAACAA	180
GTTATTATTC AAGCAAAAG ATAGTGGCTC TGACAAAAGA TGACGGTAAATGCTACGTC	240
ACACCCCTCGA G	251

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

GAATTGGCC TTCATGGCCT AAACCACTGC GCACCATATT TCTTAAGGAT GTTCTGAAGA	60
CCCATGAATG TCTGGTCAAG TCTGCTGATC TCTTAATGAG GGACAACCTG TTTGAAATAA	120
TAACAAAGCTC CAGGACATTAC TACGTACAGG CAGACAGTCC AGAAGACATG CACAGCTGGA	180
TTAAGGAGAT TGGCCGACCT GTCCAGGCCA TCAAGTGCCA CTAGGCCATG AAGGCCGAA	239

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

GAAAACCCA GATATTCCCTT ATTATGGAAG AAGAACGAGG AAATATGTTT TTGAAATAATG	60
TGGGTCAAGAG ATTGTGCAAT TTATTATTGC TAGGATGCAAT ACACACATTG AACTCAGTCA	120
ACTTACTCTC TCTAAATTAT CTCACCGGTG GAGACATTG CTCAGGAGTC GACCCCTGTG	180
GTTGCGCTCC TGCTGTCACC ACATTTGACC ACCTAACTGA CCCCACTGTG GTCACCTTG	240
CCACCAATCT CGAG	254

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

GAATTGGCC TTGCCCCAGTAT TCATGCTGTT GCTTCAGTCA AGAATGAATT CCTCAGGCC	60
ACCTCTCTTG ACCTTCACAT CTTACTTAGT GCAAATGCTG TCTCCTCTG AGACTTGCCT	120
GACTTCGGAT ACTCTCCCTG TGACATCTTA TCTAAAATGT CAAGTGAGAC TCGAG	175

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

GAATTGGCC TTCATGGCCT AAGTGGCTGT GTGGTATTC CTAAGTATTT TTAAAATTTT	60
TCTCTCATTG ATACCCCTATA AAAATGCAAC TGTTAAAGAA TTTGCTTTG TTTCTCATT	120
TATTCTTCC AGAGTATATA ACTAATTAT TCAGCATTCA TTCATTGAGC AGATATTG	180
TGAGCACTAA CTATGTTCAAG GCACTGGGCA GGGATATCGG GATACCAAGA AAGCTCGAG	239

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

GAATTCGGCC TTCATGGCCT AGAAAATAAT TTAGAGAAAG AATAGAAAAGT CATGGAAAAT	60
CTCATAGGTA GGAGACAGAA GAGAGAACAT TGTAAATAAG TTTAAAAAAG ATAAGAAAAT	120
CAGGATAAAG TAGTATGGAC TCTGAGGTGG GAGAGAATT TAAGATTAGC AGGAAAGTAG	180
TGTAGTTGGT ACTTTTTACT TATTAACAAA GCACTCACTT CTTACAGAGT CTCGAG	236

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

GAATTCGGCC TTCATGGCCT ACGAAGATTA TAATGTATT TTATTCGTT TTCAGCTTCA	60
TGTTTCCTGT TGCAAGGTGGG ATAAGACCCC CTCAAGGCCT GATGCCGATG CAGCAACAAG	120
GATTTCTAT GGTCTCTGTC ATGCAGCCTA ATATGCAAGG CATTATGGGA ATGAATTACA	180
GCTCTCAGAT GTCCCAAGGA CCTATTGCTA TGCAAGGCAGG AATACCAATG GGACCAATGC	240
CAGCAGCGGG AATCCCTTAC CTAGGACAAG CACCCCTCCT GGGCATGCCCT CCTCCAGGCC	300
CACAGTACAC TCCAGACATG CAGAAGCAGT TTGCCGAAGA GCAGCAGAAA CGATTGAAAC	360
AGCAGCAAAA ACTCTTAGAA GAAGAAAGAA AAAGACGCCA GTATCTCGAG	410

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

GAATTCGGCC TTCATGGCCT ACACATTTCG ATTGTCTGCC CATGGACTGG TTGGAGCAGA	60
AACCTCCATA CCTCACTCTC TTGGTATTTC TCTGCCCAA CTGCTCTTT TTGTTGGGAT	120
GTGTTGTGTG GCTGGGGTCT CGGCAGCATC GGCTGCTTC CGGTGCGCAC TGACATGCAC	180
TTGTTCTCCA CGATGGCTTT CTCTACCTTC TGAGATGCTC CATTATCAGT CCTGCCCTTG	240
TTCCGGAGAG TTGAGATGGT ATCACTCTC ATCCATCTT AGAAATACCC CTCTCGAG	298

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

GAATTCGGCC TTCATGGCCT AGGGGGCTGG TAGTGAATA TTTGGTACTG AAAGTGTGAA	60
GACCTCTGCT GGGGACTGAA CAGAGGGAGT GTCTTCTGCT GGTGGTGTA AATCTATCTC	120
ATCATCAAAA TTATCTTCAA ATTCCCTTAAA GTCTATTCTC GGGTCCTTAC AGCAGGATAC	180
ACAGTTTGCA ATTAACACTA TTAATATTAT TAAACTGCAC ACACACAGGA TCACAAAAGA	240
TGAGGAAACT TCTGCAGCAG GTGGCGCTCG AG	272

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

GAATTCGGCC TTCATGGCCT ACTACTTATC ATCCCTGCTC ACACACCCCT GTCCAAGGCT	60
TTATGCATCG GATTTATTTT TCCAAATCAA GAGGACAGTG ATAGATGCAT TTTCCCCAGG	120
CTGTCAGA AAGGTGCGTA AATGTATACT GTTGTGAGAA TTGCTGAGAT CTCCCCCAC	180
TTTTGGTTTT TGACGAGTA AAAACTCTTT CCACTGTGAC TTATTTCTC TCTCAGGAG	240
CAGACTCGAG	250

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

GAATTCGGCC TTCATGGCCT AGATCTTCTC CCCATTCAAGC AAAACTTTCC CATTCCGGTT	60
AATGGTTTG ACAAGCAGGG CACCACGGGG CATAAAATTG TATCATCCAG CCTCCCTTCCA	120
GCAGCTCTCT CCAGTTCTTG TCTGTGATGA TGCGTACGTT GCTCTGCCGC CTGTGGGTCC	180
AGGGAGCACC CCCAAGAAC AGTACCCAGGA CTGCCAGCGG AACTGCAAGA CTCCTGGAGG	240
GTGCCATGTC TGCCACTTGC CCACCTCACA GCAAGCGTGG CGGGCCAAACA CTAGGTTTTT	300
TAAAAACTGT GACTATCACT GTTTAAAAAA TTGCCCGGTA ACTCTAGACT TCAAAAGTGG	360
GATAAGTAT GATAAACCAA TAATAAACCC TGCCCTCGAG	399

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

GAATTCCGCC AAAGAGGCCT AAAAATTAAT ATTACCTTAT GACTGCCTTT ATCATGACTC	60
TCTTAGTGGG GATTCTGTG CTCACATGC CCTGGGGAT GTGCAGCCCC CGTGCACCTCC	120
CCGCCTTGGC CGGCCCTTC CCCATGCC AGGTAGACTC TGAGCTCTTA GCCCAGCAAC	180
TCGAG	185

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

GAATTCCGCC AAAGAGGCCT AGGAAACTAA TCTTAAACAC TGAACCTCTT TTCAGCAAAT	60
TGGCTTCTA GTTCTCAGC TCTCTCTTTA CACCTCTAAA TCTCTTCCT GGCAAGATCA	120
TTTATTTGCC TTGGTTTATG GTGATACTCT TCATTGTTAT ACTGGTGGGT GATTGTTTTA	180
ATTCA TAGCT GTTTTTCT ACCTCAGGAA GATGACACTG CTGGCTCTGC TGGCTCTGAT	240
GTTTACCTTG TGGCTAATGC CTGTGTTTGC CTGTGTTCAC ATTTATTCCA CGATTCACTTT	300
GTAAACATTT ACTAAGCTCG AG	322

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

GAATTCCGCC AAAGAGGCCT ACTCATAACA GCGTCAGAGA GAAAGAACTG ACTGAAACGT	60
TTGAGATGAA GAAAGTTCTC CTCTGATCA CAGCCATCTT GGCAGTGGCT GTTGSTTCC	120
CAGTCTCTCA AGACCAGGAA CGAGAAAAAA GAAGTATCAG TGACAGCGAT GAATTAGCTT	180
CAGGGTTTTT TGTGTTCCCT TACCCATATC CATTGCCCC ACTTCCACCA ATTCCATTTC	240
CAAGATTTC C ATGGTTTAGA CGTAATTTC CTATTCCAAT ACCTGAATCT GCCCCTACAA	300
CTCCCCACCT CGAG	314

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

GAATTCCGGCC	AAAGAGGCCT	ATTATGCTGG	TGCTGTCTAC	TAATTTCAAG	AAAAACTACA	50
AGTCTGGCTA	GACTCTGCTA	CCGCCTAGCA	CTGAGGTGTG	GTCTCTTATC	TGTTATTACA	120
TTCTTCGTGA	TAATGAAATT	CTGAAACACA	TCCTCCAGGC	ACCTTTGTA	ATGTGAAGGT	130
GAATAAAAGTA	TTTGTGTTGTT	GTCTGAAAAG	AGATCTTGA	AATGTTAAGT	TGCCACAGAC	240
CCAGACCAAG	GACCCCTGCTG	AGAGTTTAA	AGGCTCTTAT	TGGATGACAG	TAGATTCTTT	300
CCTTGAATG	TCTATAATGA	ATATCAAGA	ATGCTCATTC	TGCATGAAAT	TTGCAATT	350
AATTATCAGT	GAAAGAAAAG	ATTACACAGT	GCTAAATGAT	TGCCATGGAA	AAAGTTATGGC	420
TACCTCTTGG	AGTAGAGAAA	ATCTCAAAGG	CCGCTACTCG	AG		452

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

GAATTCCGGCC	AAAGAGGCCT	AGTGGCAAC	TTGGAGAAGA	GTGAAAAACA	CTAAAGAAC	60
ATCTCTTTTC	CGAGTCACAA	AGTCCCAGA	ACTTTGTGAC	TCAGAGACAC	TTTCGTGAA	120
AATTACCTTT	CGGCGGGACA	CCGTCTCAGG	GCAGCTTTT	CAAGGCTTCG	CTTGACATGA	180
TTCCCTTCCC	TTCATCAGTC	ACTTTGGATC	CAGCTGAATA	TCTCTCTCGG	GTGAGAGCGG	240
ATGTGGACTG	GCCTCCACAA	GAAGAAGAGT	AGGTGGCTTT	GGTGGGGTT	GGGGTGCAGG	300
CTGGCTTCT	GGTCTCGAG					319

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

GAATTCCGGCC	AAAGAGGCCT	AGTAAAAGA	AAGAGACTGT	NAAATAATT	TGCATATCCT	60
CAGTGGATAA	TTCTGTNACC	TATCTGTCAG	CTATTCCATA	TCAATAAAGG	ACACAGCTGG	120
TAATCCAAAA	GGAAAGGATC	TCTTGATGAA	AGTGTCTGC	CATTCTTATT	AAAGTCAACA	180
TACAAGATAC	ACTCTTAGTG	ATTTTGAAAC	CCATAATTAT	ATTTGCTCTGA	TAATAATTGG	240
CACTTAACGG	TTACAGAACCA	CTTTCACTGA	TATTTCCCTT	AGTGAATCTT	AACAACAATT	300
CTACCAGTAA	TTCTAAATAT	TTGCCATGAT	TAGACTTCA	AAATTAGTCC	ACGCACTCGA	360
G						361

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

GAATTCCGCC	AAAGAGGCCT	AAGAACATG	GCGGCCGCGA	CGTTGACTTC	GAAATTGTAC	60
TCCCTGCTGT	TCCGCAGGAC	CTCCACCTTC	CCCTCACCA	TCATCGTGGG	CGTCATGTTC	120
TTCGAGCGCG	CCTTCGATCA	AGCGCGGGAC	GCTATCTAGC	ACCACATCAA	CGAGGGAAAG	180
CTGTGGAAAC	ACATCAAGCA	CAAGTATGAG	AACAAGTAGT	TCCTTGAGG	CCCCCATCCA	240
GGCCAGAAGG	ACCAGGTCCA	CCACAGCAGCT	GTGGCCAG	AGCTGGAGCC	TCAGCTTGAA	300
GATGATGCTC	AAGGTAATCT	TCATGGACCA	CCATTGCTG	TTGGCAAGAA	ACGGCTTAC	360
TTACAAAACA	GTCTCGAG					378

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

GAATTCCGCC	AAAGAGGCCT	ACTCTGAATT	AATGCAAATT	CCCGTTGTAC	TGTATTTAAT	60
TATGCACAAA	ATGGTGCCTT	TGACTCAGAT	TTCAGTGAAG	AACTTCATTT	TTTTACTTTT	120
AAAGTCTCCAA	GTAGGAAATT	CAATTAGCGT	TATGAAAGAA	ACACTAAAAC	TCGAG	175

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 700 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

GAATTCCGCC	AAAGAGGCCT	AGGCAGCAAT	GTTATCTGTC	CTTCATTCTT	GCATGTTTT	60
GGAAATTGCT	TTTGCTTTA	CTTTGGTCG	TCATGGCAAT	CACGTGCCCT	CTCTGGTTCA	120
TTTGACACAG	ACCTGCCTAG	AGCTGGAACG	TTACCTCCAG	AGCGAGCCCT	GCTATGTTTC	180
AGCCTCAGAA	ATCAAATTG	ACAGCCAGGA	AGATCTGTG	ACCAAAATCA	TTCTGGCTCG	240
GGAGAAAAAG	GAGGAATCCG	AACTGAAGAT	ATCTTCCAGT	CCTCCAGAGG	ACACTCTCAT	300
CAGCCCGAGC	TTTTGTTACA	ACTTAGAGAC	CAACAGCCTG	AACTCAGATG	TCAGCAGCGA	360
ATCCTCTGAC	AGCTCCGAGG	AACTTCTCC	CACGGCCAAG	TTTACCTCCG	ACCCCATTGG	420
CGAAGTTTG	GTCAGCTCGG	GAAAATTGAG	CTCCTCTGTC	ACCTCCACGC	CTCCATCTTC	480
TCCGGAATG	AGCAGGGAAC	CTTCTCAACT	GTGGGGTTGC	GTGCCCCGGG	AGCTGCCCTC	540
GCCAGGGAAAG	GTGCGCAGCC	GGACTTCGGG	GAAGGCCAGT	GACAAGGGAA	ATGGCGATGC	600
CTCCCCCGAC	GGCAGGAGGA	GGGTGCACCC	GTGCCACTT	AACGGCTGCA	GGAAAGTTA	660
CACCAAAAGC	TCCCACCTGA	AAGCACACCA	ACGGCTCGAG			700

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

GAATTCTGGCC	AAAGAGGCCT	ACAAAATAC	TTGGGCAGAA	AGAAAATATC	ATCAAATAAC	60
ACCTATTCT	TTTCAGCTAT	AGAGATGGCT	GGATATCAA	AGCACCAACGG	GAGCTTTGCA	120
ATTTGCTGCC	TCTTTTCAGC	CCTCAGCTTG	ACTCTCAGTT	TTCAAGAGGG	AGAAAATGAA	180
TGTTTCCAG	CATTCTCTGT	CCTTTGCTCC	AAAGAAGAGA	GCAGGTGTTG	GCTTCCAAAC	240
CTTCCGTATT	TTCTTATTGC	TGTTAGGGGG	ATCAACTGCA	TGTTTCCTGA	GGGAAAAGGG	300
TGGCTCACTG	ACCTACTTGA	AGGCATTCTC	TCAGTGGAAAG	CTGGGCAAGA	GAATCCAGGG	360
ATTTCTTTTG	CAGGTTCTG	CGCAGTGCCTC	CTGCCATCAA	GCTGCCTAAA	ATGTGAATAT	420
TGCTTCCCTG	CGTTTCAGAG	GTGGCCGCTC	GAG			453

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

GAATTCTGGCC	AAAGAGGCCT	ACAAAATGTG	AATGGAACAA	ACCTGCACGT	GTACCCCTTGG	60
ATGTGTGGAT	GTTCTTTGTT	TTTATTGTT	AAACCTGATG	TCTTGTCTGT	ATGACACATT	120
TATTGGAAAC	GTTTTTCCC	TATTCTGTGT	CTTGTATTGT	ATTTTCTCGT	GTTCTCCAAA	180
GAGCAGATAT	TTTAAATTGT	TATATAAAC	CAGTTGTCA	ACATTTTAA	AGGGTTCATG	240
CTTTTGAT	CCTATTCAG	AAAACTTGG	CTACTTCAAG	GTCACAAAGA	TTTTGGATT	300
GTTTTAATCT	ACAAGTTTA	TAGCTTGAC	TTTTATATAT	AAGTCTGATT	CATTTGGAGT	360
TAATTTTGT	GTACAGTGT	ATTAAGGGT	CTAGGTTCAT	TTATTTCTT	ATGAATATCC	420
AATGGTTCC	CGAG					434

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

GAATTCTGGCC	AAAGAGGCCT	ACAAACACAG	AACATTTCCA	TCGTTGCAGA	GAGTACTATT	60
AGAGAGCAGT	ATTCAGAGC	CTGTGATCTT	AATCACTACA	CCTAAAGCCT	CCCAGTTGAC	120
AAAGTTACCA	CCTTTTTTG	GTGTGTTGTC	ACGTGCGTGT	GTGTGTTGTC	AAGTATATAT	180
AATTTAAATC	ATTCATTA	ATTACCTCT	GAAATTCAA	AGACTGAAAC	AGATCTTCTT	240
TTTATCAAAT	AAGTTGATTG	CAGAGATTAT	ATTGGTGT	ACATTCAGG	CAACCTGCTC	300
ATGAAATTAT	CCATTGCT	CGAG				324

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

GAATTGGGCC AAAGAGGCCT ACTCCTCCGC CTGCAACCAT TGTTCCTAC CACTGGATTA	60
TTCTGAAGCA AATTCTAGAC ATCATATATA TTTATCTCTG AAAGAGGACT CTTAAAAACAA	120
TGCACTTATA CCTCTATTAC ACTGACAAA TTGGTAACAA TTCCTTATA TTATCAAATT	180
TCCTTATTGA GTTCTGATG TTCAAATTTC TGATTCTCCA GATGCTCCAA ACTTCCAGAA	240
ACACAGATTG CCAGATGGAA TCCTGGGAA GGCTCGAG	278

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

GAATTGGGCC AAAGAGGCCT ATTTCTAAC AAAAACTATT TTATGGTAGG TTTTGTTGAT	60
TATTGAATAC AATCTGGCAT TCTGTTAAC ATGTATGTTT TCCTGAATGA GGGGTACAT	120
TGTAATTATA ATTATTAACAC TCACAATGTT TTTGGTTTTA AAAATAAAA TTTAGGAGC	180
AAGCAGTGTTC CCTGCCCTCT TTCTGAAGA TGATTCTCAA TCGAATGACT CAAGTGATTC	240
TGATAGCAGT AGTAGTCAGA GTGACGACAT AGAACAGGAG ACCTTTATGC TTGATGAGCC	300
ATTAGAAAGA ACCACAAATA GCTCCCAGTC CAATGGTGCT GCCCAAGCTC CCCGTTCAAT	360
GCAGTGGGCT GTCCGCAACA CCCAGCATCA GCGAGCAGCC AGTACAGCCC CTTCCAGTAC	420
ATCTACACCA GCAGCACTCC ACCTCGAG	448

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

GAATTGGGCC AAAGAGGCCT AACTTTGTAA ATTTGAATTG GGTCCCGCTT AGTTCCTTGAA	60
TTGTTATGAA AATCCTATAT CTGTTTGAT ATTTGAAAC CCTTTGTATT ATAATTGTTG	120
ATATTTCCC TTTTAAAAAA ATACCATTGA AATCAGCATG ACAAAAATAA CACTGTGGC	180
ACTCGAG	187

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

GAATTCCGCC	AAAGAGGCCT	AGACCAGAAT	AAGCCTTTA	AGGTAAAACCT	CAAATTATC	60
ATTTTATGGT	AATACTGACC	ATTTAGTCC	CCTAGTTTC	ACATGGAGA	TAGTGACTAC	120
ACTGGTGTCT	GACTTTTTC	CTAGAGATT	CTCCCTGAAA	AATACAAGGG	CTGTTGGTGA	180
GAGCAGACTT	GAGGTGATGA	TAGTTGGCCT	CTGGTCTACA	AAGATTCAT	AACTCCTTGG	240
AAAGCTTCTT	ATAATCATTC	TTAACCTCTT	GGTAGCTAGA	AATTTAGAGT	AGTTGAAATC	300
TTTAGGAATG	AACTTCTGAG	GGCCAAAAAA	TGTGACTGAC	ACACTCGAG		349

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

GAATTCCGCC	TTCATGGCCT	ACATCACCAA	TCGGCTGGG	TAAGGGTCCC	CATGAAGGCC	60
CAGCCGGGTA	TAGAGGTGCA	GGGGAGAGCA	GCCTGGGGAG	TCCCTATCTG	GATAGGCTCC	120
AGCCTGGGTC	GGGGCGGTCC	TGGTCCCCGG	TGAAGCGTCA	AAAGAGGGAG	CCTGAGCGGG	180
GCAACGCAGA	AGGGTGGAGA	GGAGGGGGTG	GCGAGGGCGG	GCAGCGAGGC	CTGGAGCCGC	240
CAGGAGAGGG	GGGGGGGGCG	GCCTTCTCC	AGGAATTCC	GGGGATCGTG	TTACAGCGTT	300
GGCGGAGCCC	GAGCGGAGTG	GGACTCGAG				329

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

GAATTCCGCC	TTCATGGCCT	AGAAAGGGCA	GGGAACGTGA	CAGGCAGGTG	TGGGATAGGG	60
ACTTCTCTTC	CGGTTCAGAGC	AAGGGTCGTC	CGAAACCAAA	ACAACCCCTCT	TCCCTTCATC	120
TCGCCCCCGA	TCCAAAGTCT	TGGGGCTAGG	CTGGGGCGGG	AGTGGCACGG	AGATGTAGGA	180
ACACTGCCCT	TCGTTACTTC	TCTGCCATG	GCTGACCTTT	TTGTCTCTTG	TTTCATGGTT	240
TTACACGTAT	GAATGGCTTG	AGACTGAGGA	TTTAGGGAAG	AAGCGAAGGC	ATCATCTAGG	300
GCTGTGCTGT	GCCAAGTTGA	GCAGTTGTTT	AAACTGTTAG	AATTTTGAC	TGGTGTAAAA	360
ACCCCTCTATG	CTCGAG					376

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

GAATTCCGCC	TTCAAGGCCT	ACGTGAAACC	CCATCGGCTT	CATTGGCTCC	TTGATTTAAA	60
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CCACGCCCGG CTNTCTGCC C TCTTGTATGC TCTGGGCCA GGTGGCCAG CCATATCCC	120
GCCCCGTCCTG CAGGGAGCCG GAGGCNGCTG CTGCTGCTAT TGTGTGGATG CCSCCGGTGT	180
CTTCTCTTCT TTCCAGAGAT GCCTAACAGG GGCCCGAGCT ATGGCTTAAG CCGAGAGGTG	240
CAGGAGAAAGA TCGAGCAGAA GATCTCGAG	269

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

GAATTGGGCC TTCATGGCCT AGATGTGTTG AACCTTATTTC TTGTACATTC ATTCAATCAA	60
GGCAAACCTT TATAATTTTT CTTTGTTC CAATGACCTT GAAATGTTAT AGCATGGTAA	120
TATTCTATGC AACTATAGTT ATACTTTTG GTTTGACACT GTATTTTTC ACATTGATT	180
ACTGGTTGAG GCTCGAG	197

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

GAATTGGGCC TTCATGGCCT AGCAAGACCT TTTAAGTATA TACTCTGAAA CTGTGGCTAA	60
TATGATCATG ATGCTGTAGG AAAAAAAGGT TATATGTCCA AGTGTATGTA CTTGTAAATG	120
TGCCTAAAGA AACCTGGAAG GATACACAGG TCTTCCCTGG GGTACAAGAC GGAGAACTGG	180
GATCATCATC TTAACCTCTAC TCTTCCCTTT TACTCTTCTG TCCTCTTGA GACTTTGCC	240
TGTATACATG GATTACTGTT ACTTAGCAGG GGCGACCGGT TGGCAAAGC CTTGGTGTGC	300
CCTTGGACAA ATTCTGCCAA GACCCTTACCA CTCTCCTCTC CTCANGGCTC CCTTAACCCC	360
TCTCCCCACA TCTGGAAAC CCTGGATACA TTTCT	396

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

GAATTGGGCC TTCATGGCCT AGGAAGAGGT TGAGAAGACT CCTGGGCTTC AGCCTCTCCC	60
ACCCAGCCCT GCCCCTCACCC TGCCCTGCCCT CCCCTCCCCC ACTCTATACT AGGGACTGG	120
TCTCAGGCTC TGATCAGTTT CACAAAGTTT GTTCCCTAAG GAAATCAAAT CCCATTTGCA	180
CCTAACTCTG AAGATCTAAA TAGCCCTTGG ATCAGTACGG GAACCCAAA TCCCACAGGG	240
CCAGATGTGG AGTCTGTGTC TGCCCCCGTC TTCTCTCCAT CCTCAAAGCC CCCACTTCTC	300

TCCAGGCTGC TTCTCGAG

318

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

GAATTCTAGA TCCTGCCCTC GGAACAAATGG GACTCGGCGC GCGAGGTGCT TGGGCCGCGC	60
TGCTCCTGGG GACGCTGCAG GTGCTAGCGC TGCTGGGGC CGCCCATGAA AGCGCAGCCA	120
TGCCGGCATC TGAAACATA GAGAATTCTG GGCTTCCACA CAACTCCAGT GCTAACTCAA	180
CAGAGACTCT CCAACATGTG CCTCTGACC ATACAAATGA AACTTCCAAC AGTACTGTGA	240
AACCACCAAC TTCAGTTGCC TCAGACTCCA GTAATACAAAC GGTCAACCACC CTCGAG	296

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

GAATTGGGCC TTCATGGCCT AGTCTCTTGA AAAGCCGCAT TTCCAGGCGC TTGGCCAGTG	60
GCCTGGAAAG TAGCTCTGTC TTGTATTGAG ACAGTCCCCC AGCAGCAAAC CATGTTCCAG	120
TCATTCCTT TCCTACTTTG GGGATTGTTG CTTTTCTGC TTGTTAAAG TAAAACAAGC	180
ATGTACTTGT TTGTATGTAT GTATGTATGT AGTTGTACGG TGGGCACAAA TAAAAGAGG	240
GCTGTATCCA AATAAAATCAT TTCTGGCTGC TCACTGGCAC AGTCCCTTG CTCCGTCCCC	300
TCCTGGCTCG AG	312

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

GAATTGGGCC TTCATGGCCT AGGCAGCGTT TCACCGCTGT GGAGGACCAAG TATTACTGCG	60
TGGATTGCTA CAAGAACTTT GTGCCAAGA AGTGTGCTGG ATGCAAGAAC CCCATCACTG	120
GGAAAAGGAC TGTGTCAAGA GTGAGCCACC CAGTCTCTAA AGCTAGGAAG CCCCCAGTGT	180
GCCACGGGAA ACCGTTGCCT CTCACCCCTGT TTCCCAAGCGC CAACCTCCCG GGCAAGGCATC	240
CGGGTGGAGA GAGGACTTGT CCCTCGTGGG TGGTGGTTCT TTATAGAAAA AATCGAAGCT	300
TAGCAGCTCC TCGAG	315

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

GAATTCCGCC	AAAGAGGCCT	AGGAAGATGG	CGAAGGTCTC	AGAGCTTAC	GATGTCACTT	60
GGGAAGAAAT	GAGAGATAAA	ATGAGAAAAT	GGAGAGAAGA	AAACTCAAGA	AATAGTGAGC	120
AAATTCTGGA	AGTTGGAGAA	GAATTAATTAA	ATGAATATGC	TTCTAAAGCTG	GGAGATGATA	180
TTTGGATCAT	ATATCACACG	GTGATGATTG	CAGCAGTAGA	CTATGGTCGG	GATGACTTGG	240
CATTGTTTG	TCTTCAGAG	CTGAGAAGAC	AGTTCCCTGG	CAGTCACAGA	GTCAAGCGAT	300
TAACAGGCAT	GAGATTGAA	GCCATGGAAA	GATATGATGA	TGCTATACAG	CTATATGATA	360
GGATTTACA	AGAACATCCA	ACTAACACTG	CTGCAAGAAA	GGCTAAAGATT	GCCATTGAA	420
AAGCCCAGGG	GAAAAATGTG	GAGGCCATTG	GGGAGCTGAA	TGAGTATCTG	GAACAATTG	480
TTGGAGACCA	AGAACCTGG	CATGAACTTG	CACTCGAG			518

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

GAATTCCGCC	AAAGAGGCCT	AATTGAATTT	CATTTCCTTT	GTAGACTAAT	GTTACAATAA	60
ATAAAATGGGA	ATTTTAAATA	CCTCATGTT	CTGTTTTCT	CTTTTTCTT	TTTCAGCCA	120
TAATGAAAGG	AAAGTGACCT	GCAAACATCC	AGTCACAGGA	CAACCATCAC	AGGACAATTG	180
TATTTTGTA	GTGAATGAAC	AGACTGTTGC	AACCAGACA	TCTGAAGAAA	AGAAGGAACG	240
GCCAATAAGT	ATGATAAAATG	AAAGCTTCTAA	CTATAACGTG	ACTTCAGATT	ATGCACTGCA	300
TCCAATGAGC	CCTGTAGGCA	GAACCTTCACG	AGCTTCAAAA	AAAGTTCTATA	ATTTGGAAA	360
GAGGTCAAAT	TCAATTAAAA	GGAATCCTAA	TGCACCGGGC	GATCTCGAG		409

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

GAATTCCGCC	AAAGAGGCCT	AGTACAGTCC	CAATCAAGAA	GCCTTATTAA	CCTTCTGTGT	60
GAGGGACTAG	ACTCAGTGT	GGGTTGGAG	GATCCACTGG	TGAGGAGCAT	TCAGTCTAGC	120
AGGAGAAATG	TCAGGATTAT	TTATTACACA	ACAAGATCTG	ATGCATTCA	ATGTACTTAC	180
AGGTCTAGGA	ACTGTTCAGA	GGAGCACAAA	TGAATGAGAG	AGAGAGGGAG	AGAGGGAGAT	240
TGAGTGAAGTT	AGAGAGTTGT	TGGTGTCTCA	CAAGGAGCAG	TAAAGTATT	AAAAATAAA	300
AAATAATAAG	GCTGACTCTG	TGTCTGCCT	AGGGGTTGGC	CATGCTCCAC	AAAAGCAGT	360
AAAGTGTGTTT	TTGTTTGTT	TCGTTTTTTT	TTTAAAGACA	GACGTCTCGA	G	411

(2) INFORMATION FOR SEQ ID NO:213:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

GAATTTCNGCC	AAAGAGGCCT	AGTTTNAATCT	TCTTACCTAT	TTACTGAATG	CNACATTACT	60
GCACACCAAG	ACAAAAGAGC	TCTCCAGGAA	AACATTGGAT	ATATTGAGAG	CATTAAAAGA	120
TACTGAAAAA	GCTCTAAATAA	ATTCAGTCG	CTTATTTC	AAATTTCAT	AACTACATAC	180
TTAGGAAACT	GTGCTTCAG	TGAGCTAAC	TTCTTTTTT	AAGTAAC	CATACTTTA	240
AGAAAAACAT	TTTAAAGAAGA	CAAAAAGTAT	TTATTAAGCC	CATCTAAAG	GCTAATGCAA	300
ATTCCCAAAA	AAGGAGCACA	TAGAGATAGG	CATCTCGAG			339

(2) INFORMATION FOR SEQ ID NO:214:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 204 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

GAATTCGGCC	AAAGAGGCCT	ATTGAATTCT	AGACCTGCCT	CGAGACACTA	GCCCTTTTT	60
CTGTTGGTTT	AGCACAAATA	CTTCCTCCT	CCGGCACCTC	CAAACCTACC	CCACAGTCAG	120
TGTACTTGTT	TTATATATAT	TTAACCTTAT	TCAATGGAAA	CCATGCTTT	GTCGTTTTAT	180
ACTTTGCTAG	GTAGACTTCT	CGAG				204

(2) INFORMATION FOR SEQ ID NO:215:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 301 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

CTCGAGAGGC	GCATCTTCAC	TGGCATATGA	CAGGCTGTCA	CTGCAGCTAA	TGTTGGTACA	60
GTTCATCCAA	AGACCTACTG	ATGCATCTAC	CGTATTGGAA	ACCAACCAGA	CATTGGCAAT	120
GGTGCTAAC	AATAGCATAA	TAACAGTAGC	GATGTGGACC	ACAAAGATAC	CAGCCAGCAA	180
TACCAACATG	TTGGCTCTT	TTTTTTGGT	AACTTGTGAG	CAAAGAGAGT	TCTGAAGGGT	240
CCCAGCGACA	GAGGCACCTCG	AGGCAGGTCT	AGAATTCAAT	TAGGCCTCTT	TGGCCGAATT	300
C						301

(2) INFORMATION FOR SEQ ID NO:216:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 319 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

GAATTCGGCC AAAGAGGCCT AAAATATTTG AGTCTAACT TATAAATTTC GCATTCTCCC	60
TAACGAAAAA ATTTCTATTA CTGTGGTGA TTTCTTTAAA TTTTGAATAT AGTTACTGAA	120
ATATTAATTC TTCAATTAA ATTATATTT ACTCACTGGT TCCTTCCCT TCTTTAAGGA	180
GACAGAAAAC ATTAACACTT TTAAACCTCT CATTGTTA AAAATTTATT GACCTCTCCT	240
CTGAGACAGT TTGTATTCT AGATCTCTT AACACATAAT ATGCTTATT TCAAGTTTT	300
GTCACAGTAT TCACTCGAG	319

(2) INFORMATION FOR SEQ ID NO:217:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

GAATTCGGCC AANGAGGCCT ATTTAGATTAAACCCAGTTT GTAGACATTT GCATAGATCA	60
ACGAAACTA GAAGAGTTT AAGAGAAAGC ATCAGAACCT TACAAGAAAT TTGAAAAAGA	120
GTTTACCGAC CACCAAGAAA CTCAGGCTGA ATTGCAGAAA AAAGAGGCAA AGATTAATGA	180
GCTTCAAGCA GAGCTACAG CTTTAAAGTC TCAGTTGGT GCCTTGCCAG CTGATTGTAA	240
TATCCCTTTG CCTCCCTCTA AAGAAGGTGG AACTCGAG	278

(2) INFORMATION FOR SEQ ID NO:218:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 298 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

GAATTCGGCC AAAGAGGCCT ACCTGGCTCA TTTATAACCT CCTCGATCCT ATTACTGATT	60
TGCATTCCTA ACTACAGGTA AGAGAAAACC AGTGCAACCT AGCTTCAAT AGACAGGAAT	120
TTGCTGGCTC ATATAATGA GACATCCAAT AAAGAAGAAA AGTTGGAAAA AATGTGTCAA	180
ATGTAGCATC CTCTCTCTCT CTTCTCTCT CTCTCTGT TTTCACCTAG GCTTGTGCCA	240
TAAACCTGCT TCTACATCAG TTACTGTGGT TATGGCGTC TTGTTGGCTG AGCTCGAG	298

(2) INFORMATION FOR SEQ ID NO:219:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 251 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

GAATTGGGCC AAAGAGGCCT ACTTAGCAGA ATATATTCTT TAATAGCTCC CATAAAGCAA	60
ACAAACCAA AATATATTCT CCTGACCCA CATTCACTTC CAACTATCAC CCTACATCTA	120
CATTCTCCTT TTCATACCAA ACTTTTCCA AGCAGTTGTC TATATTATG TCTCCACTTC	180
TTTACCTCCTT ATTCTTGCTT CAGTATGCTT CAGTTGAGCT TCGTCCCCCT GTAGTCCACC	240
ACCAAACTCGA G	251

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

GAATTGGGCC AAAGAGGCCT AGATTGATTG TGTGTTGTTG TATTGGCCCT TACATACAAC	60
TGGAGGAAGT GTGAATTTCAT TCATGTTGAT AAATTGGACT GTCATGATTC TTTATAATTAA	120
CTTCAATGCC ATGTTTGTCG GTCCGGGCTT TGTCCTCTG GGGTGGAAAC CGATGTTGTA	180
TGAAGATGGA CCATCACTGT CCTTGGATCA ACAACTGTTG TGTTACCAA AATCATGCTT	240
CGTTCACACT GTTTCTCCTT TTAGCACCAAC TGGTTGTAT CCATGCTGCT TTCATTITG	300
TGATGACTAT GTACACACAG CTTTATCATC GGCTCTCCTT TGGGTGGAAC ACAGTGAAGA	360
TCGACATGAG TGCAGCACCC TCGAG	385

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

GAATTGGGCC AAAGAGGCNT ACCCNAGATTA TAGTTTTGTT ATTGTTTTTA CAATTTTTGT	60
GAATTAGGAT CCAAATAAGG TCTGTAATAA TTACATTGGG TTTAGGTAAT CGATACTTTT	120
TTTCTTTAA TCTATAAGTT TTCTCTATC TTTTTATTGT GGTTATTCCC ATACAATTGG	180
TTTGTGAAG AACCCAGGTC TTGCCCCAT AATACTCTG AGAACCTAGA TTGTGTTGAT	240
GAGATCCAG TGGTTCATG TAATATGTTC TTTTGTCCCT TGTATTTCCT GTAAATTTG	300
TTTATTATAT TTTTTTATT TCTATTATTT GAGATGGAGT CTTGCACTGT CACCCAGGCT	360
AGAGTACAGT GGCATGATCT CAACTCACCG CAACCTCGAG	400

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

GAATTGGGCC	AAAGAGGCCT	AAGAGCCTAT	AAGGTTACA	TATTCACTG	GAGAGAGAAA	60
TAGGGACATA	CAATAAATGA	TTTTATAATA	AATTCATG	AAAAGTGAAT	CTGAAAACCC	120
CACCGGAAGG	CAGAGTAGTG	CAGCCAAAGG	AGCATGAATT	GTGGAATCAT	ACACCTCTAG	180
GTTCAGATCC	TACCTTACCC	ACTTGATAGC	TAGGCAGACT	TCAACAAGTT	AGTCTAATT	240
GAGCTTCAGT	TCTCTCATCT	GTGAAAAAGA	AAAATACAG	CCACTTTATA	ACATTATT	300
AGATGCCATA	AGGTAGGTAA	AGTGCAGAC	ACATAGATTC	AAAATCTCA	ATAAAATAGG	360
AAGGCTGGAA	TTTCAAAT	TTTTCTTGC	TTTCACAATC	TGGGTTCTAA	ATTTATTATT	420
ACTCTACCCA	TCACTTCCTC	CTTCTCCCTC	CACAACTCTA	CTATAAGCCC	AACATCTCGA	480
G						481

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

GAATTGGGCC	AAAGAGGCCT	AGTGTCAATGT	AGAGGTCTCA	GCATTTCTCT	TAGTATTGAA	60
CTGTATTAGT	TTTACATATT	TCTTCTTTG	TTTAGACTAT	AACCGCTTCT	TACATTTCT	120
TCAGTCGTTT	TCTAAAGAAG	AAATTAATCT	TTTTAGAAAT	CCTGGCAGTT	ACCCCGCAAT	180
TGATGTTTG	GTGAAAATT	AGAGCACACC	AGTTGTCAT	AACTTTAAGA	AACATTTCA	240
CTTTATTGAT	ATTCTGAGGA	TTTTAGTGAT	TTGGGTAATT	TGGGTCATAAT	AAAGAGTAAA	300
TTGTTGAATA	CTCATTTGTT	TTGAGTCATC	TATATTTTA	AACCCTTCT	TTAGTTGTTT	360
TTTCATCCCT	AATACAAATG	CAACTTTCCC	ACTTGCTCGA	G		401

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

GAATTGGGCC	AAAGAGGCCT	AAACTGATGT	CTTCCATTG	CTGGATAGGA	CATGCTGACT	60
GATGACCTCA	CAGACTGTT	TTATGCCCTC	ACTACTCACC	TCACCCACCTA	CAGTCATAGG	120
CTGACTAGGA	GTTGGTTGTG	TACATTCCTA	AACTTTTG	CCCTCTTAT	TTGCTTTCT	180
AAGTGTGTAT	TCAGTACTAT	GTAAATTGAT	AAAACATGAG	TGTGAAAATA	TTTTTTTIG	240
CTATAAAAT	GTAAATTGAA	TTCTTGGGG	AAGAGCTGAT	AAAATATGTC	ACTTAAAGAT	300
CTTGTAAAT	AGATGAGGG	AGATATAGAT	GACAGAACT	CTTTCAACAA	ATATCTAAA	360
AGATGTGCCA	CTCCAATTAT	TTTGTGAGTG	TCTTCAGTT	TGTCCCAC	TTAAAGAAA	420
ACCAAACCTGG	CCATCATAGC	CAATGAATTA	TGCAGGAGTC	TCGAG		465

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

GAATTGGGCC	AAAGAGGCCT	ACACATTATA	TTAGATTCA	TAGAAACTGT	TGAAATATC	60
TAGCACATGT	GCTTATCCC	ACAATAATTA	CATAGAAAAT	TAAAAAGAAT	TAATTCTAAT	120
GTAACCATCT	TTTACTGAA	CTTTTTTTT	TTTGCTCTG	CTCACAGTC	TAATTGTTGT	180
TATTCTCACT	TTATTTCT	ATAAGGTAGG	AATAATATCC	ACTTCATTAG	CTCATCATGA	240
GGGATAAGTA	GGATTGGAAA	AGATCTTC	AAAGGGCACC	TAACTGTGAA	GAAGATGCCT	300
TCATTTGCAT	TTCTTCTTG	GCACATTCT	TGTTATCCAG	TCATTCTTA	GGACTCCATG	360
TTTATTGAAC	ACCTACTCTG	TGCCAGGCAC	TTTCTCTGT	TCTGGAAATA	TCACCATGTA	420
AAAACAAATA	GCTGAAGAAT	GCCCTGCCCT	CATAGAGCTT	ACAGACATAG	AGCTCGAG	478

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

GAATTGGGCC	AAAGAGGCCT	AGCGTTCTG	ACTTTATTAC	TGGTAATTAA	TTGCACAGGT	60
TTTTCTGCAT	CAAAAAAGTA	TCTGCTAAA	TAGAGAAAAGT	TGTGTCTGAA	TTCACATTTC	120
CCCCCAACTT	CTAAAATAT	TTCCCTAAA	AAAGAATCCA	CTCATCTAAT	TTAAAGAAA	180
ATATACCTCT	TACACAAGAC	AATCCAAACT	GATGCAAAT	ATTTATTCCA	AGTTAGTTAT	240
TTTATGCAGT	AGTTTCCCCC	TCGAG				265

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

GAATTGGGCC	AAAGAGAGAA	ATTTTAATCT	TGAAAGACTT	TTCAGGGTAT	CTCATTCTT	60
AGGTGGGGT	GGCAGGTGTA	TTTCTTTTTT	AACAAATAAA	AGGCATTAA	GTAAAACCAA	120
AATGAAAAAA	GTAGGCCCTC	TGACATTGTG	TACTTGGTGG	TTCTGTCCCT	CTGCCCTGTAA	180
CAAATCTCAT	TTTTGTTACC	AAGAACTGTA	TGAAAGAAGT	AAATCCACCC	CTCTCGAG	238

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

GAATTCCGCC	AAAGAGGCCT	ATGCCGTGTT	TGGGTTGACA	GTGAGGGTAA	TAATGACTTG	60
TTGGTTGATT	GTAGATATTG	GGCTGTTAAT	TGGTGTGTA	GAATATTGGA	GCACAGGTGG	120
AGTAGAAACA	AATCACAAAG	ACTTTAACCA	GTTGAGGTAT	AATGAAAGTC	TCACAAACTT	180
CAGCTGTCAT	GGGAAGAATG	GAACCACCAA	TGGAAGGATC	ACTCATGGTT	TCAAGTTACA	240
GAGTGCCTAT	GAGAGTGGCC	TGATGCCCTA	CACGAATTAC	ACATTTGATT	TCAAGGGTAT	300
AATAGACTAC	ATTTCTATT	CTAAACCTCA	GCTGAACACC	TTAGGCATCC	TGGGCCCTCT	360
GGACCACAC	TGGCTGGTG	AGAATAACAT	CAGTGGCTGC	CCGCACCCCC	TCATCCCCCTC	420
TGACCACTTC	TCACCTTTG	CACAACTGGA	GCTCTTACTG	CCTTCCTGTC	CCCAAGTCAA	480
CGGCATTCTC	GAG					493

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

GAATTCCGCC	AAAGAGGCCT	AAGAAATCAA	AATTAAAGCA	ATCAAATAAT	ACTCACATT	60
ATATAAGAAA	TACTTCAATT	TACTTCCAA	TGAGTAAAGT	TTTATATTAA	ATGTTTTAAT	120
ATTTCATATT	TTAGTTTCTT	GCAATTATTT	ACTTTTTCTA	AAACCTACTT	AAATTAGGTT	180
TAAAAGCTA	CTATATATAA	TTTGAAATT	TATTCAAGTTT	GCCTACAGGT	GTGTTTTAAC	240
CACTGTGTAC	ATAGTATTAA	ACGGTCTGCT	TTTTTTTTT	TAATATGGT	TCATGNTNGA	300
ACATCTGTAT	GTTCACTATT	TTCTTGACAA	AGTTCTAAAG	GTTACTGTG	TGAAGCATAAC	360
TGAACGATTA	CTGATAATT	CTATTTGAG	GAACAGGTAT	GTCAGTTCTT	TCTCTCTGTT	420
TGATAATTCT	CTCTTTCCC	CTTAGGAATC	AAAAAAATCCT	TGTGGAGTGT	CTTACTCCTG	480
ATTTTCAAGG	TGATCTCAA	GCAATAGAAA	AAGTTGCTCT	GTCAGGATTA	GATGTGTATG	540
CACATAATGT	AGAAACAGTC	CCATTGCTCG	AG			572

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

GAATTCCGCC	TTCATGGCCT	ATCGAGATAAC	GCTTTCGCGC	ACCAGGTACG	CCTGGTGT	60
CTTTGTTGTT	TTTCGGATTC	TTTTGGGGA	GTGCGGGGAG	TCACAGTTAG	AAGGCGGCCG	120
GGTGGTGTG	GAGGAAAGTG	CTGAGGTCCA	GAGCCTAGTC	CGAGGGCTCC	GAAGTCAGAT	180
TAAAGGGCTC	GAG					193

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 608 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

GAATTCCGCC	TTCATGGCCT	ACATAATGAT	GCTGCCTCAA	AACTCGTGGC	ATATTGATTT	60
TGGAAGATGC	TGCTGTCATC	AGAACCTTTT	CTCTGCTGTG	GTAACCTTGCA	TCCTGCTCCT	120
GAATTCCCTGC	TTTCTCATCA	GCAGTTTAA	TGGAACAGAT	TTGGAGTTGA	GGCTGGTCAA	180
TGGAGACGGT	CCCTGCTCTG	GGACAGTGGA	GGTGAATTTC	CAGGGACAGT	CGGGGACTGT	240
GTGTGATGAT	GGGTGGAACA	CTACTGCCTC	AACTGTCGTG	TGCAAACAGC	TTGGATGTCC	300
ATTTTTCTTT	CGCCATGTTT	CGTTGGAC	AAGCCGTGAC	TAGACATGGA	AAAATTTGGC	360
TTGATGATGT	TTCTGTTAT	GGAAATGAGT	CAGCTCTCTG	GGAATGTCAA	CACCAGGAAT	420
GGGGAAGCCA	TAACTGTTAT	CATGGAGAAAG	ATGTTGGTGT	GAACGTGTTAT	GGTGAAGCCA	480
ATCTGGGTTT	GAGGCTAGTG	GATGGAAACA	ACTCCTGTTG	AGGGAGAGTG	GAGGTGAAAT	540
TCCAAGAAAG	GTGGGGACT	ATATGTGATG	ATGGGTGGAA	CTTGAATACT	SCTGCCGTAA	600
	TACTCGAG					608

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

GAATTCCGCC	TTCATCGCCT	ACAGCGCTGC	CTTTCCTTAT	GAAGAAGACA	CAAACCTGGA	60
TTCTCACTTG	CATTATCTT	CAGCTGCTCC	TATTTAATCC	TTTCGTCAA	ACTGAAGGGA	120
TCTCGAGGAA	TCGTGTGACT	AATAATGTA	AAAGACGTAC	TAATGGTG	GCAAATCTTC	180
CAAAGACTA	CATGATAACC	CTCAAAATATG	TCCCCGGGAT	GGATGTTTG	CCAAGTCATT	240
GTTGGATAAG	CGAGATGGTA	GTACAATTGT	CAGACAGCTT	GACTGATCTT	CTGGACAAGT	300
TTTCAAATAT	TTCTGAAGGC	TTGAGTAATT	ATTCCATCAT	AGACAAACCT	GTGAATATAG	360
TGGATGACCT	TGTGGAGTGC	GTGAAAGAAA	ACTCATCTAA	GGATCTAAAA	AAATCATTCA	420
AGAGCCCAGA	ACCCAGGCTC	TTTACTCCCTG	AAAATTCTT	TAGAATTTTT	AATAGATCCA	480
TTGATGCCCT	CAAGGACTTT	GTAGTGGCAA	ATCTCGAG			518

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

GAATTCCGCC	TTCATGGCCT	ACCTTGATAC	ATCAGCTGAC	CTCATTTCCG	GATACTTTT	60
CCCCCCCCAA	AAAGTACAACA	TCTGGGCCGC	CCCAGCCCCA	AGACAGATCG	TCGCTCCCTG	120
GACAATCAGA	CGAATTCTCC	CCCCCCCCGC	AAAAAAAAAG	CCATCCCCCC	GCTCTGCC	180
GTCGACATT	CGGCCCCCGC	GACTCGGCCA	GAGCGGGCGT	GGCAGAGGGAG	TGTCCGGCAG	240
GAGGGCCAAC	GCCCGCTGTT	CGGTTTGCAG	CACGCAGCAC	GGAGGTGGGC	GGCAGCGTCG	300
CCGGCTTCCA	GACACCAATG	GGAAATCCAA	TGGGGAAGTC	GATGCTGGTG	CTTCTCACCT	360
TCTTGGCCTT	CGCCTCGTGC	TGCATTGCTG	CTTACCGCCC	CAGTGAGACC	CTGTGTCTCG	420
AG						422

(2) INFORMATION FOR SEQ ID NO:234:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 412 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

GAATTGGCC	TTCATGGCCT	AAGAGATTAA	GTGATTTACT	CAAGGTCATA	TTCCTTGAA	60
GTAGCAAAC	TTCTGGACCA	GATTTCTGAT	TCCAAGGCG	GTACTGCTTG	TACAACACTC	120
TGAGAAGTAA	TTACTGTGGA	GCAAAGAAA	AGGAAGTCTA	AAAGCAGGTG	ATAGGTGTA	180
ATTTAGATAG	TGTAAGGGTA	GGCTAAAGTG	TTGTAACAAA	TGCACCCCTCA	AGTAGGTTAAT	240
GGCTCAAACA	CAATAGATGT	TCACTTCCC	CATCTCAGAG	CAAATTGGGT	TCTCCTCATC	300
AGCTAAAGCT	TTCCATCACATG	GGATGATTTG	GGGAGCAAGA	CACTCCATCT	ATGGCTCCCT	360
TACCCTCCAA	GGCCTTCTTA	TTGTCCTTAT	GTAACCAGTG	GAAGAGCTCG	AG	412

(2) INFORMATION FOR SEQ ID NO:235:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 574 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

GAATTGGCCT	TCATGGCCTA	GGCTTCTTCG	GAGCTGTGTA	NTCTTAATT	GCTTGCTGC	60
TGGCTGGCTG	ACAGCTGATG	GGGGACTCCT	CANGACGGAC	TCCCTTCCAG	ATGCACCCAT	120
CTCCATCCTT	CTCAACTCCC	CAACCTTGT	CCTCCCCACT	CTTCGCTCGC	GGGGCGGTCT	180
GAGACCACCA	GGACCAAGTTT	CAGGGGTTTC	CTTCTCCAGC	GAGACTTGGC	AGAACAGGCT	240
TTAAAAGCAA	AGGAGGCAGC	GGAAAGACTGT	GAATTCCTT	GGACAATTGA	TGATATTAT	300
CATTGTGCC	AGTTTCTACA	AATAAAAGAT	GGGTGGATTA	TTTTCTCGAT	GGAGGACAAA	360
ACCTTCAACT	GTAGAAAGTTC	TAGAAAAGTAT	AGATAAGGA	ATTCAAGCAT	TGGAAGAATT	420
TAGGGAAAAA	AATCAGAGAT	TACAAAAATT	ATGGGTTGGA	AGATTAATTC	TGTATTCTC	480
AGTTCTCTAT	CTGTTAACAT	GCTTAATTGT	ATATTTGTGG	TATCTTCCTG	ATGAATTAC	540
AGCAAGACTT	GCCATGACAC	TCCCACATCT	CGAG			574

(2) INFORMATION FOR SEQ ID NO:236:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 332 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

GAATTGGCC	TTCATGGCCT	AGGCGCGGCC	CGGGTTCCCG	TTCCCCCGGG	AGCCATGCGG	60
TACAACGAGA	AGGAGCTGCA	GGCTCTGTCC	CGGCAGCCGG	CCGAGATGGC	GGCCGAGCTG	120
GGCATGAGGG	GCCCCAAGAA	GGGCAGCGTG	CTGAAGCGGC	GGCTGGTGAA	GCTGGTGGTG	180
AATTTCTCT	TCTACTTTCG	GACAGACGAG	GCCGAGCCCG	TGGAGCCCT	GCTGCTGGAG	240

CGCTGCAGAG TCGTCCGGGA AGAGCCCGGC ACCTTCTCCA TCAGCTTCAT TGAGGACCCCT 300
GAGAGGAAGT ATCACTTCGA CTTCAGCTCG AG 332

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

GAATTCCGGCC TTCATGGCCT AATTGCAAGA TCACGGAATC TCCTGAATCA TTAAGAAAAG	60
ATAAAATATC ACAAGCATCT TTAGTGTATT CTGTATTCAAG TAATTCTTTG GAGTTGTATT	120
TATTAACCTT ACCAGATTT AAAGGCATAT AAAATGTGGT AAGATATGAG ACACATACTG	180
AAATATCAGT GCAGGAGGAG AATGGTAGTT GAATGGTCAG AAACGAAAAA CCCTCGAG	238

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

GAATTCCGGCC TTCATGGCCT AGAAGCATTG TTGTTTATTG TGAAACATTT TTATACCTTC	60
ATTATAATTG GTTGAGCCTA GAGTTGGCT ATTGAATAT TTATTATGAT AATCTTTGG	120
CTAATGGTAA CAGCATATCT TGTTCTAACAA AAATTACTGT TAACAGCAAT CGAACCTCGAG	180

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

GAATTCCGGCC TTCATGGCCT ACTGAGATCC AGACCAGCTC CTCCCAGACC TCTCCAGAAG	60
AAGCCATGGG AACCCCTCGT ATCCAGCATT TGCTGATCCT CCTGGTCTA GGAGCCTCCC	120
TCCTGACCTC GGGCTAGAG CTGTTTGTC AAAAGGTCT GTCCATGACT GTGGAAGCAG	180
ATCCAGCCAA TATGTTAAC TGGACCACAG AGGAAGTGA GACTTGTGAC AAAGGGGCAC	240
TTTGCCAGGA AACCATACTA ATAATTAAG CAGGGACTGA GACAGCCATT TTGCCACGA	300
AGGGCTGCAT CCCGGAAGGG GAGGAGGCCA TAACAATTGT CCAGCACTCT TCACCTCCCG	360
GCCTGATCGT GACCTCCTAC AGTAACTACT GTGAGGATTC CTTCTGTAAT GACAAAGACA	420
GCCTGTCCTCA GTTTGGGAG TTCAGTGAGA CCACAGCTTC CACTGTGTCA ACAACCCCTCC	480
ATTGTCCAAC CTGTGTGGCT TTGGGGACCT GTTTAGTGC TCCTTCTTT CCCTGTCCCCA	540
ATGGTACAAC TCGATGCTAT CAAGGAAAAC CTCTCGAG	578

(2) INFORMATION FOR SEQ ID NO:240:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 334 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

GAATTCTGGCC	TTCATGGCCT	ACATGAATCC	ACTCCTGATC	CTTACCTTTG	TGGCAGCTGC	60
TCTTGCTGCC	CCCTTTGATG	ATGATGACAA	GATCGTTGGG	GGCTACAAC	GTGAGGAGAA	120
TTCTGTCCCC	TACCAGGTGT	CCCTGAATTTC	TGGCTACCAAC	TTCTGTGGTG	GCTCCCTCAT	180
CAACGAACAG	TGGGTGGTAT	CAGCAGGCCA	CTGCTACAAG	TCCCAGCATCC	AGGTGAGACT	240
GGGAGAGCAC	AACATCGAAG	TCCTGGAGGG	GAATGAGCAG	TTCATCAATG	CAGCCAAGAT	300
CATCCGCCAC	CCCCAATCG	ACAGGAGACT	CGAG			334

(2) INFORMATION FOR SEQ ID NO:241:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 368 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

GAATTCTGGCC	TTCATGGCCT	AGGGCACCAC	TGAGTTCACT	ACTTCAAAAT	TGCCGTGCTC	60
TACCTCTCCC	CAGTGACAA	AAACACTCTC	CACACCAAGC	TGCTGCTGCT	GGGGGATGGA	120
GGGATGGCGT	CAGCGATTCA	AGACTGTTT	TCCTACCTGT	TCAGCACTTC	TTTCAGCGAT	180
ATGAAGTTAA	ATCCAGTCCT	TCCCTGTCTC	CAGGCATCAT	CGCCATCAAC	ATACAGCCAT	240
ACTCCAGGAT	TGCCCATCTT	CAACATAAAC	GGACTCTCCT	GGACTCCACT	TCCCACATCA	300
GTCACAGCCA	CACTTCTGA	GAAAGAAGTC	TACACTCTTC	ATTCACTTTC	ATTCACTTCA	360
GTGTCGAG						368

(2) INFORMATION FOR SEQ ID NO:242:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 478 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

GAATTCTGGCC	TTCATGGCCT	AGAGAAAATA	AAGAGTTATA	TCAGAAATTT	ACAAACATAA	60
CTTTTTAAAT	TTTAATTGCA	AAAATATATA	TCATACGAAA	ATGAAAATTA	TAATTCTTCT	120
TGGATTCTG	GGAGCCACAT	TGTCAGCCCC	ACTTATCCCA	CAGCGTCTCA	TGTCTGCCAG	180
CAATAGCAAT	GAGTTACTTC	TTAATCTTAA	TAATGGTCAA	CTTTGCCAC	TACAACCTCA	240
GGGCCCACTT	AATTCTATGGA	TTCCACCTTT	CTCTGGAAATT	TTACAACAGC	AGCAGCAGGC	300
TCAAATTCCA	GGACTCTCCC	AGTTCTCTT	ATCAGCTCTA	GACCAGTTG	CTGGACTGCT	360
CCCAATCAG	ATACCCCTAA	CAGGAGAGGC	CAGTTTGCC	CAAGGAGCCC	AGGCAGGCCA	420
AGTTGATCCC	TTACAGCTTC	AAACACCGCC	TCAGACACAA	CCAGGCCAC	GTCTCGAG	478

(2) INFORMATION FOR SEQ ID NO:243:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 490 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

GAATTCCGGCC	TTCATGGCCT	ACTTACAGAA	CCTATTCACT	GGGAAGGAAG	CCCTCATTAT	60
AATGATTTTC	ATTCTTATGT	GTGTTTCAGG	ACGACTGGGT	TTGGATTCTAG	AAGAGGATTA	120
TTATACACCA	CAAAAGGTGG	ATGTTCCCAA	GGCCTTGATT	ATTGTTGCAG	TTCAATGTGG	180
CTGTGATGGG	ACATTCTGT	TGACCCAGTC	AGGCAAAGTG	CTGGCCTGTG	GACTCAATGA	240
ATTCAATAAG	CTGGGTCTGA	ATCAGTGCAT	GTCGGGAATT	ATCAACCAG	AAGCATACCA	300
TGAAGTTCCC	TACACAACGT	CCTTTACCTT	GGCCAAACAG	TTGTCTTTT	ATAAGATCCG	360
TACCAATTGCC	CCAGGCAAGA	CTCACACACG	TGCTATTGAT	GACCGAGGCC	GGCTGCTGAC	420
CTTGGCTGC	AACAAGTGTG	GGCAGCTGGG	CGTTGGGAAC	TACAAGAACG	GTCTGGGAAT	480
CAACCTCGAG						490

(2) INFORMATION FOR SEQ ID NO:244:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 386 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

GAATTCCGGCC	TTCATGGCCT	AGAAAAAAGA	AACTGTCGTG	GATACTGTCA	GTGTATATAT	60
TTATGTGTA	CCTGAGAGCC	ACCCCAAATT	AGATTGACTT	TAGATCGTT	ATACAAAAT	120
AGCTTGAAGA	ACTGTTTTTT	CCATGGTAA	TGTTTTGAA	TATTAACCTA	TTTATGTTAG	180
ATTCCTACCT	CAGTGGTACT	GTACACAGCA	TTGGTTACAT	TTCTGAAC	CTTCAGAGTA	240
AGAGTTTGG	TTTTTGTGTT	TGTTTTGTT	TGTTTTTGAA	GATGGACTCT	TGCTCTGTCG	300
CCCAGGCTGG	AGTGCAGTGC	AGCAACCCAG	GTGGAGTGCA	GTGCAACCTC	CACCTCCAG	360
GTTTAAGCGA	TCCTCCTAAC	CTCGAG				386

(2) INFORMATION FOR SEQ ID NO:245:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 396 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

GAATTCCGGCC	TTCATGGCCT	AGCTTCAGTA	GCAAATAAGG	ACATCATCTG	CTATAACCTA	60
CAAGCAGTTG	GACAGATATT	CTACATTCTC	TCATTTCTCT	ACACCGTCAA	TTACATCTGG	120
TATTTGTACA	CAGAGCTGAG	GATGAAACAC	ACCCAGAGTG	GACAGAGCAC	ATCTCCACTG	180
GTGATAGATT	ATACTTGTG	AGTTGGTCAA	ATGGCCTTTG	TTTCTCAAG	CCTGATACCT	240
CTGCTATTGA	TGACACCTGT	ATTCTGTCTG	GGAAATACTA	GTGAATGTTT	CCAAAACCTTC	300

AGTCAGAGCC ACAAGTGTAT CTTGATGCAC TCACCACCAT CAGCCATGGC TGAACCTCCA	360
CCTTCTGCCA ACACATCTGT CTGTAGCACA CTCGAG	395

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

GAATTCCGCC TTCATGGCCT ACACCTTTCA CTTATCTTAT AGTCACTTAA TTCCCTCTACT	60
CTTATCATT GATATTTCA TTTTATTGTG TATCTCTGTN NGGCCAAATC AATAGATTT	120
GAACAAATCTC ACACCTAACC TTTAAAAAA ATCTAATAGG CCCAGTTTCC TCTCAAACAT	180
CTTTGAAGAA CCTTCGAGAA AGGAGAAACA CAGACCTCCC GCTTCTAGAC ATGCACACTG	240
TAACCCGGGA AGAGGGAGAA GGCGATGGAGA CAACTGATAC GGAGTCTGTG TCTTCGCCA	300
GCACATACAC ACAGTCTTCA GAGCAGCTGC TTAACTCTCC CGAAACTAAA CTTGGTATGT	360
TACTCTGTCT AAATATGTTT TTCTTATTTA ATTCACTGT CTTATTTAAT TACTANTACT	420
CTAAGTTACA TATGCTTTTT NGGGCTGCTC CAATAAAATT TCTTTCAATA TTCCACTACC	480
TGTTTGATT AGGTTCTCTA GAGGGACACT CGAG	514

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

GAATTCCGGCT TCATGGCCTA GGTTTTCTGT ACATGGAGAT TAAACTGTCT TCCAAAGTGA	60
AGAGTTTATT GTTCTAGATC TTGAGCACAA AGGTTGGTAT ACCTTAATAA AAAAATAGC	120
AAGGGAAAGAA AATCATTTC TTTCATACCAA GTAAGAGAGC ACTTATCATG GTAGGCAGTG	180
GCTTTGCAAT TATGAGACCA GTAGTAGAAA TAGCTTTAGT TTCCCTCAATT TTCCCTGGAGT	240
ATTCTTCAGA CTTTCTTAC ACTGCTCAAG GTGGGGCGAG TGGCAGGGCG GACCCTGGCG	300
ACCTGACGCT GCGGAGGCTC GAG	323

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

GAATTCCGGCC TTCATGGCCT AGGAACAGTG TGTGTTTTG TGTGTGGCTT GCATTCTCTC	60
CTCCGTTTT GGAGCAGCGT GAGATTATTG CAATGCTACA TTTCCTCCCT CTGGGCCCTC	120
CTACCCCATC AATGTCTCAT GGGTGGTGTG ATAGAGGCTA TGGGAGTGAA GACCACTGGT	180

GTAGTCGTT GTATAGTTCC TGGGGTGTGC CGACTACCAG CTCTGACAGC GGAAGAGAAC	240
TATACTGTTG ATTCGGCTTA TTCTCAGTAG GTGTGTTCTA TAAAATTGCT GCGAACACCA	300
AATTAGCGAA TCCTGAACCA TCCTTCCCAG AGGAATAGGG GGTTAGGGTC CTGTGATCTC	360
CAAGTTGCCA CATTGTCTTC GACTGATTAA TATGTAACCT TGTTTTATAT GTGCAATCTC	420
GAG	423

(2) INFORMATION FOR SEQ ID NO:249:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 124 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

GAATTCGGCC TTCATGGCCT ACCGAAACCA AATAATTCAA GCACTGCTTA TTACAATTTC	60
ACTGGGTCTC TATTTTACCC TCCTACAAGC CTCAGAGTAC TTGAGTCTC CCTTCACCCCT	120
CGAG	124

(2) INFORMATION FOR SEQ ID NO:250:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 289 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

GAATTCGGCC TTCATGGCCT ACATCTATGA CTTTTAAAC ATGCGGGCGTT TTGTGAATAT	60
CATGATAATA ACAAGAGTCA ACAGGCTAAG TGAGAGGAGA GGGATGCTAC GCCTACGCTG	120
CCCCCACAC GGCCAGCCGG CTCTCGCGCC TTTGGTGTTG GATTTTCTTT GTGATTTTAC	180
GGGGTTTGTG GTTTTTTTT TCTTGTGTTT TGTTTTGTTA TTTTTTCTTG TCCACTTGAT	240
TTGCAATGCAA CACCCACAAA AAGGAAACAC AAAACCCCGT CTGCTCGAG	289

(2) INFORMATION FOR SEQ ID NO:251:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 302 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

GAATTCGGCC TTCATGGCCT ACACATGAG AGGACCGATT GTATTGCACA TTTGTCTGGC	60
TTTCTGTAGC CTTCTGCTTT TTCAGCGTTG CCAACACAATG TCTGGCCTTC CCCAAAATAG	120
AAAGGAGGAG GGAGATAGCA CATGTTCATG CGGAAAAAGG GCAGTCCGAT AAGATGAACA	180
CCGATGACCT AGAAAATAGC TCTGTTACCT CAAAGCAGAC TCCCCAACTG GTGGTCTCTG	240
AAGATCCAAT GATGATGTCA GCAGTACCAT CGGCAACATC ATTAATAAAA GCAAAACCG	300
AG	302

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

GAATTCGGCC AAAGAGGCCT ATTTTTTTT CTGAAACAC TGTGTATAAGT GAGACTTGT	60
CTACTTTGGA GAACAGGTTA CCTTTGAAA ATGAGGTTGA GTTCTTCCT TTCTGATGCA	120
TTGATTTTG AAGATTTTT TTTCCCCCTT CCCCTCTCCC TCGAG	165

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

GAATTCGGCC AAAGAGGCCT AGCTTCTTTG TATAATTAA TCTGAGTTT GTTGAGCAT	60
CTTCAACAT GTACCATATT TATGACAATT CTCTTCATA GGATCTATCT GTTCTGCAAC	120
AAGTATTGAT CTTACAGTAA AATTTTCAC AAATTCATTA GATTCTATGT CTCTTTTCT	180
GGTAGGAATT TTGTCAGG TAGCTATCTC TTGCCCTAGA TTATTCCT TGTTTAGCTG	240
CTGATTCTTA AACTGGCCTC TAGATTCCA GATTTCTTCC GGTACAGACT TTCTCTTG	300
AAGTTCTTCC ATCTCTAAC TTTGAGATTA ATCTTCTTT GAAATGTCCT GCTGCTCTAC	360
TCTTGATGTT CTCGAG	376

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

TCTCCAAGGG AAAATAATG CTTTTACTAT CTAGTTTGTCTCTTTGAGAA TTAAACTCT	60
TTTTTTTTT TTTCATTCCA GTAGCTTTG GGGTAGAGTT TGGCTCTTTG AGAATTGCAT	120
ACTAATTAAAT TTAGGGGTG ATTGTACAT CATCTCTATA TTCCTGAAAC ACAGTAGAAA	180
CAGCCAGCAG TCAGGCAACC ATCTACCATG ACCATTAAGA CATCCCCAAA GTGAAACACC	240
AGATGTGATC TGCTAGATTT AGTGGAGGCG GCTGGCTCGA G	281

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 571 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

GAATTCCGCC	AAAGAGGCCT	AGCTAGNCTT	GCTCAGCTTT	GTGGATACCG	GGACTTTGTT	60
GCTGCTTGCA	GTAACCTTAT	GCCTAGCAAC	ATGCCAAC	TTACAAGAGG	AAACTGTAAG	120
AAACGGCCCA	NCCCGAGATA	GAGGACACG	TGGAGAAAGG	GGTCCACCAAG	GCCCCCCCAGG	180
CAGAGATGGT	GAAGATGGTC	CCACAGCCN	TCCTGGTCCA	NNTGGTCNTC	NTGGCCCCCN	240
TGGTCTGGT	GGGAACCTTG	CTGCTCAGTA	TGACGGAAAA	GGAGTTGGAC	TTGGCCCTGG	300
ACCAATGGGC	TTAATGGAC	CTAGAGGCC	ACCTGGTCA	GCTGGAGCCC	CAGGCCCTCA	360
AGGTTCCAA	GGACCTGCTG	GTGAGCCTGG	TGAACCTGCT	CAAACGTGTC	CTGCAGGTGC	420
TCGTGGTCCA	GCTGGCCCTC	CTGGCAAGGC	TGGTGAAGAT	GGTCACCCCTG	GAAAACCCGG	480
ACGACCTGGT	GAGAGAGGAG	TTGTTGGACC	ACAGGGTGT	CGTGGTTTCC	CTGGAACCTCC	540
TGGACTTCCT	GGCTTCAAAG	GCAACCTCGA	G			571

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 453 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

GAATTCCGCC	AAAGAGGCCT	ATGCGCAAGG	ATCAAGCCGA	CTACCTGTGC	TGTCTACTGG	60
GACAGCAGTC	TCCGAGCTAC	TCGGTACCTC	CCTCTGCCAG	GTCGTGGAGT	TAGGCCCGAG	120
TCCCTACTTG	TCACTGGTTC	CCACTGTGCT	CTTAACGTG	CAGCACCTGG	GAGCTCTGGC	180
CTGGGGCTGG	AGGCCCTGGT	AGGAGCTGCA	GTGGAGGCC	GTTCTGTGCC	CAGCAGCGGT	240
GAGCGGCTCC	CATGGGCCCT	GTGCTGCAG	GGAGCCAGGG	CTGCCGCACA	TGTGCTGTGA	300
AACTGGCACC	CACCTGGCGT	GCTGCTGCCG	CCACTTGCTT	CCTGAGCAC	CTCCCTACCCCT	360
GCTCCGTGTC	CTCCCTCTCC	CCGCGCCTGG	CTCAGGAGTG	CTGGAAAAGC	TCACGCCCTCG	420
GCCTGGGAGC	CTGGCCTCTT	GATATACCTC	GAG			453

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 307 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

GAATTCCGCC	AAAGAGGCCT	ATGTCATGAG	TGAACCTGGC	AATTGCCCTTG	TTAAAACCAAG	60
TTGGACATTA	TCTTCCACAT	TGCGAAGCTA	TACATGTCTG	ATATGTTCTG	AAAGAATAGA	120
ATTTATAGTT	AGATATACTA	TTTTGATTA	TTTACTCAGA	AGGAGACATG	TAATTATTCT	180
TATGTGTCA	TGAAAATCTA	TTAAATGCAT	TTATATTCTA	CATCAATGTT	ACGAAGTTC	240
ATTATTATTA	TTTTACAGAG	GGGAAGCCAA	GATACAGGAG	TGGAAATTAC	TTGGCCTATC	300
GCTCGAG						307

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

GAATTCGGCC	AAAGAGGCCT	AAGAAGATGA	ACAAGGCCA	GCTCTATTAC	CAGGTTTAA	60
ACTTCGCCA	TGATCGTGT	TTCTGCACTC	ATGATATGGA	AAGGCTTGAT	CGTGCTCAC	120
GGCAGTGAGA	GCCCCATCGT	GGTGGTGTG	AGTGGCAGTA	TGGAGCCGC	CTTTCACAGA	180
GGAGACCTCC	TGTTCCCTAC	AAATTTCCGG	GAAGACCCAA	TCAGACCTGG	TGAAATAGTT	240
GTTTTAAAG	TTGAAGGACG	AGACATTCCA	ATAGTTCAC	GAGTAATCAA	AGTTCATGAA	300
AAAGATAATG	GAGACATCAA	ATTTCTGACT	AAAGGAGATA	ATAATGAAGT	TGCTCTCGAG	360

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

GAATTCGGCC	AAAGGGGCCT	ACCTGAAACG	GCAGTCCGGT	CCCTCCGACA	TTGTCCAGCG	60
GAAGGCCTGG	GCTTCACACT	CTGTGCTCC	CGGCGCTACC	TGGCACGATG	CCGAGCACAC	120
AGCAGATGCT	CAATGAATGC	CCAACCAACC	CTATACCTGG	CTTGGATCTC	AAGCTCCCTG	180
GCCGGGGCCT	GATGGAAGGC	TTTGGGGCA	CAGGAGGCTG	CCCCCTTGGG	CGCCCCCGGC	240
CACCTCTCG	CCCTCGAACATC	TCAGGCGAGCT	TGGTCAGGAA	CTTCTCTCC	ACGTATTTAG	300
CGTGAATCCA	GGCCTCCCTTC	TCTGCGCTGT	GGGAGGGGAG	AAGCAGCGAG	TCTTCCCTCT	360
TCTGCTCCAG	GGGTCCCCCA	TTCCCCTGGG	AGGCTAAACC	CATAGCTCGA	G	411

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

GAATTCGGCC	AAAGAGGCCT	AGGGAGTGTT	TGCGTTCTT	CTCCGTTGG	CAGTGAACACA	60
CATCTCAGAA	AGGTGGAGCT	GATCAGATA	ATGTTCAGCA	TCAACCCCT	GGAGAACCTG	120
AAGGTGTACA	TCAGCAGTCG	GCCTCCCTG	GTGGTCTTC	TGATCAGCGT	AAGGCCATG	180
GCCATAGCTT	TCCTGACCCCT	GGGCTACTTC	TTCAAAATCA	AGGAGATTA	ATCCCCAGAA	240
ATGGCAGAGG	ATTGGAATAC	TTTCTGCTA	CGGTTCAATG	ATTTGGACTT	GTGTGTATCA	300
GAGAATGAAA	CCCTCAAGCT	CGAG				324

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

GAATTCCGCC AAAGAGGCCT AGTGGGGCTG TATTTTAATA CAAGAAAGAC ATTGCTCTAG	60
AACATGGCTC GCCTTGCTT CAGGGCCTAG CAGTTTATTT TAGCCATAAG GGTAAGGGAG	120
CAGGTCAAGAA ATGACTTTTA GTGTAATCCT ATCTGTAATT AAAATACAA ATGCTGTCA	180
AAGATCAAAT GTTATCAAAA ATCAGTATT AAAATTAAAT TTACCCCCAA ATTCTTTCA	240
AAAAAGTTGT AATGTTCTTT TTCAGTGAAG CCTTGCACCT GCTAGAGCTG AAGAATGTGA	300
TCAATCGGCC TGTTGAATAA TCCCGCACAG TAGGTATTCC GCTGAAGCCA ACTCTAGCTG	360
GGGGCTCGAG	370

(2) INFORMATION FOR SEQ ID NO:262:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

GAATTCCGCC AAAGAGGCCT AAGAAATAGG ACTATACAAA TTTTCAACTT CTTTGATAT	60
CAGTTTGCTT AAGATGCATT TTTCTTCGAA GAATTGTTT CATTGAAATT TCCAAATTAA	120
TTAGCATGAA GTTGTAAATA AAAATCTTAT ATTTTACTC AAATTTGAG ATAGTTGTAG	180
ATTTACATGA AGTTGTAAG AATAATAGAA AGATCCTGTG TACCTTTCC CAGTTTCCC	240
CAAAGTAAC ATTTGCATA ACTCTAGTAC AGTAGCACAA CTCGAG	286

(2) INFORMATION FOR SEQ ID NO:263:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

GAATTCCGCC AAAGAGGCCT AGGCAAAACCG TGTACTAACG ATCAGTGCAG AGATAGTGAA	60
TGAGACACAG TATTCCACC TTGAGCAGT GCCAGTCAG TATTAGAATA TTTTTGGCTA	120
AAAAATTATT TTGAAGCATA AAGAAGCTT TGTTTGCTCT GGTGATTTTC ATAACATATT	180
CACATTCTTA ATGTATTTTT GGTTTTTCAG AAAGTTACTT CTGGCCTGTG TTCTTTCAGA	240
ATATAGTTG CAGCTTGTGT TAAGTGCAGG AACTATTGAT AGACTGAGTT TAGAAGAAGG	300
GAAACTCGAG	310

(2) INFORMATION FOR SEQ ID NO:264:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

GAATTCCGCC	AAAGAGGCCT	AGGACTTGG	GGCAGGTGAT	TAAATTATA	TAGGTACCTC	60
AAGAAAAAAGA	ACCTGAATAT	SCTGCATTTC	CTTCTTTAG	CTTTACATG	TAGCATTTG	120
TTTGCTTT	GTTATTTTG	TTTGATATA	TGCTTTGG	ACCCCAATAG	ACTGTTGAAA	180
GAAATTAAA	AATTACTCTT	GTAGGGATAT	AGTATCCTTA	AAAAATAAAA	ATTAAAAAAA	240
ATTTAAAAAA	ATTGCTGCAA	TATCTGGCTC	GAAGGTTGCC	CTATATTAGA	ATAACTTT	300
AGCCAAACAC	ATCAGCTCGA	G				321

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 550 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

GAATTCCGCC	TTCATGGCCT	TGTGATTCTG	CAAAGGAGGA	ACAATAATT	ACTGTTCCC	60
AAACTTATCT	GACCATAGAA	CATATNTCTC	AGAGTATT	TCAAGAGTAG	TATTTCTGT	120
AATATATGAT	GAAAAATAAT	CGTATCGGCC	ATCTTGTAC	ATAAGGTCAA	AATGTCAGCC	180
AGCCCTGAAA	AAATGCAAG	CCAAAAGGTA	GAGAGATAA	TGAATAAGC	TGGCACACTG	240
TCAGTCGGGA	GTACCATGCT	GCATTCTGAG	TCAAGCTCCA	GGAAACTGAG	CTAGGGTTG	300
TCTCTAAGAA	AAAAAACTGG	AGCGTCCAAA	GCTTCTGGAT	TCCATTAA	AAAACCCCTT	360
TTAAATTAAA	TCTCTGTAAC	TGAAGAGTAT	CGGTGGATGA	AGAAAAATA	GTCTCACATG	420
TCTTCATTT	CATCCTTGGC	TCACTACAGC	TCCAGTTCCA	TTATTCTAA	ACATCTATTA	480
ACATGATTGC	AAATAAATTA	CACAGGCTAA	CTGCCAAGCA	TTTTTCACAG	GAAGCAAGGC	540
ACTGCTCGAG						550

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

GAATTCCGCC	TTCATGGCCT	AGTTAAGTGG	GAAGTTAAC	GGCAAGTACT	AGAATGCCAC	60
CTATGCCAAG	CACTAGAATG	GTCTAGGTGT	GAAATGAGGG	AGTAATGTCA	GGGAGTCAAG	120
GTGGCCATCC	ATAGCAGTGA	TTCTTATCTG	GGGTAGGGGG	TGAATTTCAC	GTGGAGGGAG	180
GTCTCTGGAC	ATGGACCCCC	AGGCAGGGCT	ATCCAATCAT	CTGAGGGGTG	AGCAGTGTTC	240
AGCTCAGTAA	AAAGTAAGGGA	AAAAAAATAG	CAGTCTCTAA	AAGGAACATA	GAGCGCTCGA	300
G						301

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

GGGGAGAGCA TCAGGAAGAA CAGCTAATGG ATGCTGGGCT TAATACCTAG GTGATGGGAT	60
GGTCTGTGCG GCAAACACCA TGGCACAAAGT TTACCTATGT AACCTGCACA TCCTGACATG	120
TACCCCTGAA CTTAAAATGA AAGTTGGAGA CCAAAAAACA AAACACCATA AACTACAAA	180
ACTTCTTAAA CAATAAACTA GTAGAAAATT TCTAAAATAT ATAATTCAAG AATTATATAA	240
GAGCTTTT TATATGAAA TATAAATTAA AATACAAGAG AAACATCTAA AACAGGTTGC	300
TTCTGAGAAA CGTGAAGGGT TATTAAGAAG AGGTATATAG GGGCTCACTC GAG	353

(2) INFORMATION FOR SEQ ID NO:268:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 241 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

CATTATTTAA CCTTTTAAAC AATCAAGAGA TTGCTTTTA AATTTGTCCT AAAAAGGTTT	60
GATTTTTTAC GAAAGAGAGA GCACCTGAAT ATATCTTTAT GTACCACCGT GTCTCTTTT	120
GTTAGATTT TCATCTGTGG GTATAATATA AAATATTCTT AAAATGAAAG CTTAACGCTT	180
GTGTTGAGA CTAAGCAACT TGCATTGTGT CATGACCCCTT CTAATACAC AAACCCCTCGA	240
G	241

(2) INFORMATION FOR SEQ ID NO:269:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 330 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

GAATTCCGGCT TCATGGCCTA CACTCAACCA CTGAAAAGC TGAAAATCAA TGTTTTTAAG	60
GTTCACAAAGT GTGCCGTGTG TGGCTTCACC ACCGAAAACC TGCTGCAATT CCACGAACAC	120
ATCCCTCAAGC ACAAAATCGGA TGGTTCTTCC TACCAAGTGCC GGGAGTGTGG CCTCTGCTAC	180
ACGTCTCAAG TCTCTCTGTG CAGGCACCTC TTCATCGTAC ACAAGTTAAA GGAAACCTCAG	240
CCAGTGTCCA AGCAAAATGG GGCTGGGAA GATAACCAAC AGGAGAACAA ACCCAGCCAC	300
GAGGATGAAT CCCCTGATGG CCCCTCTCGAG	330

(2) INFORMATION FOR SEQ ID NO:270:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 297 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(iii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

GGGGGCACCA TTTCCAGTAT GTACCAAACC AAAGCCGTCA TCATTGCAAT GATCATCACT	60
GCGGTGGTAT CCATTTCAAGT CACCATCTTC TGCTTTCAGA CCAAGGTGGA CTTCACCTCG	120
TGCAACAGGCC TCTTCTGTGT CCTGGAAATT GTGCTCCTGG TGACTGGGAT TGTCACTAGC	180
ATTGTGCTCT ACCTCCAATA CGTTTACTGG CTCCACATGC TCTATGCTGC TCTGGGGCC	240
ATTGGTTCA CCCTGTTCCCT GGCTTACGAC ACACAGCTGG TCCCAGGGAA CCTCGAG	297

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

GCCAGACTAC CACAAGCCCC ACCCACACTA TGCCAAGCCC TACCCATACC ACAGCAAGCC	60
CCACTCATAC TTCCACAAGC CCCACCCATA CCCCCCACAAG TCCCACCCAC AAAACCAGTA	120
TGTCACCTCC CACCACTACA AGTCCTACCC CCAGTGGTAT GGGCCTAGTC CAGACTGCCA	180
CAAGTCCCAC CCATCCTACC ACAAGCCCCA CCCATCCAC CACAAGCCCC ATCGTTATAA	240
ATGTAAGCCC TTCCACTTCT CTAGAACATTG CTACCCCTCTC CAGCCCCCTCC AAACACTCAG	300
ACCCCCACCTT CCCAGGCAAT GACTCCCTTC CCTGTAGTCC CCCAGTCTCC GATTCCCTACA	360
CTCAGGAGA CCCTATGGCC CCCAGAACTC CCCACCCAAAG TCTCGAG	407

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

ACTGAGCTCA AGGACCCCTC CAAGAAGAAG ATGCAGCAC A TCTCCAACCT GTCCATCGCT	60
GTCATGTACA TCATGTACTT CCTGGCTGCC CTCTTGGCT ACCTCACCTT CTACAAACGGG	120
CTGGAGTCGG AGCTGCTGCA CACCTACAGC AAGGTGGACC CGTTTGACGT CCTGATCCTG	180
TGTGTGCGCG TGGCCGTGCT GACAGCAGTC ACGCTCACAG TGCCCATCGT TCTGTTCCCG	240
GTGCGCCGCG CCATCCAGCA GATGCTGTTT CCAAACCAAG AGCTCGAG	288

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

GAATTCCGCC	TTCATGGCCT	AGTCAAGCTA	GGTAAGCTAA	AAAGAAGAAA	ACCTGGTAC	60
AGCCGGTGA	ATTGATTTT	TTCCAGCCGA	GAAATAGATA	TTTCTCTCAC	ATATATTTGG	120
AAAACCTTAG	TCATCTTCAT	AAAACCTAAA	AAGTTACCTA	AGCACACACA	GCAAGTTCT	180
CCTTCTCTCC	TTTCCACAC	CCTTACCACT	TCACTATGTT	TCTACCAATC	CAGTGCAG	240
TTGCCAATGA	TGTGCTCTC	ACATGAATT	ACTGCATTCC	CTTCTGGTTC	CCCAGAAGGT	300
CTTGAAGAAA	GAGGTCAGA	CTAGTGGACC	CAAACAGAAAT	TTCTTGCGT	GTGATACTCA	360
GATTGTGTT	AGAGCCTGGT	ATGAAGAAGG	GGCCAGGTGT	AAGAAGTAGT	TAATCAACTG	420
CACGTGATT	TCAGGCTGAA	TATTCACCA	TCTGAGCCA	CCCGTCTCTA	AAAGTCTAGC	480
TGAAGCACAA	TTGATTGTGC	CATAGAATGA	GCAAACGCTT	GAAAACACAA	GCTCGAG	537

(2) INFORMATION FOR SEQ ID NO:274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

GCGAGCTCGT	TTTTAAAGG	ACCAAATAGA	AGTTTACCAAG	GAGAGAAGTG	ACAGAAGTGC	60
TGTCTAGATA	GAGGAAGGGC	ACACACAGAT	GCAAGCATGT	GCAGAAATGA	GCAAACCACT	120
GAGACGCTGC	CTTGAGCTCT	GTGTCACACT	GCTATGTTGC	AGCCTGGGAG	GCTGTTCCCA	180
GTTGAGCCCT	TCGGAACCAAG	CCATGAGATG	GCACGGGTAC	GCGGAAGGGA	GCAGTCTCCA	240
TGGCTGGGTG	GTGATGGGGG	CTTCTCGAG				269

(2) INFORMATION FOR SEQ ID NO:275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

GATGGCTCCC	CAGAGCCTGC	CTTCATCTAG	GATGGCTCT	CTGGGCATGC	TGCTTGGGCT	60
GCTGATGGCC	GCCTGCTTC	CCTTCTGCCT	CAGTCATCG	AACCTGAAGG	AGTTTGCCT	120
GACCAACCCA	GAGAAGAGCA	GCACCAAAGA	AAAGGGAGAGA	AAAGAAACCA	AAGCCGAGGA	180
GGAGCTGGAT	GCCGAAGTCC	TGGAGGTGTT	CCACCCGACG	CATGAGTGGC	AGGCCCTTC	240
GCCAGGGCAG	GCTGTCCTG	CAGGATCCCA	CGTACGGCTG	AATCTTCAGA	CTGGGGAAAG	300
AGAGGCAAAA	CTCCAATATG	AGGACAAGTT	CCGAAATAAT	TTGAAAGGCA	AAAAGCTCGA	360
G						361

(2) INFORMATION FOR SEQ ID NO:276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

GCCACAATAG CGGGATTGAT CTCCCTTAGGA CCTATCTTTC	60
CTTTTGAG TTTAGGTTG ATGTGCTTTC GGGCTTTGAT CGGACTTTGT GCTTGCAATT	120
GCGAAGCTT ATATCCCACC ATTGCCACGG GCATTCTCCA TCTCCTTGCAGT GGTCTGTGTA	180
CACTGGGCTC AGTAAGTTGT TATGTTGCTG GAATTGAACCT ACTCCACCAAG AAACTAGAGC	240
TCCCTGACAA TGTTCCGGT GAATTGGAT GGTCCTTCTG CCTGGCAGAA CTCGAG	296

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

GAATTCCGGCC TTCATGGCCT AGGATGTAGA ATCCTGCTTA TCTGTGAAAT GCAGTTGACA	60
CATCAGCTGG ACCTATTTCC CGAATGCCAGG GTAACCCCTTC TGTTATTTAA AGATGTAAGA	120
AATGCGGGAG ACTTGAGAAG AAAGGCATG GAAGGCACCA TCGATGGATC ACTGATAAAAT	180
CCTACAGTGA TTGTGATCC ATTTCAGATA CTTGTGGCAG CAAACAAAGC AGTTCACCTC	240
TACAAACTGG GAACAATGAA GACAATGAAC TCGAG	275

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

TCGTTCCCTT CATCTCTTCC CTTGCCAGAG CAGGGACTCT CTCCATATAA ACAAAAGGAA	60
AACCACCTGGC CAGGGTATGG TCAATACCTC AACATATCCA GACATCACAG CACCAAGAAC	120
CCAGTATGTA TATTCCACAA GTACTCGAG	149

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

GCAATCAGAT AAAGAAAAGAC CTGGCTGACA AGGAGACACT GGAGAACATG ATGCAGAGAC	60
ACGAGGAGGA GGCCCATGAG AAGGGAAAAA TTCTCAGCGA ACAGAACCGC ATGATCAATG	120
CTATGGATTG CAAGATCAGA TCCCTGGAAC AGAGGATTGT GGAACGTCT GAAGCCAATA	180
AACTTGAGC AAATAGCAGT CTTTTTACCC AAAGGAACAT GAAGGCCAA GAAGAGATGA	240

TTTCTGAACT CGAG

254

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

GACAGCCTGG AAGTTGGAG ACCCTGACAC ACCCACCTTC TCACCTGGC TCTGGTATC	60
CCCCAGCCTT GAGGAAAGAT GAAGCCTAAA CTGATGTACC AGGAGCTGAA GGTGCCCTGCA	120
GAGGAGCCCG CCAATGAGCT GCCCATGAAT GAGATTGAGG CGTGGAAAGC TGCGGAAAAG	180
AAAGCCCGCT GGGCTCTGCT GGTCTCATT CTGGCGTTG TGGGCTTCG AGCCCTGATG	240
ACTCAGCTGT TTCTATGGGA ATACGGCAG TTGCATCTCT TTGGGCCCCA CCAGGCCCA	300
CCCCCTGCT ATGACCCCTG CCTCGAG	327

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

GCCTGGAAACC TGATTCTCCT GACCGTCTTT ACCCTGTCCA TGGCCTACCT CACTGGGATG	60
CTGTCCAGCT ACTACAACAC CACCTCCGTG CTGCTGTGCC TGGGCATCAC GGCCCTTGTC	120
TGCCCTCTCAG TCACCGTCT CAGCTTCCAG ACCAAGTTG ACCTCACCTC CTGCCAGGGC	180
GTGCTCTTCG TGCTTCTCAT GACTCTTTTC TTCAGGGAC TCATCCTGGC CATCTCCTA	240
CCCTTCAAAT ATGTGCCCTG GCTCCATGCA GTTATGCAG CACTGGGAGC GGGTGTATTT	300
ACATTGTTCC TGGCACTTGA CACCCAGTTG CTGATGGTA ACCGACGCC GCTCGAG	357

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

GCGGGCTGCA GAATGATAGA CGAGCTAAC AAAACGCTGG CCATGACCAT GCAGAGGCTG	60
GAAAGCTCTG AGCAGCGGGT CCCCTGTTCC ACTTCTTACC ACAGCTCTGG GTTGCACTCG	120
GGTGATGGGG TCACCAAAGC AGGACCTATG GGCCTTCCAG AAATAAGACA AGTGCCTACT	180
GTTGTGATTG AATGTGATGA CAATAAAGAA AATGTGCCTC ATGAGTCAGA CTACGAAGAC	240
TCTTCTTGCCT GGTATACAG AGAAGAGGAG GAAGAGGAGG AGGACGAAGA CGACGACGAA	300
CTCGAG	306

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

AATCAATCAA CTAGGCATAT GACACAGTAG TCCATTATAA AAGAACAGAT ACATCCAGCA	60
CCATCAACTA ATTCTTAAGA TAAGTTATCT GGGAAAATTG AAGAACAAAT AAATTCAACG	120
AAATACTGTA AAGTGAACGA AGACATAAAA CCAAAGAAAA CTGAGGCCAT TTCTGCCAAG	180
AAAGGAACAG CAAAGAGTAA AGATGAAAAA TATTCTAAGA TAATACCAGA AAAAGATAAT	240
TCCTACATGG ACAAAAGATGA GCATGGTTCA TCCTCTGAAA GTGAAGATGA AGCGCTGGGT	300
AAATATCATG AGGCCTTATC CAGAACACAC AATTCCGGAC TACCACTCGA G	351

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

AAGTTAAAGG TATTAAATAA ATGAGTTCT CCTTAATTCTT GTTAATGCTC TTTTAGCTAA	60
TAAGACTTTT TCTAGAGTTA CATATTAA TCTGTTTCAT TTTTATTTTT TCCTTTGGTT	120
TTATATTTTT AAAAGCCATT ATATCCCTCC CACTGGTAAC ATACACATAC ACAGACACAC	180
ATCTATTTCATTA AATGAATACT TACTACTTAA TCATTTTCAG TCTTAATTGT ACT	233

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

GCGGCGCCGC AGCAGTTCCA GGAAGGATGT TACCTTGAC GATGACAGTG TTAATCCTGC	60
TGCTGCTCCC CACGGTCAG GCTGCCAA AGGATGGAGT CACAAGGCCA GAATCTGAAG	120
TGCAGCATCA GCTCTGCC AACCCCTTC AGCCAGGCC GGAGCAGCTC GGACTTCTGC	180
AGAGCTACCT AAAGGACTA GGAAGGACAG AAGTGAACCT GGAGCATCTG AGCCGGGAGC	240
AGGTTCTCCT CTACCTCTTT GCCCTCCATG ACTATGACCA GAGTGGACAG CTGGATGGCC	300
TGGAGCTGCT GTCCATGTTG ACAGCTGCTC TGGCCCTGG AGCTGCCAAC TCTCCTACCA	360
CCAACCCGGT GATCTTGATA GTGGACAAAG TGCTCGAG	398

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

GAATTTCGCC	TTCATGGCCT	ACACCCAGCC	AATTTTTTG	TATTTTTAGT	AGAGACGGGG	60
TTTCACCATG	TTAGCCAGGA	TGGTCTCTAT	CTCCTGACCT	CATGATTGTC	CCGCCTCGGC	120
CTCCAAAAAA	AGAACATTTT	ATATTTGAGT	CCTATTTCTT	TTGCGGCACC	AAAACTTTAT	180
AACACACTGC	CTTCTGAATT	TTTTTTTTTG	GTTTCTGCTC	AGCTCATTTGT	TAATCATATT	240
GTTCCCATGT	ATGTCAATGAG	TTATTTTTCT	CCTAGTCTTT	TCAAAATTAT	CTTGTCTTTG	300
ACTTTTAACA	GTTTAATTGT	AACAGTGTAT	ATCTTTAAAG	TTAAATTAT	GCTTGTGAAT	360
TTTTATAAGA	GCCACAAAGG	CCTTCCTCTG	TGTTTTGTTT	TTGTTTTGT	TTTGTGTTTC	420
ATTTTGAGA	CAGGCTCTCA	CTGCCCCTCA	GTGGCTCTCG	AG		462

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

TGGACAGTCT	AGAAGATGCT	GTGGTCCCC	GGGCTCTGTA	TGAGGAGCTG	CTGCGCAACT	60
ACCAGCAGCA	ACAGGAAGAG	ATGCGCCACC	TCCAGCAGGA	GCTGGAGCGG	ACTCGGAGGC	120
AGCTGGTACA	ACAGGCCAAG	AAGCTCAAGG	AGTACGGGGC	ACTTGTGTCT	GAAATGAAGG	180
AGCTCCGTGA	CCTTAACCGG	AGGCTCCAGG	ACGTGCTGCT	CCTGAGGCTT	GGCAGCGGTC	240
CCGCCATTGA	TCTGGAAAAA	GTAAAGTCAG	AATGTCTCGA	G		281

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

AATGGAACGT	CTGACACAAT	ACTCGTGTAA	CTGTGTGGAA	CCGCATAATC	CCAGCAATGG	60
CACATTGAAG	GAATGGAGGG	AATCCAATAT	TTCTGCCTCT	GACATAATTT	GGGAGAACCT	120
AACTGTGTCA	GAATGCAAAT	CATTGCAATGG	AGAGTATGTT	GGACGGGCCT	GTGGCCATGA	180
TCACCCATAT	GTTCAGATG	TTCTATTTTG	GTCTGTGATC	CTGTTCTTT	CCACAGTTAC	240
TCTGTCAGCC	ACCCCTGAAGC	AGTTCAGAC	TAGCAGATAT	TTTCCAACCA	AGGTTCGATC	300
CATAGTGACT	GACTTGTCTG	TCTTCTTAC	AATTCTGTGT	ATGGTTTAA	TTGACTATGC	360
CATTGGGATC	CCATCTCCAA	AACTACAAGT	ACCAAGTGT	TTCAAGCCCC	CTAGGCTCGA	420
G						421

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 417 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

AAGCCAATGG CTGGTCGTGA TCCTGAATCC CAAACGACAG AAATGATTAA CAAAGAACAA	60
GAACGTTTGA GGGCTTCCAT ACGTAGGGAA TCTCAGCAGC GCCGAATGAG AGAGAACAG	120
CACCAGCGGG GGCTGAGCGC CAGTTACCTG GAACCTGATC GATACTGATGA GGAGGAGGAA	180
GGCGAGGAGT CCATCAGCTT GGCTGCCATT AAAAACCGAT ATAAAGGGGG CATTGAGAG	240
GAACGAGCCA GAATCTATTC ATCAGACAGT GATGAGGGAT CAGAAGAAGA TAAAGCTCAA	300
AGATTACTCA AAGCAAAGAA ACTTACCACT GATGAGGTAA GACCAAATTT ATTCAATTCT	360
AGGGTTTAT CCTGTACTCA GGAGCCAACT GCTTTGAATG AAAAGCTCAC ACTCGAG	417

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 314 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

CAAGCATACA ATCAAACCTCA AGCTCGGTAT CACCTGAGCC CAGGAAGTGG AGGCTGCAGT	60
GAGCTATGAT CAGTAAAACA CAAGACAGGT TCACTGGCTC CCATCCAAAC CCGGACCAGC	120
TCCCTAGTAT AACAAACTCAC ATGCATGTGG ACTATACCCCT TACAGCCTTC TTCTGTGTGT	180
TTATGTGCAT ATATGTAGCC ATAGGAAAAA AAATCAAAAT CCTTTGGTGT TCTTTCTTAT	240
TTTTTCAAAT ATTCACCTG CCCCATTCTC TTTCCTTTCT CCTTCTAGTA CTCCCATTGC	300
ATGCAGTTCT CGAG	314

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

GTTGTATGTGG GGGGTAAGTG TGTGTGTGTG CGTGTGCGTG TATGTGCACG TGTTGTGTGT	60
GTGCGCTGC ACACGGAGAG CCCACTCATA CGTAGCAGAA AATCAAATGG CCCCAATCA	120
GAAACATGGC GCATGTGAGC ATGCCACTTC TTGTGTGCCCT GTGACTGTTC AGAATGTACA	180
CGGCCCTGCA GCTCCCGAAG GCCAGCTCTG CTGCAACCCCC TCCCTCTGCC AACACAGTCC	240
TCACTGGTGT CTTTTCTCTC TCAAATCTAC AGCATTCTG ATCTCTGCAA ACAATTAAAC	300
CCAAAACCAA GTTCTGGCTG ACAAGGCTAC ATCTTGTTC TTGTGCGTGA TTAGCCTCGA	360
G	361

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 237 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

GCGATTGAAT TCTAGACCTG CCTCGAGTCG ATGCACCGAA AAGGGTGAAG TAGAGAAATA	60
AAGTCTCCCC GCTGAACATAC TATGAGGTCA GAAGCCTTGC TGCTATATT CACACTGCTA	120
CACTTGCTG GGGCTGGTT CCCAGAAAGAT TCTGAGCCAA TCAGTATTTC GCATGGCAAC	180
TATACAAAAC AGTATCCGGT GTTTGTGGGC CACAAGCCAG GACGGAACAC ACTCGAG	237

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 292 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

GAATTCCGGCC TTCATGGCCT ACTTTATTTT TTTAATTATT ATTAGTATTA TTTTGAGACT	60
GAGTCCTGCT CTATCACCCA GGCTGGAGTG CAGTGAGCTG AGACTATGCC ACCGCACTCC	120
AGCCCCGGCG ACAGAACGAG ACTCCATCTC NAAAAAAA AAAAAAATCT ATGTTCATGC	180
CTTNACACCT GTTTCTGCAC ATAGCTGTGC AGTATATTCT TCTTCTAAGC AACGACCCAG	240
TGAAGATCCA AACAAAAGTT CACAAATATG TAGTTATCCA AGGCACCTCG AG	292

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 136 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

GAATTCCGGCC TTCATGGCCT ACAATCTTTT AACTTTGGGG GTCACAGTTT TAGCCACCTT	60
TCGGGGGGTG ACTGGAGCAG TAGGAGGTGT GGGGTCATT TATGAATATA ATAAAATGGA	120
GCTGACTGTA CTCGAG	136

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 264 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

GAATTCCGCN	TTCATGGCCT	AAAATAACAC	ACAATTAGTA	TAGAAAAATT	GCAAACACAG	60
ATAAAAGTCC	TTTCCCTGTG	AATTCTGAA	TGCACCTTTG	AATATTACA	TCTTACTGCC	120
AAAATGAGAT	TGTCTTGTGT	GCCGTTCTGG	AATTGCTTT	TTTCCAGCTT	ACATGTTCTA	180
GGTCCTTCCA	GATCAATAGC	TGCACCCCT	CCTTCCTCTG	CTGGTTCTC	AGCTCGATGG	240
GCTGTAAGTG	GCATTACTCT	CGAG				264

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

GAATTCCGCC	TTCATGGCCT	ACAAACCTCAT	AAATCTCATT	CTTAATTTCAT	CTCTAGGACA	60
GAATTATTGT	AGCACCTGTG	TTCTGTTATT	TTAGATTCTAT	TTAACCTTAC	CTAGACACGG	120
GTACTGTGGT	AGTTGTAGAG	GTACAGATGT	TGAGTTCCCA	TCCTCCTGGC	TTAATGTCAC	180
TGGGGTTATT	AATAACACTTC	ATAAGCATT	TAGGGACACC	TGCTGTCG	TCAACCCCCA	240
GCAAACCTCGA	G					251

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

GAATTCCGCC	TTCATGGCCT	ACATCTGGTA	AATTTTTCTT	TCTGCCTGAG	GAACACCCCT	60
TAGCATTTAT	TTAGTCTGCT	GGTGANCAAT	TCTCATATTT	TGTTTGTCTG	AAAAATACCT	120
TTATTTTGT	TTAATTCTTG	AAAGATATTT	GCACGGTGT	GATTGGATTC	ATGATTGCTT	180
ATTATTTCT	TTTCTTTTT	TCTTTTTGA	GACAGAGTCT	CGCTGTCGCC	CAGGCAGGAG	240
TGCAGTGGCC	CGTACTCGAG					260

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

GCTCTGAATC	TATTTTCTAG	GACATTTTT	TCCCATTAG	ATTAAGCCAG	AGAGAGCCCT	60
TTCTTGCTC	CCAAGAGTTT	TTCTTGTGT	GACTGTTGGT	ATTCTGAACC	TCTTGGATT	120

GATGCCTGGA ATTGTCTAG AGACTCTCT GATTCTGTC TCATTCTTG ATTTCACCC GGGGAGCTGG GGAAGAGATA CCTTCCCCTG GCATCACTTG TTAAGAGTGG ATCCCCCTTC CCCCCTTCCT TCTGTCCCCC TCGAG	180 240 265
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(2) INFORMATION FOR SEQ ID NO:299:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 311 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

GAATTCGGCC TTCATGGCT ACCAAAACAA AAGAAGAAAAT CATTTCACTC ATGCTTAGAA AGATGTCAG AGGATGGAGG ACTCACATTC TGTTAACCTCT TCTGCCTGTA ATATATGCTT TAAACACTAA AAATGATGAG CATGAATCTG CAATTCAAGC CCTCAAAGAT GCTCATGAAG AAGAAATTCA ACAAAATTCTT GCTGAAACAA GAGAAAAAAAT ATTGCAGTAT AAAAGCAAAG TAACAGAGGA GCTAGACCTT AGAAGAAAAGA TTCAAGTTT AGAACATCA TTAGAAGATC ACAATCTCGA G	60 120 180 240 300 311
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(2) INFORMATION FOR SEQ ID NO:300:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 255 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

GCGATTGAAT TCTAGACCTG CCTCGAACTC GTGGCCTCAA GTGATCCACC TGCCCTCACCC TCATCACCTG CCAAGTCCTA CCCATTCTAA CCCTGATAGC TCTTAAATCA GGTCTTTCCA CCTCAACCTC ATTATCACTG CTCTAGAGCT CAAGCCTTCA GTGTCCTTTC ACTTCCTGAA TTTACTGTCT TAGTGTCTT GCTCACATTG TATTCTNTGC CCAAATGCT CTTACCACTC CCNTCTTTTC TCGAG	60 120 180 240 255
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(2) INFORMATION FOR SEQ ID NO:301:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 345 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

GAATTCGGCC TTCATGNCTT ACTTGGATTG ATCACAGTAG CATTCTGCTT CAATCTGTGT GTAACTAGA AATCAAGGAA AGACATGAGG AGATTTGTCT ACTGCAAGGT GGTTCTAGCC ACTTCGCTGA TGTGGTTCT TGTGATGTC TTCTTACTGC TGTACTTCAG TGAATGTAAC AAATGTGATG ACAAGAAGGA GAGATCTCTG CTGCCCTGCAT TGAGGGAGAT CGCGACGCAG CTGGTGGAGC AGTCAAATG TCTGGAGCAG CAATCAGAGT CGCGACTGCA GCTGCTTCAA GACCTCCAGG AGTTTTCCG CGGGAAAGCT GAGATTGAGC TCGAG	60 120 180 240 300 345
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(2) INFORMATION FOR SEQ ID NO:302:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 300 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

GAATTCGGCC TTCATGGCCT AATCCTCCAG ATTATTATGG ATATGAAGAT TATTATGATT	60
ATTATGGTTA TGATTACCAT AACTATCGT GTGGATATGA AGATCCATAC TATGGTTATG	120
AAGATTTCA AGTTGGAGCT AGAGGAAGGG GTGGTAGAGG AGCAAGGGGT GCTGCTCCAT	180
CCAGAGCTCG TGGGGCTGCT CCTCCCCCGC GTAGAGCCCG TTATTACACAG AGAGGAGGTC	240
CTGGATCAGC AAGAGGCAGT CGAGGTGCGA GAGGAGGTGC CCAACAACAA TGATCTCGAG	300

(2) INFORMATION FOR SEQ ID NO:303:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 258 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

GAATTCGGCC TTCATGGCCT AAAAAAAAAGA AGTTTATTTA AAGAAACTCT ATAAGAGCAG	60
CTTGGATTT ATATCTTAG ATCCAGAGTT TTTACTTTTC TGGAATTAAA TATAATTGTT	120
TGGAATTAC TCTTTATTGT TGAATTAA AGCGTGACTA AAGTAGTGCT TCTTAAGATA	180
ATTGTATGT GTTTTGTTT TGTTTTGTT TGTTTTTG TGCTGAGTGT TGCTCTGTCG	240
CTCAGACTGG AGCTCGAG	258

(2) INFORMATION FOR SEQ ID NO:304:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 262 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

GAATTCGGCC TTCATGGCCT ACAATTCCGA TAAAGTTAA GGTCAGCTGA TGAAGAACAC	60
TCAAACCAAA GTCGCCATT GGAGGAGCGC CCTACCTCAC AGGAATAGGC CTGCATTATT	120
AGTATACCTT CTTCATTCAG TTATTGTTAT TCTTATGGAA ACAACCCATG GGAATGTAG	180
CCTTGGCATG ACTGTATCAA TGGATTCAAGA GAGCAGTAGC GGGGACCCCC CCAGTCATT	240
ACGTTCCACA GCAAGTCTCG AG	262

(2) INFORMATION FOR SEQ ID NO:305:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 298 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

GAATTCGGCC TTTCATGGCC TAAATCTCAT AAATAGAAAG NAAAATAATC TAGAAATT	60
TCAAAGCTAG TACTCTTCT CCTTATAAAAT GTACACAATT TTAATCTTT TACAAATT	120
TTTAACTGTA CCTACTGTAC TTATTGAGA TTCATGACG CAGTTAAGTC ATCACCAAG	180
GATTTATGAA TTGAGGATTA CTGACCTGTT TTCTTCATAT TGCAATTACA TCAATATTG	240
TGAATTGTT GTTCAGCTT TCATTCAAC AAAAAATATT CCCCAAGAA AACTCGAG	298

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 263 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

GCGATTGAGT TCTCCCTGCT GGTCTTTTG AATCACACCA AATGAATGGC TTGCTACTGT	60
TCCCTCACAC CTTCATATTG TCCATGGTTT TTCCCACCTC CTTAGCTATA CAGCTGCTGT	120
TCCTCTGCC TAAAATGTCT GAACATTCCC TCAGTGTCA GCTCAGCCA CATCTTACAT	180
CTTCCCTAACG GATGTTTTTC TGCTGCTATC ATTCAATTTC TTCCTATGAG TTCCTCTGTT	240
ATATTGCGCC ACCAGAACTC GAG	263

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 267 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

GAATTCGGCC TTCATGGCCT AGCCCCACT AGCTTGCCTC TAACTCCTTC ATCAAAAGAC	60
CCCCCGCCAG CTTCCACAC CTCATACGCA GCCACATCTG CCCTATTCTC CATGCTTCC	120
AGCTTGCCTG CCCCCTCTCA TCTCTCCCTG CCTGTGCAGA CCTCCACCT TCTTCTCTCC	180
ACCCCTCCAT CCCCAATGC TTGAGACCT TCCATTCAATT CCGTCTCATC GTGCCGGTC	240
TCTGATCGTC CATCACCTGA CCTCGAG	267

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 261 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

GAATTCCGCC TTCATGGCCT AGCCAAATC ACAAGAAAAA TAACTTGAC TTTGAAAACA	60
AATAAGTTAG AAATGCAGTG TTTGCACTTC GTGGTTTATG TTTGCTTTGG TGGCCTCTCA	120
TTCCCCACTTA GCCTCAGTCT CCAGGGCCTG GGCTCCACCA AGGAAGACTC CATCTGCTCT	180
CTCTATTGCA ACACGTGGAA CTTTTTCCC CAAGGTACAG GATATGATTC AGGGTTTATG	240
GATGACCTCC CACCCCTCGA G	261

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

GAATTCCGCT TCATGGCCTA CCTATTCCCA AACTTTAAAT GTTGTCTACC AAATACTGAC	60
AATTATGAAA ATTCTACCAAG TAGAACACAC CTCCCCTTTG AGCTCCAGAG CACATGCTTG	120
ACATCTCATCA TTAGAAAGAA TCTTGATTT CCCTCCAGTC TAGTCTTCA TGTTTTGTTT	180
TTCTTTGTGA GAGTCTCCCT CAGCCTGCMA TGGCGTGATC TCGGCTCACT TCAACCTCCC	240
GTGCTCGAG	249

(2) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

GAATTTGTTT NAAAAAAA AAAAAAAA AGGGCNGGGG GGAAAAAAA AAAAAAGAAC	60
TCTCTGGAGAG GGAATAGCA AATGTGTCTT GCCTTTGTT GCTCTCTCTC TCTTTTTTTT	120
TCTCTCGCTC TCTTCTTCTC TCTGTTTTA AGTCAAGCAT TGGTCTCGAG	180

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 742 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

NNNNNNNNNN NNNNNNNNNN NNNNNNNNANN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN	60
ANNNNNNNNNN NNNNNNNNNN NNNNNNNNNN ANNNNNNNNA NNNNANNNNAN NNNNNNNNNNN	120
NNNNNNNNNN NNNNNNANNA NNNNNNNNNN NNNNNNNNANN NNNNNNNNNNA NNNNNNNNNNN	180
NNNNNNNANN NNNNNNNNNN CNNNNNNNNN NNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN	240

NNNNNNNNNA	NNNNNNNNAN	NNNNNNNANN	NNNNNNNANAN	GNANNNNNNN	NNNNNNNNNN	300
NNANANANNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNC	CCCCTTTGTC	360
ATNGTTNTCG	TTCCCNNTCT	TCCTTGTTC	TTTTTCGGCA	CAATATTCA	AGNTATAACCA	420
AGCATAACAT	CAACTCCAAG	NTCGGAATT	TAATTACTTC	ATGGCCTACT	TGATGCAGGC	480
TGGAATCTTA	TCCCTGGGT	GTGCTTGAC	CCCACCTGCT	TTCTTTCTCT	CCTGCCCTC	540
CCCTACTCTC	ACTGTAATT	ATGGACCCCTG	CCCGCCTGCG	TGTTGTGTGT	ATGTCTGTG	600
CCTTTCTCA	CTATTGTTTC	GGTGTGGAG	GGGGTGGTTT	TTCACTGAA	ACGGGGGTAC	660
ACCTATAAGT	TTCTTGATGT	TCATCAATC	AGTCACTGTG	TCCCAGACAT	ATTCAATAAA	720
CACAGATTG	TACCATCTCG	AG				742

(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

GCGATTGAAT	TCTAGACCCG	CCCCAGGAGC	CTCCAGCTGC	CTAACCCAGTG	CCATTCTTTC	60
ACAACACGAT	TTTCTACAAA	TCTACAGCAC	AACCGAGTT	GTAACCCGTG	GGTTAGTATG	120
AGGACCGGGT	TCGTGTACTC	TCTGTATCTC	CTCTTAAGCT	TCGTCCAGGG	TTCTTTATTT	180
TTGTCTGCTG	CCAATGTCGT	CTCGCATGCC	TGCACCCTCG	CATGCACGCT	GCCCCATGC	240
CACGTGCCAC	GCTGTAGCCA	CATCCTCGAG				270

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

GAATTCTGGCC	TTCATGGCCT	AGTTGATGTC	CTCTCATATT	TTGTTGTTA	AATAACGCACT	60
GTGGTGGTTG	TTATTCTAGGA	CTGCCTCTGC	TCTGACAGAT	GTGTCTACTC	TACAGAGAGA	120
GAGAGAGACT	GTGTCATTG	TCCCACCAGG	CTGTCCAGAT	CCAAACTCCA	ATGACCTTTC	180
TGCACCTCTGC	CTGGCTATTG	GTTACAGTTT	ACATTCTACC	TTCTCCAAG	GTATTGAGGG	240
AGGCTTGCAT	GCAATTCTCG	AG				262

(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

GAATTCTAGA	CCTGCCTCTC	CTGACACGGG	CCACCAAACC	CCTTACCTGG	TTCCCTTGCTG	60
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TAAAACTTCA CCAAATGAAG CCAGAGTTGA TCATGACCCCT CTCGTGCTCG AATCCCTTCT	120
GGGCTCCCCT CTGCCCCCTG CAAAGCCCAC ATGATACCAAC AGAGAAGACC TGTCCCCCTGC	180
AGGCCAGCTG CTTCAGCCTC TTCCCTCACCA CACATCGTCC CGCACACGGC AGCCACCATG	240
GACTAACAT CCCCGACACA CGGTGCTGCC CTCTGCATGC ACCGACCCCC TGCCCCCTCCC	300
ACCAAGCTCGA G	311

(2) INFORMATION FOR SEQ ID NO:315:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 232 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

GAATTCCGGCC TTCATGGCCT ACCTAGGTGC TTTTTAAAAT ATTCAAGACAA ATATCTATCT	60
TACATTGATT AAACCCGTGT AAATTCAATT GCAGTATCTA CATCGAATGT CAAAAAAAGTA	120
TACTTATTCTT TGTTCCATAC TTATGTACAA TTTTTCCCT CTTCAAGGCTT TTTCAATTAC	180
CTTTTGAAA AAGCACTTAC TCTCCCTTC CCTATCACCC CATCCCCTCG AG	232

(2) INFORMATION FOR SEQ ID NO:316:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 205 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

GAATTCCGGCC TTCATGGCCT ACAGTTGTTTC ATACTTCCTT TACAAATATA AAGATAGCTG	60
TTTAGGATAT TTTGTACAT TTTGTAAAT TTTTGAAATG CTAGTAATGT GTTTTCACCA	120
GCAAGTATTCTT GTGCAAACACT TAATGTCAATT TTCCCTTAAGA TGGTTACAGC TATGTAACCT	180
GTATTATTCTT GGACGGACAC TCGAG	205

(2) INFORMATION FOR SEQ ID NO:317:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 299 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

GAATTCCGGCC TTCATGGCCT AGGGCTTGTC TTTTCATTG TTGAGTTGCA GGAGTTCTTT	60
ACATATTCTG GATACTAGAC CCTCATCAGA TATGGTTTTA AAATACTTTC TCTCATTCTT	120
TTCACCTTCA AGTATCCCTT TGATGCACAC ACCCAAAAAA GCAAATAGTG TCCAATTGCA	180
TTCTTTGATG AAGAAGATA CAAGCAGTAA GTCAATTACA GCCTTATTCTT TTCTTTCTT	240
TCTTCTCTT TCTCTCTCTC TCTTTCTTC TTTGAGGCAG GTAGGCCATG AAGGCCGAA	299

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 95 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

GAATTCTAGA CCTGCCCTCGA GCTCCAGCTG CCAACACCCCT TGGACACAAT ATTCCAGTCT	60
CCACTGCCCA TCTCATGTGG TTCAGGTTCC TCGAG	95

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 109 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

GATGCTTGCG TCACTCCCCG CTACTGGCCC CCAGACTTTT CCACCCCAAG AAATGTCTCC	60
CCTGCCTGCA GCTTCAGCGA AAGCCCAGGA GGCAGGCCAA TCACTTGAG	109

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 253 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

GAATTCCGCC TTCACTGGCCT ACACATTCT GTACCTGGAA AAAAATGTA TCTTATTTTT	60
GATAATGGCT CTTAAATCTT TAAACACACA CACAAATCG TTCTTTACTT TCATTTGAT	120
TCTTTTAAAT CTGTCTAGTT GTAAGTCTAA TATGATGCAT TTTAAGATGG AGTCCCTCCC	180
TCCTACTTCC CTCACTCCCT TTCTCCTTGT CTTATTTTC CTACCTTCCC TTCCCTGTG	240
CTCCCCACTC GAG	253

(2) INFORMATION FOR SEQ ID NO:321:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 334 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

GAATTCTGGCC	TTCATGGCCT	AGGTTGTAAG	TGATTTTATT	TTTCTTTTC	TATTTCCAG	60
TGTTTCTGTA	ATGCTTTCAT	ATTTCTTTG	GTAGTTAGAA	AATAAAGGCT	AATTTTAAA	120
AAGAATATCA	TAGTCTAAAA	AATTAAGGAA	TGCATAGAGT	TCCCTCTTGA	CTATGTGACA	180
TCTAAACTGA	ATGAACTGTC	TGGTGGCAC	AGTGGAACAG	CGCAGTCTCA	GGATTCTGAC	240
AGATTTTGG	ATCCCAGCTC	TACCACTAAC	CTTGGCAGG	ATTTAGTCC	CTCTGAGACC	300
TGCTTCTCG	ATTGAATTCT	AGACCTGCCT	CGAG			334

(2) INFORMATION FOR SEQ ID NO:322:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 226 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

GAATTCTGGCC	TTCACCTAAA	TACTCCTCCT	TTTGTATCAT	TCAGCCTTT	GTTTAGTTT	60
GGTAAGTTT	AAGAAATTTC	AGCAGCAAAG	TTGTTATTCA	GTGGGCACGA	TGGACTCCAA	120
ATGCCTCAAG	TTATGTATAC	CTGTGGAGGT	CACGTACTTC	CAAATTGTT	TCTTCCTCAT	180
CTTCTCCCTT	TACCTGCACG	CCCAAGTGCG	CCAGCCGGC	CTCGAG		226

(2) INFORMATION FOR SEQ ID NO:323:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 164 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

GAATTAATAAT	AAACAAAAGG	CAGCCAAGGA	TGAAAGGATT	TAGTTCTAAG	ATGTTTCACA	60
GTTGTGATTT	GTAAATTCTA	ATCCTTAGTA	GTAAATTAGT	ACTAGAAAGGA	TCAGGTATAT	120
CTTCCTTAAT	TCTTCCCAGG	GGAGAGAAAAG	TCCCATTCT	CGAG		164

(2) INFORMATION FOR SEQ ID NO:324:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 494 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324.

GAATTCTGGCC	TTCATGGCCT	AAGCCTATGT	TGATCTTGAA	CTCCTGGGCT	CAANCCNTCC	60
TCCTGTCCTCG	GCCTCCAAA	TTGCTGGAAT	TATAAGCACA	TTACACAGT	CCCAGTCTAC	120
CTACATTTCG	ACAGACATAT	AATATTCCAT	GGCATGGTTA	CATTATTCA	TTAAGAATGT	180
TCCCGGTTTT	CTCTAAGATA	ATGCTGCCA	TCTGTGTC	ACTCTGGACA	TGTAGAGTAC	240
CTGCAAAGAC	TTGGACTGCT	TGAGCAGAGG	GCCTGCTTT	GTTTTTGTT	CTTCTGCCT	300
GTTGTAACCT	GATGCTGCCA	AATGATCCTC	TTAAATGATT	GTACCACTT	CCCTGCCACC	360
ACCAGATTT	AAGGATTCTC	TGTACCTCCC	AACACATGAT	GACATCATAC	ATGAAAAGTT	420

TTGCCTGCCT GATGGAATAA TTGAGTCAAG AAATAGGATG CTAATGGCAT CTTCGCTTAC	480
CCGGTCTCCT CGAG	494

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

GAATTCCGCC TTCATGGCCT AGTTGGGTGT TGAGCTTGAA CGCTTTCTTA ATTGGTGGCT	60
GCTTTTAGGC CTACTATGGG TGTAAATTT TTTACTCTCT CTACAAGGTT TTTCTCTAGT	120
GTCCAAAGAG CTGTTCTCT TTGGACTAAC AGTTGTCTG ATGAATAATT TCATTTCTCT	180
CAAGTTATG ACACTCGGAA CGTCAAGAAC TGGAGGTTTG TGCAATTGAA GACCGGTCGG	240
CACTGTGCAAG AGATCAGAGT ACTAAGAGAC AGAGATTAAA ATGGCTATCC TCGAG	295

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

GAATTCCGCC TTCATGGCCT ACAAGGATAG AATTCAATTCC ACCTATATGT ACTTAGCAGG	60
GAGTATTGGT TTAACAGCTT TGCTGCCAT AGCAATCAGC AGAACGCCCTG TTCTCATGAA	120
CTTCATGATG AGAGGCTCTT GGGTGACAAT TGGTGTGACC TTTGCAGCCA TGGTTGGAGC	180
TGGAATGCTG GTACGATCAA TACCATATGA CCAGAGCCCA GGCCCAAAGC ATCTTGCTTG	240
GTTGCTACAT TCTGGTGTGA TGGGTGCAGT GGTGGCTCCT CTGACAATAT TAGGGGTCC	300
TCTTCTCATC AGAGCTGCAT GGTACACAGC TGGCATTGTG GGAGGCCTCT CCACTGTGGC	360
CATGTGTCGCG CCCAGTGAAA AGTTTCTGAA CATGGGTGCA CCCCAGGGAG TGCTCGAG	418

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

GAATTCCGCC TTCATGGCCT ACAGACATCT AATCCGAATC TTGCTCTTGT TGCCCAGGCT	60
GGAGTGTAAT GGCACAATCT CGGCTTACTG CAACCTCTGC CTCCCTGGATT CAAGTGATTC	120
TCCTGCCTCA GCCTCCCAAG TANCTGGGAT TACAGCCCTG AAAACCCTC GCTTGAGAG	180
CGCTGGATCA GCAATGCCCTA CTAGTTCTTC ATTCAACAC CGGATTAAG AGCAGGAAGA	240
CTACATCCGA GATTGGACTG CTCATCGAGA AGAGATAGCC AGGATCAGCC AAGATCTTGC	300
TCTCATTGCT CGGGAGATCA ACGATGTAGC AGGAGAGATA GATTCACTGAA CTTCATCAGG	360

CACTGCCCT	AGTACCCACAG	TAAGCACTGC	TGCCACCACC	CCTGGCTCTG	CCATAGACAC	420
TAGAGAAGAG	TTGGTTGATC	GTGTTTTGGA	TGAAAGCTCA	ACTTCCAAA	GATTCTCCA	480
TTAGTTCACT	CCAAAACACC	AGAAGGAAAC	AACGGTCGAT	CTGGTGATCC	AAGACCTCAA	540
GCAGCAGAGC	CTCCCGATCA	CTTAACAATT	ACAATGCCGG	AACTCGAG		588

(2) INFORMATION FOR SEQ ID NO:328:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 385 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

GAATTCCGGCC	TTCATGGCCT	ACGACTGGGG	GAAATGTCTA	TTCTCCTGTG	TATCTCTGGG	60
CTTTTCTTGT	TTTGGCTGC	CTCTGCTCA	GTTCCCTCTCT	TTAGGTATTT	AGTAAGCGT	120
TCATGTAATG	TCATT CCTGA	GGACCCAAAG	TGATGCTCTT	TAACATGGTG	AACAATGGTC	180
ACTATATGTT	GGGAAACAG	TTCTGAGGGG	CTACGCTGAG	ACTGAGCTGA	TTGTATGTGC	240
TGGAAAATGG	AACGAAACTC	CTGTTCCCTT	TTGTTGCTAT	GGACTAGATC	TCGGCAAAGC	300
TTGGTTCCT	GAGCCAATAA	GCCACTGGGT	CGTGCAGGTT	CCTCATCAA	AGAGTCCATC	360
CGGACATTGA	CCTGTGCCTC	TCGAG				385

(2) INFORMATION FOR SEQ ID NO:329:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 482 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

GAATTCCGGCC	TTCATGGCCT	AGCAGTTCAC	CACTGCAAA	CCACGGGGCT	GGGTGGAGGT	60
ATTCATGGGA	CACCGAGTGG	TATCACTAGC	AGCGGACTCT	GCATGCTTAC	TTAGAGCATA	120
AAAGGATAGC	ACCCCTGGCC	ATTGCCTGAC	ATGAACCTAG	TTTGGAAATT	GCAGAGGTGT	180
GGAGAGCCAT	GGATGGGTTT	TATAATTTAT	TCTAATGTAA	TCTCTGTGCT	AAAGGCTGTT	240
TGAAAAAAAT	AATGAAGTTG	ATGGTGCTTA	AGTTATATGC	AAATGTAAC	TGGTCTTCCT	300
TCAAGATGTT	TGGAATGGAA	TGAATGCCCT	TCCCCTGGGT	ACCTCCCAAT	ACCTACCCCTC	360
AAAAGACCTC	CAGTAAGGCT	TCCTTATCTT	TCCTTGCCCT	GCTTCCTACA	CTGCTGCTGC	420
AGGTGTCTCT	GGGTGATTGT	GGGGGAAACC	ACTGTGGTTA	AGCACCAACA	CCAAGACTCG	480
AG						482

(2) INFORMATION FOR SEQ ID NO:330:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 532 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

GAATTCCGGCC	TTCATGGCCT	AAGCCCTTGG	TGCCCTGTGG	GTGGACTCTG	GGGAGGCCAG	60
GGGCCCAAGG	CCACCTTCTA	GGGCCGTGAGG	AGCCCTCTGA	GACCTGCACA	CCCACCCAG	120
GGAGCGCCCC	TCCCTCCACC	TCTGTGCCCC	CCCAGTGA	CTCGAACCTC	TGTCTGTTTT	180
GCAGATTCA	CCGGAAGGGC	CGCCAGCCAG	TGGATTTCCC	GGGCCCTCA	CCCTCTGGAG	240
TGTACGGAGTT	TTGGAGAAC	CTCTTCTCT	GTATATGCTT	TTGACTTTCC	TGGACTGATG	300
TAAAAAAACT	CTTTTCTTG	ACCTGTTTAT	TTTTAAGACA	CGACGTGATT	GTGTCAGCTT	360
ATATTTTATT	GCTGAAGTAA	ATTTTCAAAT	TTTTTATTAG	TTTTTTGGA	TCTTTGCTG	420
CTCATTTG	AGTTTTGTA	ATTTTGTAG	GTGTTCTTT	ATGCTTGTA	TTGTTTTCTT	480
AATGACTTTT	ACCTTAGTTT	TTAACAAACC	CATAGTACAG	TGTACCCCTCG	AG	532

(2) INFORMATION FOR SEQ ID NO:331:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

GAATTCCGGCC	TTCATGGCCT	ACATTTTGG	AAAAAAAAAA	ATCTACTTTG	TGTATGTGTG	60
GGGTGTGGGG	TGTGAGAGAT	ACATTCCTTT	TNGTGTCTA	AATCTCACAG	TCCACATATG	120
ACTTTCCCA	CTTGAGAATT	CTCTCTCATC	TGTGTGGCTC	CCTGCATTCT	ATAAAATAT	180
AAATAAAATAA	AATTTTAAA	AGTATAAAGC	CGGTGCCATG	AGACCCTTGG	GTTGGGCAA	240
GCCTGTGAAG	TTTGAACCGG	TTAACGCACG	AATACAAGGG	AGTGATTATT	ACAAGGCCAT	300
CCCGCTTAGC	ATCGGGAAAT	CATTGGGGA	GAGAGATTCA	ATTCATAAA	GATGATTTTC	360
AAGGGCTGTC	TCGAG					375

(2) INFORMATION FOR SEQ ID NO:332:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 344 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

GAATTCCGGCC	TTCATGGCCT	ACACGGGTC	AACTCTGCAG	GGCTGATGAT	AAACATGCCT	60
CTTCTCCTAT	TGTCCTTCTC	CTCTCTAAAG	CAAGTCATT	TCTGTGCTCG	TCAGGCCAGTG	120
GCAGGGTTG	GGAGGAGGAG	AGAGGAAAC	ACTGTGGTCA	GGCTCTGGGG	AGAGTTGACT	180
ACAGTGTAGC	TCTTGGATTA	TTTATGAATA	TTGCCCTCAG	ATTTATTTTC	ACTCTGCTCC	240
TTCCATTCTAT	ATTCGGAGAG	ACAACCAAGA	GCCGACTGTA	AAAAAAAGACT	TCCAGACACC	300
TAGAATATAT	ATCAATAGAC	ACTGTTAAA	AGGGAGAGCT	CGAG		344

(2) INFORMATION FOR SEQ ID NO:333:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 422 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

TGGCCTAAAG	GGGGTGGGTA	CTCCGGTGGG	GTAAGGTCAG	AAGGTCCCTG	TGCAGGGAGG	60
GAECTGGTCCC	TTGAGAAAGGA	ACAGAGGGCA	AATCCTGAAC	AGTCCTGGAG	GCCCAATGTA	120
GACAGCAGAA	GCTGGGAGCT	GACCTAGGAG	TGATCGGGGG	CCTGATCCAG	ACAGGACAGA	180
CACAGGCTGA	CACCGGAGAG	TCCCAGGTGC	CAACATGAAC	AGTTAACGGCA	GGGGCTGACC	240
CCAAAGAAAT	CAGGGGCCG	CAGCTGACCC	CGGAGGGTCC	CAGGTGCCGA	CCTAGACAGC	300
AAAGGCAGGG	CTGACCCCCAG	AGGGTCCCGA	GCCGACCCAG	ACGACACAGG	CAGGGCTGAT	360
CCCGGAGGGC	CCCGCCCCGA	CCCCGACAGG	CAGTGAAGGC	ACAGGCAGGG	CTGACACTCG	420
AG						422

(2) INFORMATION FOR SEQ ID NO:334:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 329 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

GGGAACGAAA	GATGGCGGCG	GAAACGCTGC	TGTCCAGTTT	GTTAGGACTG	CTGCTCTGG	60
GAECTCTGTT	ACCCGCAAGT	CTGACCGGCG	GTGTCGGGAG	CCTGAACCTG	GAGGAGCTGA	120
GTGAGAGTCG	TTATGGGATC	GAGATCCTGC	CCTTGCTGT	CATGGGAGGG	CAGAGCCAAT	180
CTTCGGACGT	GGTGATTGTC	TCCTCTAAGT	ACAAACAGCG	CTATGAGTGT	CGCCTGCCAG	240
CTGGAGCTAT	TCACCTCCAG	CGTGAAAGGG	AGGAGGAAAC	ACCTGTTAC	CAAGGGCCTG	300
GGATCCCTGA	GTGTTGAGC	CACCTCGAG				329

(2) INFORMATION FOR SEQ ID NO:335:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 377 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

GAATTCGGCC	TTCATGGCCT	AAAACAGATA	ACGCTATAGA	GAAAACACTG	TTTACTGAAC	60
AGTGCTTGT	AACCACGAGG	GTGATCAGAG	CCCCATTCTG	CCTTCTAGAG	ATAAACCTGT	120
CTCCCTTCT	GCAGAGCTAG	CTCCCTCTAT	TGCTTCTGGT	TGTCGTTGT	CTTCAGTCTG	180
CTTCCTGCCA	GTGCAGCAGC	TCTCTGCTAGA	TCTTGACATC	CTAGTGGCCA	GATCCCAGGG	240
GCGGTGCTGG	TCTCTATCCGA	GCTCTCTGCC	TCATCTCCA	TTCCCTTTT	CCACACTCAG	300
TGTGTATTCT	CTTGGATTTC	CATACCCCTGT	TCCTCCTACC	ATCCACCTCT	CTACCTCATC	360
TCCCGACCTG	CCTCGAG					377

(2) INFORMATION FOR SEQ ID NO:336:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 356 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

GAATTCCGCC	TTCATGGCCT	AGCAGGTCAG	GAGCCCCGGG	AAGGCCCAGA	GGTACTCCAA	60
AGGGGGCCCG	CTGGTATCTG	AAGGCCCCTT	GCAGTTAGTG	TGTTGTTGAG	CTGTGGGCAT	120
GAACATGCCA	CAGGCAGACA	CTGTTAGCC	AAGGTTTAA	GAAACACCGA	GGGTCTGTG	180
GATCTGGAGT	TCATTGTC	GGACAGGGAT	GGGGACCCCT	CTGAAGTATT	CACTGTGGC	240
TGAGGGGTGC	TGGCCACACA	ACCTCTGTGG	GAGGCATCTC	TTGCAGTGAA	GCTGTTGGTC	300
CTCAGTTCA	TGCCCACTGA	GGGTAAACCAG	CCCCCAGCTC	TGCACCCCCA	CTCGAG	356

(2) INFORMATION FOR SEQ ID NO:337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

GAATTCTAGA	CCTGCCGCAG	CACAATCCCG	TGGACAGAGC	TTACTCCATC	TAACTCGTT	60
TCAAGTCAT	GATTTCACT	TTCACTTTTC	CTTTTCCCTT	ATTATGTTGC	TTAACCTGTA	120
CAGTGGCAAC	TGAAATGCAT	TCAGAAATA	GGAGGTTTCG	TCCAGCACCC	TCTGCAGCCT	180
TGGTGCCTGT	AGCTCTGGAC	TTCCCTGGGC	CTTCCCTGT	GGGAGGGCCC	TGTAGACCAC	240
ATCAGGGTGG	GGTGGGGGTC	ACTTGGAAA	AAGGGCCGAG	GTCTGGTGAT	GTGGTTCCA	300
GGATCTGAA	CCTCTCCAC	CCCTCTGCA	GTGGACTGA	ATTCTCCCT	TTCATCCGAA	360
GAAACCCACT	TGCTGTTCC	AGCCAACTCG	AG			392

(2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

GCAAGATGGC	GACCGAGACG	GTGGAGCTCC	ATAAGCTAAA	GCTTGCGAA	CTAAAGCAAG	60
aatgtttgc	TCGTGTTTG	GAGACCAAGG	GAATAAGCA	AGATCTTATC	CACAGACTCC	120
AGGCATATCT	TGAAGAACAT	GCTGAAGAGG	AGGCAAATGA	AGAAGATGTA	CTGGGAGATG	180
AAACAGAGGA	AGAACAAACA	AAGCCCATTG	AGCTCCCTGT	CAAAGAGGAA	GAACCCCTG	240
AAAAAACTGT	TGATGTGGCT	CTCGAG				266

(2) INFORMATION FOR SEQ ID NO:339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

GAATTCCGCC	TTCATGGCCT	AAACAATGAA	TAAAGCCAAG	CCAGTTCTG	CCCCCGTGG	60
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GCTTGTACTC AAGACATTGA ACAAGTGATC AGAAAGATGT TGACTGCTGC AGCAGAGGGT	120
TGCAAGCTGC TCATGAGTAT ATAACAAGTA GCCCTAACCA AAGCATTCTC TCCCTTGGTT	180
TAATGTCCAC CCATTGAGGT GACTGCTAAA TACTAATCCA TGACTCTATC CCTTGGCATT	240
CAAACTCACA CATCCACTTA CCTGCCTCTC AACACCTCCCT GCCTCGAG	288

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

GAATTCCGCC TTCATGGCCT AGTCTCTGCC ATGTTCTAAA CTGAAAACCT CCTAGTCAAC	60
TTCACACTTT ATTCCCTGAT CCTCAATTGG TTCCCCTGTC CCGTTAGTGT TTCTTGTAAG	120
CCTCTGCCAC CACCGCAGAT CGAACTCTAA TCACATCTCA CCTGAATTAT GGAAAAGTCA	180
CCTCAATTCT CTCACCCATC CCAGCCTCCA CTATGGATTA ATATGCCCTAA AGCAGAGCTG	240
ACCACAAACGG TGAGAAGAAT CTGAGAGGGA AGCAGCAGCA AACACAAGAG TCACTGGACA	300
TGCATGCCCTC GAG	313

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

GAATTCCGCC TTCATGGCCT AAGAAAAAAAG GATAGACAAA TAGTATTTTT GTGATTTTAC	60
AGTAGCTTAA AACTATAGGA TTTTTTTTCC CCATTACTTT GCAACAACTG ATACTTTGA	120
CCAGTTCTCT TTCTCTAAGCA TTTCTCTCTC TGAGCTATTA CCCAAATTGT CCTAGTTCTT	180
CTCTGCTTGT CCCTCAGCTA TACACAGTCA CTGAGGCTCT GTGCTTGGCT TCTGTTCCCTC	240
TCTCCTCATCA GGGATTCCTC ATGTTGGAGT TCATCAAGCT CGAG	284

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

GAATTCCGCC TTCATGGCCT ACCACGATAG ACCAGCTGTA GCTCATTCCA GCCTGTACCT	60
TGGATGAGGG GTAGCTCTCC ACTGCATCCC ATCCCTGAATA TCCTTTGCAA CTCCCCAAGA	120
GTGCTTATTT AAGTGTAAAT ACTTTAAGA GAACCTGCGAC GATTAATTGT GGATCTCCCC	180
CTGCCCATTC CCTGCTTGAG GGGCACCCT ACTCCAGCCC AGAAGGAAAG GGGGGCAGCT	240
CAGTGGCCCC AAGAGGGAGC TGATATCATG AGGATAACAT TGGCGGGAGG GGAGTTAACT	300

GGCAGGGCAC TCGAG

315

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

GAATTGGCC TTCATGGCCT	AAAGATGTTA GATATTACAA	TTTGACTGAA	GAACAGAAGG	60
CGATCAAGGC	CAAGTATCCG	CCAGTCATAA	GGAAGTACGA	120
TCTCTTCTGT	TTCACTTTT	GGATGAATGG	CTTATAAGT	180
ATACCCCGG	TGGGGAGAAG	AATTTTCATT	TCAGTGTGA	240
AGCAATAACA	TATTCAACAA	TGCAAGGTCTA	TGAATGAAGAG	286

(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

GAATTGGCC TTCATGGCCT	ACCTCTGTGA	AAATTTAATT	TTTTATATCC	TGATTAATAT	60
ATTGTGACTT TAGGCCATT	TTTCATGTGC	TTCACTTTGA	TAGAGTTAAT	CCATAAAATT	120
GCTCTTTACT TTAGCTTATC	AAATGAAGTA	TTATTTTGTC	GAUTGGAGGC	AAAAAAGTC	180
ATGTGAGCTT CTCACAGGTT	TTTAAAGCTC	CACTAAAAAT	AATTATCCAC	TTGTCTTAC	240
TTTTGTTGAC CAGAATAGTT	GGTAACTCTG	CCAGAGCCTG	TACTTACCTG	CCAAAAAACAA	300
TTAAATCTGG TTAATGCC	AAACCAAATC	TCTCAGTCTC	AAGTGTATA	CTATCCAAGT	360
TTAAATCTGG AAGGTAAC	TGAGGTAAT	GAATTTTG	TTTACTGTG	CCTTTGCTA	420
TCAAGATAAT ATTCA	TTGTGTTT	GAATCTTGT	AAATTAGTTA	CTGTCGCTT	480
TTAACCTTGT	CTTTCTAA	GAAAGTTGA	GATCCAGAGA	GTTCAAGGGA	540
TCGAG				TCGGGGAGTC	545

(2) INFORMATION FOR SEQ ID NO:345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

GAATTGGCC TTCATGGCCT	ACAATAAGTG	TGTTATACIT	GCTTTGGTGA	TTGCAATCAG	60
CATGGGATTT GGCCATTCT	ATGGCACAAT	TCAGATTCA	AAGCGTCAAC	AGTTAGTCAG	120
AAAGATACAT GAAGATGAAT	TGAATGATAT	GAAGGATTAT	CTTTCCAGT	GTCAACAGGA	180
ACAAGAACAT	TTTATAGATT	ATAAGTCATT	GAAAGAAAAT	CTTGCAAGGT	240

TACTGAAGCA GAGAAGATGT CCTTGAAAC TCAGAAAACG AACCTTGCTA CAGAACTCGA G	300 301
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(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

GAATTCCGCC TTCATGGCCT ACACATTTG ACAGCTTC TTCAAGTTTC TTGAGCTCTC AGAAAAATTA GAAGGAAGTG GGCTGGGAT ATAGAGACAG TCCAAACTAC CAACTAATGA ATGAATCTGA AGGAGACACA GAAGGCAAG TAGAGTTAG AGTTTGAGAG TGCAAGGAAAG TTTGAAATG GTCAAGACTG CCAGAGTAAT TTCTGAGATC TTACTAAGCA CTCTCCCACC GTTTGCCTTA AAAGATCCCC TTCCCCCAA TTGAAACATC ACAAACTCTGC AGAGCTCTTT AATCAGGTGT GTTATACACA ATGAATTAA TTCTCTTATT GCCCTGGAAG AAAGATAAAC CAGATGTGGC CCTTGCCCT TTTCAGTAAG TATTTGTTAG ATCTTCATTA CATTAGGC CTCCTAGGCC ATGAAGGCCG GCCTTCA	60 120 180 240 300 360 420 447
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(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

GAATTCCGCC TTCATGGCCT AAAATTCGGC TGATTTCCCC CTTGGCTAGC CCAGCTGACG GAGTCAGAG CAAACCAAGA AAAACTACAG AAGTGACAGG AACAGGTCTT GGAAGGAACA GAAAGAAACT GTCTTCCTAT CCAAAGCAA TTTTACGCAG AAAAATGCTG TAATTTCTTG GGAAGATTTT AATGTACACC TATTTGTAAA GTCATCAGAA TAGTGTGGAT TATTAATAT CTAGTTGGA AGAAAATAAT TTATATAAT TATTGTAAAT TTTTATGTAA ACTCGAG	60 120 180 240 297
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(2) INFORMATION FOR SEQ ID NO:348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

GAATTCCGCC TTCATGGCCT AGAATAAAAC AAAGCCTTT CTGCCTTTA CATTCAAGTC AGTAACCGTC AACACCCAC CCATATACTC CCATACCATG AGGTGAATT TTCAAACCTCC TCGCATACTT TTAATTACTA GTTTAATTAT TTGCCTCTC ACTGAGTCTA TAATCTCACT TAGGGTAAGA ACAGAACTCA ATTACAGATG CTCAGTAAAC ACTGGAAAGGC CGGGCTCGA G	60 120 180 240 241
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(2) INFORMATION FOR SEQ ID NO:349:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 172 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

GAATTCGGCC TTCATGGCCT AGGGCTGCC AAGATTGTGA AAGGTAAGTA GTATCTTAT	60
TTGGGGTAA CTTAATTATA GATAAAAGAT GGTCCAATAC TGGAAACTGT TCGTTCTTC	120
CCTTGGATCT AGTCTTCTTC TGCTTTATAT AGAATCCCAC CATCATCTCG AG	172

(2) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 253 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

GAATTCGGCC TTCATGGCCT ACACGTGACA GCCTTCACT TTTCAGATCA CCTTCCTCAC	60
ACTGATGGTC TCATACAACA TCATTTGAA TGTCCTCAGC TCTCTGCACC ACCCACCAA	120
CTCCACTCTG GGCCACCGCT GGTGTATCCA AGATCAGGAC ACCAGTCCTT GGGCACCAAGG	180
GAGTATGCTG CCCACTGAAG CACGTTCTGT TTTCCGGCAC CCATGTTGTA AAATCGACTC	240
CCCCAAACTC GAG	253

(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 240 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

GAATTCGGCC TTCATGGCCT AGAAAGTTA AAGATTAGCG TACTGATTAT GATGGGATTT	60
TTACTGAAAA TTAGTTTGT CAGGCTGCTT GCTTGTCTGT GTATTTCTA TTCTAATTAA	120
GTTTTTATTT TTATCAAAGC TGATTTACT TATAATGAA AAAGTCAATT AGTTTTCCAA	180
GGCTTATTAT GGAAAACAGT AGTCCCCAG GCTCCCATCC CTATGTCCAA CAAACTCGAG	240

(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 334 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

GAATTCGGCC	TTCATGGCCT	AGACCTGCCT	CTAACGCCTT	GATTATTCA	CTGCCACTGC	60
CTACAGGCC	TCTCCCATAT	TCCCTCCTTC	TTGCTAAGTC	TGACTTAAC	TAGGCTTAGG	120
CACCAACTCC	TATAGGAAGC	CTTCCTTGAA	CCTGGCCCTC	TACTTTCA	TCACTGACTA	180
CCACTCAATT	AACTGAACGG	TGAAAAGTAA	CCCACAGCTA	CGCATTCA	CAGACAACAG	240
AATTTACTA	CTTCTTCTCA	CTACTGGTTC	ATATTTCTGC	AACCAGAAAA	TATCATTCA	300
TCCCTAGTAA	CTATGGCTTC	CATCTGTTAC	TTCC			334

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

GAATTCGGCC	TTCATGGCCT	AATAATGACT	TGTTGGTTGA	TTGTAGATAT	TGGGCTGTTA	60
ATTGTCAGTT	CAGTAGGCCA	TGAAGGCCGA	AG			92

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

GAATTCAGTT	CCTTATATAT	TCTAGTTATT	AATCCCTTAT	CAGGTGGATA	GTTTGCAGAT	60
ATCTTCTCCC	ATTCTTCTAGG	TTGTCTCTTC	ACTCTGTTGA	TCGTTTCCCTT	TGCTCTGCAA	120
AAGCTTGTA	GCTTGAGATA	ATCCCCATTG	TCTGTTTTTG	CTTTTGTGTC	CTATGCTTTT	180
GAGGTCTTAC	TCAAAAAATT	TTTGCCAGA	CCAGTACCCCT	TGAAGCATTG	CCCCAATGGT	240
TTTTTTTTT	AGTCATTCA	TAGTTCA	AGTTCAGGT	CTTACTCGAG		280

(2) INFORMATION FOR SEQ ID NO:355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

GAATTCGGCC	TCCATGGCCT	ACATAGATGG	GCACACTCAC	ACACAGAAGT	GTGCTTGTAC	60
AATCACCACA	CACGCACAAA	CACACACACA	CACTAAAAAT	ATAAAACACA	TGCGTCACAT	120

GGGCATTCA GATGATCAGC TCTGTATCTG GTTAAGTCGG TTGCTCGGAT GCACCCCTGCA	180
CTAGAGCTGA AAGGAAATTG GACCTCCATG CAGCCCTGAC AGGTTGTGGG CCCGGGCCCT	240
CCCTTGTGC TTTGTATCTG CAGCTCTTGC GCCTTTATA AGTCCATCCT AGTCCCTGCT	300
GGATGGCAGG GGGCTGGATG GGGGGCAGGA CTAATACTGA GTGATTGCAG AGTGCTTTAT	360
GAATTACACT TATTTTATCG AAACCCATTG GACTCGAG	398

(2) INFORMATION FOR SEQ ID NO:356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

GTGTCAGAGC AGGCATTCC CAACCTAAGG AAATCTTGT TTTCAAATAT TAGGGTTTTT	60
TTTTAATTGT GGTAAAGGA TTTGGACAT GCTTTGAAA TTGTTAGTAA AAGGACCTAT	120
TTTCCACCTG TATTCTAAGT TATTTTTTC CCTCTTTTG AATTTTCAG GTCAGCCCTT	180
CATAAACCCA GATGGGAGTC CAGTTGTGTA TAATCCTCCT ATGACTCAAC AACCAAGTAG	240
ATCCCAAGTG CCTGGACCTC CACAGCCACC TCTGCCACCC CCACCTCAAC AACCAAGCAGC	300
TAATCACATT TTCTCACAGG CGCATCTCGA G	331

(2) INFORMATION FOR SEQ ID NO:357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

GCTGCCTCGA GGTCTCCAAG ACTTTTTCAT CTCGTATCGT TTCGGGATCC GTATCCATAC	60
TTTTATTTTC ACTTTCTTCC TCTTCCTCCT CGAACTCCTC GTCGCCATCC TGTCTGCCA	120
GCTTCCCGTA GCCATCCTCG CCTTCTTCT CGTGCTCCTT CTCGCTCTCG CCATCCCTCG	180
GCATACTCTC CCTCTTCCTC TCGAG	205

(2) INFORMATION FOR SEQ ID NO:358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 584 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

CAAAAGAGAT GGTACCAGCA AGAGATTAAT ACTAAAGAAA TGCAAGTCAGA TTTTAAAGAA	60
ACTGGAAGAA GAGCCATTTC TCCCAGGGAG AAGATTCTAG ATGTGATTGA TGACACCATA	120
GAAATGGAGA CAGGTCTGAA AGCAATGGGA AGAGAGATTT GTCTAAGGGA GAAGACGCCA	180
GAGGTGATTG ATGCCACTGA GGAAATAGAC AAAGATTGG AAGAAGCTGG AAGAAGAGAA	240
ATATCCCCAC AGAAAATGG CCCAGGGAG GTTAAGCCTC TAGGTGAAGT GGAGACAGAT	300

TTGAAAGCAA CTGGATATGA GAGTTCCCA AGGGAGAAGA CACCAAGAGGT GACTGATGCC	360
ACTGAGGAAA TAGACAAAAA TTGGAAAGAA ACTGGAAGAA GAAAATATC CCCAAGGGAA	420
AATGGCCCAAG AGGAGTCAA GCCTGTAGAT GAAATGGAGA CAGATTGAA CGCAACTGGA	480
AGAGAGAGTT CTCCAAGGGAA GAAGACACCA GAGGTGATTG ATGCTACTGA GGAAATAGAT	540
TTGAAAGAAA CTGAAAGAGA AGTATCCCCA CAGGAAAAGT CGAG	584

(2) INFORMATION FOR SEQ ID NO:359:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 344 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

GAATTCGGCC TTCATGGCCT ATGCTTCTG AATTGGCAAG ATATTCCAGG CTTATTTGGC	60
ATTCATCTTA CTCTAGACCT ATTATCAACC ATGTCTCCAA GGATAAGTAG ATCCTTTAA	120
GGGAAAATGG TATTTTGAAA GCATAGTGTG GGATCTGAGG ATACCTATTCT GTGTCAGGTT	180
GTTTATTGTT TGTTTTCACT GAGTAGATCT TGGACTTTAT TAATTTTATT TATTTATTAA	240
AAGAAAAGTA CATCATGAGT TATAAGTAAT ATTCCAACCAAAATTTAA TATTGCTTAA	300
CTTCTTGTAT TTTATTTTA TCTTTAACAC TGAAAAGTCT CGAG	344

(2) INFORMATION FOR SEQ ID NO:360:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 362 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

GCGGGTGGAC AAAATGAAG CCAATGAAGA AGGCATGCAC TGGCCTTTCA GGTCTGGCA	60
GTGGCAGCAA GTCCCCCCCACCA GCCACCAGGG CCAAGGCTCT GAGGCGGGCA GGGGCTGGGG	120
AGGGTCACAA GCCAGAGGGAG GAGGATGAGC AGGCACAGCA GCGCAACCA CAGTCGGGC	180
CCGAAGAGGC TGAGGAAGGGAG GAGGAGGGAGG AGGCTGAGGC GGGCCCTGGG GCTGAAGGTC	240
CTCCACTGGA GCTGCACCCCT GGCGACCCCG CTCCAGGCC AGCAGAGGAC CCCAAAGGGG	300
ATGGGGAGGC AGGCCGCTGG GAGCCCTCAC TCAGCCGCAA GACAGCCCCG TTCAGTCTCG	360
AG	362

(2) INFORMATION FOR SEQ ID NO:361:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 378 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

GCACCACCTC TTGCACTGTG AGGAGTTAT TGATGAATTCA AATGGGCTGC ACATGTCCAA	60
GGACAAGAGG ATCAAGTCAG GGAAGCAGTC CAGTACCTCC AAGCTGCTGC GTGACAGTCG	120

AGGCCCGTCG	GTTGAGAAAC	TGTCACAG	ACCTTCAGAT	CCTGGAAAGA	GCAAGGGGAC	180
CTCCCATAAA	CGGAAGCGAA	TTAACCCCTCC	CCTGGCCAAG	CCAAAAAAAAG	GGTATTCAAGG	240
CAAGCCCTCT	TCAGGAGGTG	ACAGGGCCAC	CAAGACGGTG	TCTTACAGGA	CTACCCCCAG	300
TGGTTTGCAA	ATAATGCC	TGAAAAAGTC	TCAGAACGGG	ATGGAAAATG	GGGACGCCGG	360
CTCTGTAAGG	ACCTCGAG					378

(2) INFORMATION FOR SEQ ID NO:362:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 266 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

GATTGTATTG	AAAGTCAGAC	ATAGGTGTGG	AACCAGTTAT	GGGAGTGAGG	ATAAGTCTAG	60
ATTTGGGAAT	CAGTCGCAGA	GAGGTGGACG	ATGAAAGTCT	GAGAAGAAAG	GATCTTGCTA	120
ATGGAGTGAA	CTCAGAGCTT	GATAAAGGGA	GGATGAGTG	AAATGGAGCT	CAACGCTGTG	180
CCTTGGGAAA	TACCTCTGTG	GATTGGTGGG	AGCACAGTGA	CAAATTCAAG	AAAGACACAG	240
ACAATGGAAT	AACCAGAGAA	CTCGAG				266

(2) INFORMATION FOR SEQ ID NO:363:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 367 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

GAATTCTAGA	CCTGCCTCGA	GCATTGCC	CGGCCTAAGA	AGCTCTCTTA	TCTTGCATCT	60
TGGGCTGGAC	TCCTACAACA	GCCACAACTT	CCGTGCTGGT	CTCCCAGCTT	CTAGCCTTCC	120
CCCATCTCCT	GTCGTTTCG	ACACAGCAGC	CAGAAGGATC	CTTTAAAAAC	AGAGGTTGAT	180
CCTGTCGTT	CTCAAATCC	TCCAATGCTT	TTCCTACTGC	ACTCAGAGTA	AAAGCCAGTC	240
TCTGCCCTAG	ATGCTCTGGG	ATCCGTAC	CTCTTTGGTC	TCATGTCCTA	CAATCTGCAT	300
TCTGGCCATA	ATGGCTTTCT	CTGCTGTTCC	TTGAACATT	CGGAACATT	CCCCCATAC	360
CCTCGAG						367

(2) INFORMATION FOR SEQ ID NO:364:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 383 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

GAATTCGGCC	TTCATGGCCT	ACTGGGTTCT	GAGAAGCAGT	GGCCCGAGCT	GAAGCATCCA	60
GACAATGAGT	GTTCAGAACG	TGCCAGATTC	TCACCTAGCC	TTAGAAGTAA	CACAGCCACA	120
TTCTGTCGGT	TACAAACACA	TTTCTAAGGC	CAGTCCAGAT	TCAAACCGAG	GGCAATTAGA	180

TTTGACCCCT TGATGAAGGA GGGCAAGGTT ACACTGAAAA ACAGCATAGG GACTGGGAGA	240
TATTATGATG TCCATTTTG GAAAATCTGC CACAGACACA GTGAAGACAG AGAGCCCTTC	300
TCTCTGATCG AGGACCTCCA GAATGATCTG CTGAGTCACT CAGGTATGCT GGACCATTCA	360
CACTCACCC GGAAAAGCTC GAG	383

(2) INFORMATION FOR SEQ ID NO:365:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 356 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

GAGGTTTCACA GGTAAAGCA TTTGTTTTA CAAAAAGGAA TGGGATATGG GGGTGGTCAA	60
GTTTACGGG TAATAACAC ATTCTCTCTA GATGGCAGGG GTTAAGTCTG CCTGCTCTCC	120
ATTGCTGGTA CCACATAAGG GATACATTAG TAAAGTAGGG AAAGGGTCAT ATGTGTGGTT	180
GACCTGTTCT TCAGAGAGGA ACCTGGGATG GTATCTGCTG TGTACCTGTC TCAGACCAAA	240
CCTGGGGGTG GACCAGTGCC CCTTTCTTCT CAGCCTTCTT CCACAGCCTG ACTGTACTGC	300
CACCCGCACC CATGAGAAGG AGGTNNNTGAA GGAAGCTTGA GGACATCCAC CTCGAG	356

(2) INFORMATION FOR SEQ ID NO:366:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 246 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

GAATTCGGCC TTCATGGCCT ACAACCATTG AAAAATATA GACTTAGAAA ACGAAAGTTC	60
CCCTTAATCA CAAAGAACCA CAGTTGACAG GGTGATAGA TGTTTTTCA GATTTTTTTT	120
TTCATATGTC TGCTATCTT CCCACAGGA ACTGGTTTT ATTGTTAGCTG TTGTTTTGCA	180
ACCTCTGTTT TTCAAGTGCC AGTTTATCTC AGACATTGTC CTATGTCAGT ACAGGCCAT	240
CTCGAG	246

(2) INFORMATION FOR SEQ ID NO:367:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 238 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

GAATTCGGCC TTCATGGCCT ACAAAAAAAC AACTTTCCAG TGGCTTCTCA CTGCTCTGAG	60
AATAAACTCC AGGCTCTTCC ATTGCAACCA ACAGGATCTG GTGATTGAC CCCAGCCCT	120
CTTTCCAGGC CCTCATCACC TTGATCCTCC CTTAACCTAT CCTGCTCCAG CTGCACTGGC	180
TGCCCTCCTA TTCCCTCCAGC ATACCAAGAT TGTTTCTGCC ACAGGGCCGC CACTCGAG	238

(2) INFORMATION FOR SEQ ID NO:368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

GAATTCCGGCC TTCATGGCCT AGTTTTTCT ACTCCTACAA GTGTAAATTG AAAAATCTTT	60
ATATTAAGAAA AGTAAACTGT TATGAAGCTG CTATGTACTA ATAATACTTT GCTTGCCAAA	120
GTGTTGGGT TTTGTTGTTG TTTGTTGTT TGTTTGTGTT TGGTTCATGA ACAACAGTGT	180
CTAGAAACCC ATTTGAAAG TGAAAATTA TTAAGTCACC TATCACTCGA G	231

(2) INFORMATION FOR SEQ ID NO:369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

GAATTCCGGCC TTCATGGCCT ACTTGGTCTT CTGCACCTTT GTCTCTGACG TACTTCCTTT	60
CTTCACAAGT GCCATTTACA GAAAGCTGGG CTTAAACCAT TCCCAGCTAT TCCTCCTACA	120
GCTTTCTGA ATTATTCAG AATACAAAAT TCTGTATCTC CAAGAAACTA TTACAGATTT	180
AGATTTAAAA ATATGCACTA TTTCTACCT TGTATGTTT GCTTACTATT TTTTTTTGCG	240
AGAGGATATG TCTTAAAAT TGAAATGCAT CAAAAAT	277

(2) INFORMATION FOR SEQ ID NO:370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

GAATTCCGGCC TTCATGGCCT ACCAAGTCAA AAAATAGAAC AGTTCCGGCA CCCCAGAAGC	60
CCTTTGCCAC GTGTCACAA CCCTCCCTGT TTCCACCAAC AGTAACATTC TACTTTTAC	120
AGTAATTCTC TCCTTGCTTT TCTTGTAAAT TTTACTGCCC TGTGTTCTT AATATGATT	180
AGTTTTGCCT GGTTTGCCCT TCATATAAAAT GAAATCATAC TGAATATATT ATTTCATATT	240
TTGCCCAATA TTTTGTGTTA AAGATTTCATC CATCTTGAG CTCCAATGTA TTATTTCA	300
TTTTGTATA ATTATATGAT TATGCCACAG TTGTCAGTT CACTCGAG	348

(2) INFORMATION FOR SEQ ID NO:371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

GAATTCCGCC	TTCATGGCCT	AGAATTATTA	GGAAACAAAT	GGTTTGCTG	TCTTTGGTC	60
ATTAGCTTGG	CCCCATGTTT	AAGCATTCTGG	TAACAACGT	GAAGAGCTG	CTACAAATAA	120
AGTGGTAGGT	GCTCTGAAGA	AAAATAAACG	TGTTAAAGGG	AATAGAAAGT	GATGAAGGCA	180
GGGGCTGTTA	GACAGGCTGG	TCAGTGTCTG	AGGAAGTAGC	CCTGCACCTGA	GACCTGAAAA	240
GTAAAGAACG	AAGCCATGGG	GAGTTGGGGA	GGAGCATTCC	AGACAGAGGC	TTGATGTGTT	300
GAACCATCTT	TTCCAAGCTC	TTCCTCTGTT	ACCTTCTCTT	TAGTCACTAT	GTCCCCTTTC	360
TATCCCAGAC	CATAATTCCA	CCATTTATCT	TAAGGCTGAG			400

(2) INFORMATION FOR SEQ ID NO:372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

GAACGATTGA	ATTCTAGACC	TGCCCTCGAGA	TCAGCACTAA	CCCCCCAAC	TCCCAGCCTT	60
TAGTTTGCTG	TAGGCTGTCA	AACCAAGATAA	CCAAACTTGT	AAATTGAGA	ATCAATAGGC	120
TGTACATAGG	GACTACAACA	GAATGACGCT	CATTATTGAC	AGAATCAAGT	TCAAACCTCCT	180
TGCTCTGGCC	TCTGTTGGCC	TCTGGCAGCT	GGCTCATCTG	GCATTAGCTG	GTTGCACGAG	240
TTGCTGCAAC	CCTCCCAACCC	CGCTCGAG				268

(2) INFORMATION FOR SEQ ID NO:373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

GTGAGGTTTT	AACTGAGCTC	GAAGAATTGG	AATCAAAAGA	GATAGGTTG	TCTCAGTCCA	60
GACAGTGGAT	AGCATAAGGA	AACTACAAC	GCAGAAAAGA	GGGGGACAGC	GAAGAGACTG	120
GATTGATGCG	TTATCTAGGC	GGTACCTGTC	TCCATTCTTT	TCTAGCCAGC	CTTGAGCAT	180
TTCATCAAGA	ATAGAGGAAT	TCAAACTACT	GCAGTCTGCT	TGAACCACTG	CTTGTGAGTG	240
GCTCTAAAAA	AAATACCTGA	ATTGAACTT	GAAAGAACAC	TCAAATAAGG	TTTGGGGCTT	300
CTCTTTGTTT	AATACTTTAA	GGCTCTTATT	TCTAACATAA	ATATACTGAT	TGCACAGAAAT	360
TTGATTGTTG	ATAGCAGCAG	TTCCTGTAC	TTTGAATTC	TCAGATATTA	GAGCTGAAAG	420
ATCATCTGAG	TTACTTTATA	AATGGGGAAA	TCTCGATCTC	GAG		463

(2) INFORMATION FOR SEQ ID NO:374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

GAACGGCGAG CATTGAAGCA TATTGGAAAA GGAACGTGGG AATTTATTAA AGCACTCATG	60
AAGGAAATTC CAGCGCTGCT TCATCTTCCA GTGCTGATAA TTATGGCATT AGCCATCCTG	120
AGTTTCTGCT ATGGTGCTGG AAAATCAGTT CATGTGCTGA GACATATAGG CGGTCTTG	180
GAGAGAACCT CCCCCAGGCAC TTCCGCCACG GGATAGAAGA CGGCAGGAGG AAATTGATTA	240
TAGACCTGAT GGTGGAGCAG GTGATGCCGA TTTCCATTAT AGGGGCCAAA TGGGCCAAC	300
TGAGCAAGGC CCTTATGCCA AACGTATGA GGGTAGAAGA GAGATTTGA GAGAGAGAGA	360
TGTTGACTTG AGATTTCAGA CTGGCAACAA GAGCCCTGAA GTGCTCCGGG CATTGATGT	420
ACCAGACCCA GAGGCACGAG AGCCCCTCGA G	451

(2) INFORMATION FOR SEQ ID NO:375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

GAATTCCGGCT TCATGGCCTA CTCAGATCTT AAAATTCAAGG CTGTCAAAGA GATTTGCTAT	60
GAGGTTGGCTC TCAATGACTT CAGGCACAGT CGGCAGGAGA TTGAAGCCCT GGCCATTGTC	120
AANATGAAGG AGCTTTGTGC CATGTNTGGC AAGAAAGACC CCAATGAGCG GGACTCCTGG	180
AGGGCAGTGG CCAGGGACGT CTGGGATACC GTCCGTGTTG GGGATGAGAA GATCGAAGAC	240
GTCATGGCCA CTGGGAAAGG CAGCACTGAT GTAGATGACC TCAAGGTTCA TATAGACAAG	300
CTGGAAGATA TTTTGAAGA AGTCAAAAG CAAAATAACA TGAAAGACGA GGAGATAAAA	360
GTCTTAAGAA ATAAAATGCT CAAAATGGAA AAAGTCTTGC CACTGATCGG ATCTCAGGAA	420
CAGAAAAGCC CAGGAAGCCA CAAAGCAAAG GAGCCTGTTG GTGCTGGTGT TAGTAGCACC	480
TCTGAGAATA ATGTAAGTAA AGGAGACCTC GAG	513

(2) INFORMATION FOR SEQ ID NO:376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

CAGAAATGGGA TCGAACGCCG CCTCCTTAGG NTCTTTGCCN TCATCCTCTC TGGCAAATGC	60
AGTTACAGCC CGGAGCCGA CCAGCGGAGG ACGCTGCCCT CAGGCTGGGT GTCCCTGGC	120
CGTGCAGGACC CTGAGGAAGA GCTGAGTCTC ACCTTTGCC TGAGACAGCA GAATGTGGAA	180
AGACTCTCGG AGCTGGTGCA GGTGCTGTCG GATCCCAGCT CTCCCTAATA CGGAAAATAC	240
CTGACCCCTAG AGAATGTGGC TGATCTGGT AGGCCATCCC CACTGACCCCT CCACACGCTC	300
GAG	303

(2) INFORMATION FOR SEQ ID NO:377:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 334 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

GAATTCTGGCC TTCATGGCCT ACTTCATTGT AAGGTACTTC TTTGCGGCGC TGACAGTGCT	60
CACGCTCTG GGCCTCTCC ATGGACTCGT GCTGCTGCC GTGCTGCTGT CCATCTGGG	120
CCCGCCGCCA GAGGTGATAAGATGTACAA GGAAAGGCCA GAGATCCTGA GTCCACCAGC	180
TCCACAGGGGA GCGGGCTTA GGTGGGGGGC ATCCTCTCC CTGCCCCAGA GCTTTGCCAG	240
AGTGAATACCC TCCATGACCG TGGCCATCCA CCCACCCCCC CTGCCTGGTG CCTACATCCA	300
TCCAGCCCCCT GATGAGCCCC CCAGGTCCCT CGAG	334

(2) INFORMATION FOR SEQ ID NO:378:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 305 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

GGATTTTAAG GATCACATTCA AAGGGAAAC TGATATGAAG GTTGCAATGA ATGTGTATGA	60
GTTATCATCA GCTGCCGGAT TACCTTGTGA GATTGATCCT GCATTGGTCG TAGCTCTTTC	120
TTCACAAAAAA TCGGAAAACA TTAGTCCAGA AGAAGAGTAA AAAATTGCCCT GCCTTCTCAT	180
GGTGTGGTG GCAGTTCTT TGCCAACACT GGCCAGTAAT GTGATGTCTC AGTACAGCCC	240
TGCTATAGAA GGGCATTGCA ACAACATACA TTGTTGGCC AAAGCCATCA ACCAGATTGC	300
TCGAG	305

(2) INFORMATION FOR SEQ ID NO:379:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 329 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

GAATTCTGGCC TTCATGGCCT ACCCAAACAT TATCCCTCTA CACTGTCCCC ACTATGCTAT	60
ACCCCTGCAC TATACCCCTA TGCTGTCTCC CTTACGCTAT CCCCCATGC TATGTCCCT	120
ACACTATCCC CCTTTGTTGT CCCCTCATGC TACTCCCTAC GCTATCCAC TACTCTATCC	180
CCCTGACGCT GTCCCCCTAC GCTATCCCAG TACACTGTTC CCCCTACACT ATCTCCATAC	240
ACTGTCCCCC TACACTCTCC CCCTACTCAA TTCCCCCTAC ACTCTCCCGC TACACTATCC	300
CCGCTACACT ATCCCCCGAC GCTCTCGAG	329

(2) INFORMATION FOR SEQ ID NO:380:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 273 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

GTTCGAATGC TCTTACTTC CTTTGTGGAG CCTCCCTGCA CAAGCAGCAC TTTCTTTGC	60
CATAGCAACA TGTGCATCAA TAATTCTTA GTCTGTAATG GTGTCAAAA TTGTGCATAC	120
CCTTGGGATG AAAATCATTG TAAAGAAAAG AAAAAGCAG GAGTATTG ACAAATCACT	180
AAGACTCATG GAACAATTAT TGGCATTACT TCAGGGATTG TCTTGGTCCT TCTCATTATT	240
TCTATTTAG TACAAGTGAA ACAGCATCTC GAG	273

(2) INFORMATION FOR SEQ ID NO:381:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 338 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

GAATTCGGGCC TTCATGGCCT ACATAACTCT CCACAGGCTC CCCTGGGAGG GGTGCCCGCA	60
CCTCACCCCGC CACCTCACTT CTCAGCCCCCT CTTCCCATCC AAGGGCTCCC TGGGCTGCC	120
CCACCCCTAGT CATGATCTCG CTCCCTCACT CTCTCGTAGT ACTTTATTTC TACCTTGCTC	180
CTGGCTCACA TTACATGCTT ATCTTGATT TATAGATGGT TCTACATATG TCTCCTTTG	240
CATCCTTTTC TCAAAGCTCC TGTGAGGCCA GGGATGGTT TATGCCCTTT CTCATCCCT	300
TATGTTCTAG TATAATGCTT TACACATGTT TACTCGAG	338

(2) INFORMATION FOR SEQ ID NO:382:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 334 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

GAATTCGGGCC TTCATGGCCT ACTTTCTCTC CTTTTTTCT GTAACTGTGC TGGTTTTGTT	60
TTGGTCTTCC TCTCATACCC GTTCTGCTAT TTCACTTTTT CTTTCTATTG GGACTTCATT	120
TCATTTTTTT TTAACCTTAT CTTTGTTTC TCTTGTTTAT CCCATCCTTT TTGATAAAAT	180
CCATCGCATG TGTCTCTTT TTTCTTTAT TTCTCTTCTT TTCCCTTTTC CTTTTCTTT	240
CTCCCCAAACT TTTTCTTTT CACAGCATTG GAACACGGGA GGTAGTCACC CAGAAGAACT	300
TGAGCGGCCCT GGTGCCCATC CGAGACCACT CGAG	334

(2) INFORMATION FOR SEQ ID NO:383:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 232 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

GCAGAAAATA TGGTATCGGT TTCAATTAAAT AAAAATGAAA AAATAATTTC CAGTTATCAG	60
TAATTCTCA GTTACACAAC CTCTGCCCTC ATTTCCGCTT AGCCATGAAC TTTTACTGC	120
ACAAAGGAAT TTAAATAGC CAAATTCTAC AATTCTGGCT GGGTGTGGGG GCTCATGCCT	180
GGGATCTCAG TAGTATGGGA CCCCGAGGCA GGTCAGAAT TCAATCCTCG AG	232

(2) INFORMATION FOR SEQ ID NO:384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

GCCTCTGCTT TTAATTCAATT GGCAACTGTT ACGATGGAAG ACCTGATTG ACCTTGGTTC	60
CCTGAGTTCT CTGAAGCCCG GGCCATCATG CTTTCCAGAG GCCTTGCTT TGGCTATGGG	120
CTGCTTGTGTC TAGGAATGGC CTATATTCC TCCCAGATGG GACCTGTGCT GCAGGGCAGCA	180
ATCACCATCT TTGGCATGGT TGGGGGACCG CTGCTGGAC TCTTCTGCT TGGAATGTT	240
TTTCCATGTG CTAAACCTCC TGGTGTGTT GTGGGCTGTG TGGCTGGCT CGTCATGGCC	300
TTCTGGATTG GCATCGGGAG CATCGTGACC AGCATGGGCT TCAGCATGCC ACCCTCTCCC	360
TCTAAATGGGT CCAGCTCTC CCTGCCAACC ATCTAACCG TTGCCACTGT GACCACACTT	420
CTCGAG	426

(2) INFORMATION FOR SEQ ID NO:385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

GAATTCCGCC TTCATGGCCT AGGCCCTAA ACTGGATTCA AAAAATGCTC TAAACATAGG	60
AATGGITGAA GAGGTCTTGC AGTCTTCAGA TGAAACTAA TCTCTAGAAG AGGCACAAGA	120
ATGGCTAAAG CAATTCTACCC AAGGGCCACC GGAAGTAATT AGAGCTTGA AAAAATCTGT	180
TTGTTCAAGGC AGAGAGCTAT ATTGGAGGA AGCATTACAG AACGAAAGAG ATCTTTAGG	240
AACAGTTTGG GGTGGCCCTG CAAATTAGA GGCTACCTCG AG	282

(2) INFORMATION FOR SEQ ID NO:386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

GATTGAATTC TAGACCTGCC TCGAAGGCCG AGAGGGAAAG TTGAAAGGTC CCAAATTCAA	60
GATGCCTGAG ATGAAACATCA AAGCCCCCAA GATCTCCATG CCTGACATTG ATCTAACCT	120
GAAAGGACCC AAAGTGAAGG GTGATATGGA TGTGTCCTG CCAAAAGTGG AAGGTGACAT	180
GCAAGTCCCT GACTGGATA TAAAGGCC CAAAGTGGAT ATTAATGCC CAGATGTGGA	240
TGGACTCGAG	250

(2) INFORMATION FOR SEQ ID NO:387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

GAATTCTAGA CCCACCTCCA CCTTTAACTC GAAGTAACAC TGCAATCGT TTAATGAAAA	60
CACTCTAAA ACTGAATTAA TGTGTTGATA AAACAGAGAA AGGAGAAAGT AGTAGTCCTT	120
CTCCATCAGC TGAAAAGGA AAGATTCTAA ATGTTTCAGT GATTGAAGAA AGTGGCAATA	180
AAAACGATCA AAACTCTCAA AAAATTATGA AGAAGAAAGA GTCATCTCT ATGTTGGCTA	240
CAGTTAAAGA AGAAGTCTCT GGTAGTTCA CAGCTGTTAC GGAGAATGCT GATAGTGATA	300
GAATTCTGTA TGAAGCAAAT AGTAATTTA ACCAAGGGCT CGAG	344

(2) INFORMATION FOR SEQ ID NO:388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

GGAGTAATCA GAGGTGTTCT TGTGTTGTA TAAGGGTGGC AGGAGTGGAC ATTCTTCACA	60
TACACCCATT ATTGTTTGA AGTGTAAAT TACCTTTTA GCTACATTTT TGAGCTGAG	120
TTTGAATGA AAACCACAAAG AGTTTTATG TTGGCTGTAC TCGAG	165

(2) INFORMATION FOR SEQ ID NO:389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

GAATTCCGCC TTCATGGCCT AGAACAGAGC TTACTTATTC TTTCTGAAAC CAAGGCTTCT	60
CTAGTGAGCA CCATGAGCCT TTGGAAACAA CAGATGTATA CAATAGCAA GTTTCATTTT	120
TTTACCTTGA AACGTGAAAG TAAATCAGTG AGATCAGTGT TGCTTCTGCT TTTAATTTT	180
TTCACAGTTC AGATTTTAT GTTTTGGTT CATCACTCTT TAAAAATGC TGTGGTTCCC	240
ATCAAACCTCG AG	252

(2) INFORMATION FOR SEQ ID NO:390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

GAATTCCGCC	TTCATGGCCT	AGGATGTTCA	CTTGCATGCC	TCTGGATTT	AAAATTATTG	60
TTCATGAC	TCCTTTCTG	TGCGTTGGGA	AGCAGCTACA	GAGCAGTAGA	ATCCACTGAA	120
TTGGTACACT	GAAGCAGGCA	TGCATTTAA	ATGAAGGCAG	TTAACCTTGA	CTGTTGTATC	180
ACCAGACTTAA	AAGAACTCTG	GTCGCCCCCTCT	TIAAGTCTTC	AGGAAGTGT	TAGAGGCTTA	240
TTCACATTAG	TTAAAACAGG	CCCCCCCCAC	CTTCCCCCAAG	GCAACAGAAA	ACATAACCAT	300
TAGCTCTCTT	CCTGTTTCC	TTCTCTATT	CATGCTTGCT	TCGGCTGCTA	AACTGAATT	360
TTGTTACTTA	GAATATTATA	AAGTGTGGAT	GCTTTCTATA	ATGCTATTGG	TCTAAGTGTG	420
ATTAAATTTC	ATTAAGGTGT	ATAAGCCTCT	AATTATTACA	TAACGGCAC	TGGCTCGAG	479

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

GAATTCCGCC	TTCATGGCCT	AGCCTATTAC	ACAGTAAGTT	AATAATTGTG	TCCTTGCAAA	60
TAAGCATTGT	GTTCTGAAAT	GGAATCAGCA	TATTTCCCTA	TAAAGACACT	TCCACTCATT	120
CATTAATTGA	GCAGCCCCAG	TTGATAAAGA	ATCAGTATAT	CATGTTCTGA	TATTTAATCA	180
GCAAACCTAT	TTATTCTAGTA	CAAATTGAA	TTCTCTGTAT	GTGCCAGGCT	TGTGAGGAGG	240
GAGACTCGAG						250

(2) INFORMATION FOR SEQ ID NO:392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

GAATTCCGCC	TTCATGGCCT	AGTCGACTCC	TGTGAGGTAT	GGTGCTGGGT	GCAGATGCAG	60
TGTGGCTCTG	GATAGCACCT	TATGGACAGT	TGTGTCCCCA	AGGAAGGATG	AGAATAGCTA	120
CTGAAGTCCT	AAAGAGCAAG	CCTAACTCAA	GCCATTGGCA	CACAGGCATT	AGACAGAAAG	180
CTGGAAAGTTG	AAATGGTGGA	GTCCAACCTTG	CCTGGACCAAG	CTTAATGGTT	CTGCTCCTGG	240
TAACGTTTTT	ATCCATGGAT	GACTTGCTTG	GGTATGGAGA	GTGGCTTGA	CTACACTGTG	300
TGGAGCAAGT	TTTAAAGAAG	CAAAGGAAC	CCTCGAG			337

(2) INFORMATION FOR SEQ ID NO:393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

GCGATTGAAC TCCTGACCTC AAGTGATCTG CCCACTTGTG CCTCCCAGAA CTGGGATAAA	60
AAAAAAAAAAA ATAGATCCTT GGTTATTATTC CATTACATAC GGATTGTAAT ATTCAAGTTAA	120
ACATTCACTCT TTGGTGGGC ATTATATGTAT TTCTTTGTG TGTTTGTGTTG CAGCATTGCT	180
CTGTTAACCT TTTTATAAG TACATCTCGA CTCGAG	216

(2) INFORMATION FOR SEQ ID NO:394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

GAATTCCGCC TTCATGGCCT ACCACATTTG TAACGGAGCC ATTGAAGCAT ATTGAAAAAG	60
GAACCTGGGA ATTTATTTAA GCACATCATGA AGGAAATTCC AGCGCTGCTT CATCTTCCAG	120
TGCTGATAAT TATGGCATTA GCCATCCTGA GTTTCTGCTA TGGTGCTGGA AAATCAGTTC	180
ATGTGCTGAG ACATATAGGC GGTCTGAGA GCGAACCTCC CCAGGCACTT CGGCCTGGGA	240
TACTCGAG	248

(2) INFORMATION FOR SEQ ID NO:395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

GAATTCCGCC TTCATGGCCT AGCCTTCCTC TACCATTTT AATTTTTTA GACTTCATTT	60
TGTGATTAT TGCTGCTCTG GGGCCTTCAC ATCCAATCCT TTTATGTTT CATCTTCCCT	120
TTCCCTACAT TTGTTGCATA TAACAATGGC GTGTTTAGCT ACTGCAGTGA AAAATCAATC	180
AAGCCTATTC CATATTCAACA GGCTTGAAAT GGCACCAACG GCTCCCTGGAT CTCTCGAG	238

(2) INFORMATION FOR SEQ ID NO:396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

GAATTCCGCC TTCATGGCCT AAGTTGATCC GGATACACAC CTGCTAAAAC TGCTTAAAAC	60
ATTAGAAGGA CATGCTTATG GCCTTCTTA TATTGCATGG AGTCCAGATG ACAACTATCT	120
TGTTGCTTGT GGCCCAGATG ACTGCTCTGA GCTTGGCTT TCCAATGTAC AAACAGGAGT	180
CTCTCGAG	188

(2) INFORMATION FOR SEQ ID NO:397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

GAATTCCGCC TTCATGGCCT ACAGGCATGT TGAGATTGG AAAAGTGGAT GTAAGTGAAA	60
TTCAGATAGC TTTAGTGATT GTCTTGTGT TGTCTGCATT TGAGGGAGCA ACAATGTGGG	120
ACTATACCAT TCCTATTCTA GAAATAAAAT TGAAGATCCT TCCAGTTCTT GGATTCTAG	180
GTGGAGTAAT ATTTTCTGT TCAAATTATT TCCATGTTAT CCTCCATGGT GGTGTTGGCA	240
AGAATGGATC CACTATAGCA GGCAACCAGTG TCTTGTACC TGAGACTCCAC ATAGGACTAA	300
TTATTATACT GGCAATAATG ATCTATAAA AGTCAGCAAC TGATGTGTTT GAAAAGCATC	360
CTTGTCTTAA TATCCTAATG TTGGATGTG TCTTGTCAA AGTCTCACAA AAATTAGTGG	420
TAGCTCACAT GACCAAAAGT GAACTATATC TTCAAGACAC TGTCTTTTG GGGCCAGGGC	480
TCGAG	485

(2) INFORMATION FOR SEQ ID NO:398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

GAATTCCGCC TTCATGCCTA GTGGATCCGG AAACCTCTGTG GCTCTAGACT TTCAACTATT	60
TTATTTTTTC TTTGTATTTT TTGTTTGTT GCTTGTCTTT TTACAATGGG AACTAGAATG	120
TAAGATGCCA AACTCAGCCT GTGGGGAAACA TGGATTTCA CAACAGCAAC CACAGAGCGT	180
GGTTTCCATT TCTATCCCT GTTATGTGG GAGGCAGAGA AGGAAATCAG GTGCTCAGTT	240
CCAGGGACAT CACAGGACAG GACTCGAG	268

(2) INFORMATION FOR SEQ ID NO:399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

GAATTCCGGCC	TTCATGGCCT	ACACCTCTTC	TGCCAACCAG	CTGCTTGGGA	TGACTGCGAT	60
CCC GTGTGCT	TGTCTGGTA	TCTTCCCTGGG	AGGTCTTTG	GTAAGAACGC	TCAGCCTGTC	120
TGCCCTGGGG	GCCATTCCGA	TGCCCATGCT	CGTCAACCTG	GTGTCCACTG	CTTGCTACGT	180
CTCCCTCCCTC	TTCTGGGCT	GCGACACTGG	CCTGTGGCT	GGGGTTACTG	TTCCCTATGG	240
AAACAGCACCA	GCACCTGGCT	CAGCCCTGGGA	CCCCTACTCG	CCCAAG		286

(2) INFORMATION FOR SEQ ID NO:400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

GAATTCCGGCC	TTCATGGCCT	ACCTGCCTCG	AGATGATCAT	TCTTTTCTTG	CTTCTAGGCT	60
CTGTGTCCCTC	CTGGTTTCCT	CCAACCTCTC	TGGCCTGTT	TCATTTGCTG	TGGGTTCCCT	120
TTGCTTTGCA	CACCCCTCAA	ATGGGGCTTC	TCACTCACAC	TAGTGAGTTT	TCAGTGCTTG	180
CAGACCCAAAC	ACCCCTTTTT	TATAACAAAT	ATTTTTAAT	ACGTCCCTTT	CCACAACCTCG	240
AG						242

(2) INFORMATION FOR SEQ ID NO:401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

GAATTCCGGCC	TTCATGGCCT	AGTCCCCATCA	GAGGGAGCTG	ATGAAGAATG	GTCCCTGTAA	60
GTAAGTCACT	ACGTTCAACA	ACTGCCTGGC	CGAGCACTCA	GCCCCTGGAG	CTCAGGCCAA	120
CACCAGAGCC	CCGGTTTTAG	GGGCCAGGAG	AGCAGGTGAC	CAATTATTTG	GGGAGTCTTG	180
GGTAGAATTTC	CCGCCACACA	TTCTCCCCAG	GGCTGCAGGG	GTCTTCCGAG	GCAGGGCGGT	240
GGAGCAGGAT	TCAGGATGTG	GTGGGAATAG	AGTGAGGGC	AGTGGGTGTT	GTCAGGAG	297

(2) INFORMATION FOR SEQ ID NO:402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

GAATTCCGGCC	TTCATGGCCT	AAAAAACTAG	AATAATGGAA	GAGTAATAA	ACACAATTCT	60
TAATGTATTA	CAAGAAATAA	AAGGTTTAAA	AGTAGATTTT	TTAATTGAAA	AGAATTAAAT	120
CAGATAAAAA	TATTGAGAG	GTAATGCAAA	CATTTAAGTT	TGTCAAGAA	GCTTCAACAT	180
CTGGATAATA	GGAAAGAAAA	AAACCAAAGC	AAAAGAAAAA	TAAGCCACAA	ACTAAAAAAT	240
GTGGATTTCT	TGAAATTAA	AAAAGTAAAT	ATTGAAAGAG	CATGCTGTG	ACCTGAGATT	300

ATTTACCCAA AACTCGAG

318

(2) INFORMATION FOR SEQ ID NO:403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

GAATTCTGGCC	TTCATGGCCT	AGATTGAATT	CTAGACCTGC	CTCGAGTCTG	GGCACCCCTGA	60
GCAGCGCC	GAGCCGGGCC	AAGTCTGAGC	CCTTCCGCA	TTCTCCGGTC	AACCGCATGT	120
ATGCCATCTG	CCGCAGCTAC	CCAGGGCTGC	TGATCGTGC	CCAGAGTGTC	CAGGACAACG	180
CCCTGCACCG	CGTGTCCCCG	TGCTATCGCC	AGAACCGCTT	CCCCGTGGTC	TGCTGGCGCA	240
GCGGGCGGTG	CAAGGCGGTG	CTGCTGCGCT	CTGGAGGCCT	GCATGGCAAA	GGTGTCGTCG	300
GCCTCTTCAA	GGCCCAGAAC	GCACCTTCTC	CAGGCCAGTC	CCAGGCGGAC	TCGAG	355

(2) INFORMATION FOR SEQ ID NO:404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

GAATTCTGGCC	TTCATGGCCT	AGTCATGGAA	CAAGTCCTTG	CTAAACTAGA	AAACAGGACT	60
AGTATTACTG	AAACAGATGA	ACAAATGCAA	GCATATGATC	ACCTTTCTATA	TGAAACACCT	120
TATGAAACCC	CACAAGATGA	CGGTTATGAT	GGTCCAGCCT	GGGTGACAGA	GCGAGACTCT	180
GTCTTIAAAA	AAAAAAAAAA	AAAAGAAGTG	GCAGCTCTGT	CTGCTTCTCA	CAGAGTTGCT	240
AGGGACAAC	GCTGAGGCAG	GCACCTGCC	TTGGGCTCCC	CGGGTGGGCT	GCTATTGCC	300
TGTGGGCTCT	GCCTGCCCGC	CTGTCCAGTC	CCCGGGGTGG	CTCGAG		346

(2) INFORMATION FOR SEQ ID NO:405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

GCGATTGAAT	TCTAGACCTG	CCTCGAGAAC	AGGAACTTT	CAAACAAAAG	ATATATCATA	60
GGAAAGTCAGG	TGAGAAAGCTG	TCAACTGGGC	AGGCAGTGT	GAGAATCGTA	GTTGTCTTAC	120
TGTACTTTTT	TGTTTGTTC	AAAAAACCTA	AAGCATCACG	CATTTGAAA	GCAGAGTTG	180
CAGAGAGCCC	CCAACAGAGC	CAGAACTTGC	CAAGAGGAC	TGATATTCT	AGAATCCAC	240
GAGGCAG						247

(2) INFORMATION FOR SEQ ID NO:406:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 442 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

GAATTCGGCC TTCATGGCCT ACAACATCAA AACTCCCAAG CAAATGGATG AATTCAATTGA	60
GATCCAAGT TCAACAGGA CCTGGTACCA GCGCTGGCTG GTCAGATTCA AGACCATTAA	120
CAAGCAGGTC TGGGATAATG CCCTGTACTG TGTGATGGGG CCCTACAGAA TGAATACACT	180
GATTCTGGCC GTGGTTGGT TTGCCATGGC ATTCAAGATGA TATGGACTGA CAGTTGGTT	240
TCCTGATATG ATCCGCTATT TTCAGATGA AGAATACAAG TCTAAAATGA AGGTGTTTT	300
TGGTGACCAT GTGTACGGCG CCACAATCAA CTTCACAGATG GAAAATCAGA TCCACCAACA	360
TGGGCCTCGA CCTGACTTTG CCCCTTGCC CATCAGCCAT TTGCCATCAC CCCAAACAAC	420
TCAGCTTCGG GGAAGTCTCG AG	442

(2) INFORMATION FOR SEQ ID NO:407:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 154 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

CCGAGTGACC TTCTTGATGC TGGCTGTTTC TCTCACCGTT CCCCTGCTTG GAGCCATGAT	60
GCTGCTGGAA TCTCCTATAG ATCCACAGCC TCTCAGCTTC AAAGAACCCCC CGCTCTTGCT	120
TGGTGTCTG CATCAAATG CGAAGCTCCT CGAG	154

(2) INFORMATION FOR SEQ ID NO:408:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 146 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

GAATTCGGCC TTCATGGCCT AGTTTACTTC TGCTTGATCT TTATTCTTCC TTGCTACTAA	60
TTTTGGATTT AGTTTGTCTT TTTCTAGACA TTCATTGTTA GATTGTTAT TTACAATTT	120
TCTAGTTTT TTGATGTAGA CATTAA	146

(2) INFORMATION FOR SEQ ID NO:409:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 285 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

GAATTCCGCC	TTCATGGCCT	AGATGTTGCC	AGTTTTCATG	GAGGAAGTAG	ACATGAAAGC	60
TTGTTTGAA	TGTGTTGAC	AGAGTAGAAA	GACATTGAAG	AACGTGATGG	TATACATCAC	120
TTGAAATATT	TTATTGAAAA	GGGAGGGAGG	AAATGGAGCG	TTAGTTGTAG	GACCAGATGA	180
TGTAAGAGA	GTTTTTAAA	GTGTACAAAA	CAATGGCATG	TTGTGATACT	AATGAGAAGG	240
AGCCAATAGA	GAACAAAAAA	TTGATGATGC	AGGAGACGAC	TCGAG		285

(2) INFORMATION FOR SEQ ID NO:410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

CTCGAGGGAT	CTGGCTTTCT	CTGTCTTCTC	ATTTACTACA	TNACGCTGGT	GAATTAATAG	60
ATNTCTCAAC	AAAAGGACAT	TTAAATCAAC	ATATGACACC	TGTTTAAATT	CTTAAGAACG	120
CATTAATTAC	ACATTCTAA	GAAAATGAGC	TATGACACAA	CTCTTCTCAC	TGTATAACTC	180
CTATCTGTGA	TTCTCAATCA	GGTGACTTTT	CAGCTNCAAG	ACGGATCTTT	TCTATTCATC	240
TCCTCTGGTT	CGGACCAATT	AAATGTNTTC	TTTGCAATC	ANAACATCTC	ANNTGCCAAA	300
TCTTCAAAAG	CAAAGGAGTT	NGTTAGCAAC	ATATTAGGCC	ATGAAGGCCG	AATTC	355

(2) INFORMATION FOR SEQ ID NO:411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

GAATTCTAGA	CCTGCCTCTG	TATGTTGCTT	TAGCCAGGAT	TCAGAGCTAA	AGTGTAAAGTG	60
TGTGCTTCTG	CTTTCTGGAT	GTATCTCTCA	AAATTGCTCT	GTCTGTTTAT	TCAGCTCCTG	120
GATCTACCTT	CTCTTTCTT	TGAATTGGAC	ACCATTGATG	TCATTGCTCA	CTCAGAACTT	180
CAGCTGTTCT	CATGATCACA	TGCTTCTTC	CCTGTTTATG	TCCAAT		226

(2) INFORMATION FOR SEQ ID NO:412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

GAATTCTGGCC TTCATGGCCT ACTCTGCTGC TTAGCTTGTAA	TTTCAGTTT AATATATTG	60
TGATCATTAA CAAAACAGCG AAGTGAATAA TGGGCATAAA	TTTCCTAAG AAGAACATT	120
TTCCATACTT ATTTTCAAT ATTATCAAAA AGTATGTAAT	TTTGGGGGT TTTTGCTTT	180
TTTTTTTTTG TGAAACAGAA TCCTGCTCTG TTCTCGAG		218

(2) INFORMATION FOR SEQ ID NO:413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

GAATTCTGGCC TTCATGGCCT ACTTTGAACA ATTCCGCATG AATTGAAACC AGGTTTTCCCT	60
GTTGAAAGTT ATAGCTTGAT TGGGAGATAG AAGTTGAATT GAGTTCTTTC TTGCAACTCT	120
TAGTGTITAT TTTTATATCT CAGTAAGACG AGGATACCTT CAGTTTGAAT CTGCATAATG	180
TTCACTGCCA AACTCTTCT CATTAAATGC TTATGGCCTT CACATTCTG TATAATAAAG	240
ATCAATTATC AGCACTCGAG	260

(2) INFORMATION FOR SEQ ID NO:414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

GAATTCTGGCC TTCATGGCCT AAGCATATGA ATTTTGGAGA GACAGACATA CAGACCATAA	60
CAGTTCTATT TTCTATACT ATAGTAGAAAT ATCGAAATGA GAACATTGAC ATTGGTAAAAA	120
GGTGTATGTA TAGTTTATAT GTTATCTTAT CAAAAGGTA GATTACAGA ACCAACACAA	180
GTAAGCTATA GAACTAGCCC ATTACCAACAA AGATCTCCA CAAGCTACAG CTTTACAGTC	240
ATACCCACCC GGCTCGAG	258

(2) INFORMATION FOR SEQ ID NO:415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

GAGGACCTTT ATAATCTACT ACTAATTACT GTGAAAGTAA ACATTGTTA ATATAACCACT	60
TCTTAAAGAA ATATTTGTC TAGTCATTAA TATTCTAGTT CATCTCAAAG CTTCCATTG	120
ACAATTAAATTTAA ATTACTTAAATTTAAAGGAAACA GTTTCTGA TTCTCATGAA	180
AGTTCCATT TGCACCTGAAG ATGACTAACAC CTTTTAGTCA TAGTTTTAGA AGAATTGGCT	240
TTTTTATAGC CATTAAATTT ACATATGGGT ACGGACTCGA G	281

(2) INFORMATION FOR SEQ ID NO:416:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 118 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

GAATTCCGCC TTCATGGCCT ACTCAGAAAA GAAAATGAAA ATACCTCTAC ATGTGGTCTT	60
CCTGCTAACAT TCTCTGACCT TCCTATTACAC CACCCCTCCCC ACTGCCCACT TACTCGAG	118

(2) INFORMATION FOR SEQ ID NO:417:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 273 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

GCGAGGGATGG CATGGACGCT TATCGAGCAG CTTCAGGGTG GCAGCTACAA GAAGATTGGC	60
TACTATGACA GCACCAAGGA TGATCTTCCC TGGTCCAAA CAGATAAAATG GATTGGAGGG	120
TCCCCCCCCAG CTGACCAAGAC CCTGGTCATC AAGACATTCC GCTTCCTGTC ACAGAAACTC	180
TTTATCTCCG TCTCAGTTCT CTCCAGCCTG GGCATTGTCC TAGCTGTTGT CTGTCGTCC	240
TTTAACATCT ACAACTCACA TGTCCGTCTC GAG	273

(2) INFORMATION FOR SEQ ID NO:418:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

GAATTCCGCC TTCATGGCCT AAGCAGTTGC TAATGCCAGC AGTACATAAA TTGAGGGATGG	60
AGCAAAGGA TCGACACCAC CAATGGCTGC ATTGTGATAG GTGTGGACAG AGCCTGCCAG	120
AATTAAACAC ACGCCAGGAC TCGAG	145

(2) INFORMATION FOR SEQ ID NO:419:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 290 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

GGATTTCGCC	TTCATGGCCT	AGTGTGTTATA	ATTAATCCCT	TAATATTATG	GTTATTAACC	60
TCTTAAACAT	GAATGAATTG	TTGATTGTTT	TAACACAGTA	CCTAAGACTA	ATGCTTCTG	120
TGGACACCA	TGAGCTCTGC	CTCAACTCCA	CCCTCTGCAG	CCGGAGGACT	ATGCCCTAG	180
TAACTGCTGT	CGGTGTGGAC	GCTGTGCTGG	TTCTGTTTC	TAAAGGAGCA	GAAGGACAGG	240
TCTCTGAGAC	AGGATCGTTG	TCCCTACAGG	AGGAACAGTG	GCCACTCGAG		290

(2) INFORMATION FOR SEQ ID NO:420:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

GCGATTGAAT	TCTAGACCTG	CCTCGAGCCT	CCCAAAGTGC	TGTGATTACA	GGAGTGAGCT	60
GCCACGCCCA	GCCTACAAGT	TTTTCTTTAA	CTACTGCTTT	AGTCAACCAT	ATCCTCTAGC	120
TTCTGATATT	TTCATTGTTT	GTGTCATTT	TCTAGATATT	CAACAATTTC	AAATTAGATT	180
TTCTCTTCGA	CTAAAGTGGAA	AGAATTTTTT	CCGGTTTATT	TTCTACATGC	AAAAGATTTT	240
TATTTTCATT	TTGTTATTAA	TTCTAGTGT	TACCGTATTG	TCATTAGAAA	ATATGGGCTG	300
GCTCGAG						307

(2) INFORMATION FOR SEQ ID NO:421:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

GAATTCTGAA	AATATTAAGA	TTTATCCTAG	CACTTACGT	CAACATACCA	TAATTTTAT	60
ACTTCTCCAT	CTAAATAAAA	CCAAGTTGT	TCCTACACTA	GTCCAGCCTG	CATTCTCAAG	120
AACTCCAGTG	ATTATAACATC	AACATCTAGA	GATCAGGTAT	CCCAATCCTT	TCTTCCTATA	180
TCTAAGCTAA	CTCCTCTTAA	GCCAAATGGT	ACCCCTTGAT	TTTGTGTTAA	TCCTTCCTT	240
CCCTCCACTC	TTAACCCCTC	TCATTCCATC	TTCTCCCTCC	CTTTCCACC	CCACTCTCGA	300
G						301

(2) INFORMATION FOR SEQ ID NO:422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

GAATTGGCC	TTCATGGCCT	AGTTAAAGT	TGTCTGGTAA	TAAGGTGGAG	TGGATTGGG	60
GCAGGTTTA	TGTTGTGTG	CTTCTCTTAG	AAGTCAAAGA	GTTGGTGAGG	TAACTGCAAT	120
CCTGTCTATA	TCAGTGTAGT	GATAATGCAC	TAGTGTAAATG	AAGAAATGGAG	CTGCACGTGT	180
GAGGTTTTC	AACTCACAA	AGTCAGGTA	TIGTCTACGG	TCAATAAAGA	TTTTTTAAA	240
AAACCCCTTT	AACTAAAGAG	AGGTAACCTTC	CTTTTCAAAA	CTCTGAAATT	TACATGTGCT	300
GACTTATAAT	ATGTGTGATC	CTCGCTGCTT	TTCTGATCCC	TGGTGGTTGG	GGTGTGTG	360
TGTGTGTGTC	TGTGTGATGG	GCTCTCGAG				389

(2) INFORMATION FOR SEQ ID NO:423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

GAATTGGCC	TTCATGGCCT	AATCTTAAGT	GTTCACATG	CTCTACCTGC	CGGAATGCC	60
TGGTCCGGG	AGATCGGTT	CACTACATCA	ATGGCAGTTT	ATTTTGTGAA	CATGATAGAC	120
CTACAGCTCT	CATCAATGGC	CATTGAAATT	CACTTCAGAG	CAATCCACTA	CTGCCAGACC	180
AGAAGGCTCG	CTAAAAGGTC	AGAGTAATGC	AGAATGCCGTG	CCTTCATCTC	AGATTGGTTC	240
ATCACAGGTG	GATCCCATGT	GTCTTCAGTA	GACAAGTCAC	CTTGTAGCT	AGCACCCAGTG	300
CCAGCTCCAT	GCCATTGAC	CTCGAG				326

(2) INFORMATION FOR SEQ ID NO:424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

GCGATTGAAT	TCTAGACCTG	CCTCGAGCCA	ATCATTGTTA	AATCTAAC	GAACCTTAAC	60
TGGTTAGTTG	AGTGCAATTT	TATGTGTACT	GATGTATTG	CATTTATTCC	TTACCAACCTT	120
ATTTTGTGCT	TTTTATGTTT	TTTCCTTCCA	CTCTTTTTT	TTCTTTGGA	ATCTCGAG	178

(2) INFORMATION FOR SEQ ID NO:425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

GAATTGGCC	TTCATGTACA	TAGATCTTCC	TAGTGTCTT	GACAAAGGTG	ACATTGCAA	60
GGCTTTTCT	TCATCAGATG	CAGGGATCTG	GACTTCATGT	GTATCCTTT	ATCCACTCCT	120
CCTCGAG						127

(2) INFORMATION FOR SEQ ID NO:426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

GAATTCGGCC	TTCATGGCCT	AGAATTAAAT	TGCAGAAAAT	TATTCATATT	CTTATAATCC	60
TTTAATGTC	TATAGGATT	ATGATGATAT	CTCCCCCTCC	ATCCGTATT	TTTCAAGTTT	120
TTGTTTTTC	TTTTTCTTA	AAATTCTGG	AAATGTTA	TTAATTAT	TCATTTTAA	180
AAAGAACCAAG	CTTTGGTTT	CATAAAAGTT	TATAATTTTT	TTGTTTCAC	TTTCATTAAT	240
TCTACTCTT	ATTATTCCT	TCATTTGTT	TACTTTGGGT	TTGTTTGCC	ATTTTTTCC	300
TAGTTCTTA	AGGTGCCAGC	TCGAG				325

(2) INFORMATION FOR SEQ ID NO:427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

GAATTCGGCC	TTCATGGCCT	AGGCACACAG	GGCGGGCAGC	AACATAAACG	GCACCCATTA	60
AAAAGCAAGA	CTCGCTCTTG	AGACTAAAGG	AGAAGTTACC	AAATTTCTG	TATAAACTCA	120
GTAATTCAATT	CACTTACTA	GTATTACATT	TATGAAATTG	ACCTTTGTGG	AAAAAGGAGC	180
GGGAGACCGA	TAAGAAAATG	CCTGTTCTA	GAAAACGCTC	GAG		223

(2) INFORMATION FOR SEQ ID NO:428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

GAATTCGGCC	TTCATGGCCT	AAATTCAAC	AGAAGACCTT	ATTGTGATAA	AGTTCAACGG	60
TATAGGTAAG	CAACAAACAA	AAAACATATCA	ACCATAATT	TTTCACCTA	CCAACATTCT	120
CTGAACCTTT	CAGTAATATT	TTATACACAT	GTGCATATT	TGCCCTTTTC	ATTTACTATA	180
TCATAAACTT	CTTTCTAGAT	CATTATTTT	CTGCTGCATT	TTTCAGGAT	TTATCACCTT	240
TATTTTGTAGT	TTTAGTTTT	GTGAGTGTAC	TCTCGAG			277

(2) INFORMATION FOR SEQ ID NO:429:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

AAATGAGCCC TATCACTGAG AAATACGTGT TTCACTGATT AACTCTGTGT GTGTGTGTGT	60
GTGTATTTTT TTTTTGGTTG TCTTCAGCTG ACAGTATGAA AAATGAAACT GCTGAAAAAG	120
CTGAGCACCT GGTCACCCCTT GGCTTCCAT TGCTTTGGCC TTCAGTAAAA AGCAGCCTCC	180
CTTCTAGGTC AGGGAACCAT GCCATTGAGA CTAGTAACGG GCGTTCTGGG CACAGTCCA	240
CTGTGCACAG GTTGAGAGG ACAAGTTCAT CAGAAGGAAG GCAGTCCTTA GAAGTCACAT	300
ACGTTGAGCC CCTCGAG	317

(2) INFORMATION FOR SEQ ID NO:430:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 271 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

GAATTCGGCC TTCATGGCCT ACATTCAGAA AACAGAAAAG TTTCAAGAAG CAGGAAGAAA	60
AGACTCACCT ATGATCCAA CACCCAGAGG TAATAATTAA CCATTTTGG TGTATCTTCT	120
TTGTCTTTTC CTATGTGTTG CCTTATGTAG ATATGTAACA GGTTGTGGTT TAAACCGAAG	180
CTATACCCAT TGTTGGAGT CAGGCAGGTG CGATAAAATT GTAGGTGGCT CACCAGAAAT	240
CTATTTGCAT GATGAACCTA CAGGACTCGA G	271

(2) INFORMATION FOR SEQ ID NO:431:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 349 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

GAATCATTTC TGGTCACCAA TCTCTCATAT ACCACTACTG GATATTTACA ACATGCTTCA	60
GTGGAGGAGA AGACACTGCT GCTTTGCAAAT GATGACCTGG AATGCCAAA GGTCTCTGTT	120
CCGCACTCAT CTTTATGGAG TACTTTCTCT AGTGTGTTCTT TTTGCTATGT TTTTGTGTTT	180
CAATCATCAT GACTGGCTGC CAGGCAGAGC TGGATTCAA GAAAACCTG TGACATACAC	240
TTTCCGAGGA TTTCGGTCAA CAAAAAGTGA GACAAACAC AGCTCCCTTC GGAACATTG	300
GAAAGAAACA GTCCCTCAA CCCTGAGGCC TCAAACAGCA ACTCTCGAG	349

(2) INFORMATION FOR SEQ ID NO:432:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 261 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

GAATTCGGCC	TTCATGGCCT	ACCTGGATT	CTCAATTAT	TAAGTTGAC	TTACCTGATG	60
CTGATGATGA	TTACTGTATT	TACACATTGT	CTCAGAGCTC	ACTCTGGCG	AGGTTGTGGC	120
CTCGAAAATG	CCTTGTGTC	CCTCTGGAAT	CTGTCTTTTC	AGCTTCATCT	CCTCCCTCCTC	180
ACCTCCCTGCT	GTGGTGCACA	GATACCTATA	GGCAGGCTCC	ATCTCCCTCCT	CCCCAGCTCC	240
TCCCTAGTG	CACACCTCGA	G				261

(2) INFORMATION FOR SEQ ID NO:433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

GAATTCTAGA	CCTGCTCTCGA	GTCTCTACGGG	AAACCTCCAG	GGTTTTAGGA	AGCTGACGAT	60
GCAAGTTTAT	CCAAATGGGA	ATGATAATAA	TCATGTTTAT	TATCCTGGGG	TGCTTTCTCC	120
ATAGCAAGTA	CTCACTTAGG	TCCGTGTCAT	TAGTCAGTCT	TTTAATCTGT	ACTGAAATAG	180
GTGCTGTCGC	ATCCATGGGG	AATGAACCTCG	AG			212

(2) INFORMATION FOR SEQ ID NO:434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

GGTTGCAGTG	AGCTGAGATC	GCACCACTGCG	ACTCCAGCCT	GGGCAACAGA	GTGAGACTTC	60
ATCTCCAAAA	AAAAAAAAAA	AAAAAAAAGA	CAACCACAAAC	AAAAACGAAA	CACCACCAAC	120
AAAAAAAGTT	ACTGCTAGAG	TCTCTCTAG	ATTGTTTCT	TTTCAATACT	TGTTTCATAT	180
TCTCCAAC TG	CCCTCGTCCC	ATAATGTTGG	CTGTGCTTTT	CTTTGTGCTT	ACAGGTCATT	240
GCTGGGATGG	ATATGGT GAG	TTTTCATGTA	CATTGACCAA	ATACAATCTC	GAG	293

(2) INFORMATION FOR SEQ ID NO:435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

GAATTCGGCC	TTCATGGCCT	AGGCTTGAAA	GGAAATGAGG	GAAATTTCAG	TGAGTTTGAG	60
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GAATGGCAGA CTGGGTATGT GACAAATGAG TGGGTAAATA AGGAAATCTC AGATTGAGAA	120
TCCCTGGCAGA TCTTTCAATG GGTTAGACTG CAGGAATATT GATTTTAAAG CCAGACTGAA	180
GCAAATTCTA GTGATAAAGG AAGGGAAAG GCTGGCTGAA TCAAATGTC TACCAATACT	240
CCTTTTTTA GTATTTGAGT TAAAATTCAAG ATTANATGCT TGGCTTAGAA GAATGCAAAG	300
CTTCACTGAG CCTAATAATA TGGATCCCAG TGGGTGAGTG GAGGTGAGTT CACTCGAG	358

(2) INFORMATION FOR SEQ ID NO:436:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 258 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

GCTCGAGAGA GCTTTTTTTT TTTTTTTAA ACATTGTATC ATTAATTAT CACGTGTATC	60
CAAGCTCCCT TGAGTTCCC TGCCCCCATC CCTGTGTATC TCCAGCCATA TCCAGCTACT	120
CCTTCCATGC TTCCCCCATT CTGTGTTCTG ACTCTATTAC TCCCAGTCCA AATTTGCTC	180
TTCACTGTCT GCACCTGTG CTCTCCTCTC TCTCAAAAAA TCTACCCAAA TTCCACCCCT	240
CTTCACAGGC CCCTCGAG	258

(2) INFORMATION FOR SEQ ID NO:437:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 299 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

CAAGCCGGCC ATATTAAGAGA GATGAAATA AAGCTTCCTT AATGTTGTAT ATGTCTTGAA	60
AGTACATCCG TGCATTTTTT TTTAGCATCC AACCAATTCTC CCCTTGATG TCTCGCCCCC	120
TCAAATCACC CTCTCCCGTA GCCCACCCGA CTAACATCTC AGTCTGTGAA AATGCACAGA	180
GATGCCCTGGC TACCTCGCCC TGCCCTTCAGC CTCACGGGGC TCAGTCTCTT TTTCTCTTTG	240
GTGCCACCCAG GACGGGACCAT GGAGGTACACA GTACCTGCCA CCCTCAACGT CCACTCGAG	299

(2) INFORMATION FOR SEQ ID NO:438:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 238 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

GAATTCCCTAC TAAATAATAT TAAGCAGGAA TTTTTTAGGT GTTGCCTTTT AGCTCCTTTT	60
TATCAGTTCT GGGAAAGAAA CAGTGCTGCA TCTCCCTTTGC TCTCATAGAA TTCTGTAATT	120
TTTATACAC AGGTCTCTGC TAAAAGGCGG CATGTGTTTA GAAATTCTAA AAATGAGGGC	180
TCTGAACCTT GTAATGTCC TGATACGTTT TCCCTTTTTT AATCCCAACC CCCTCGAG	238

(2) INFORMATION FOR SEQ ID NO:439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

GAATTCTGGCC TTCATGGCCT ACAACTTGCA CTTCGCTCCA GCATCACTGG CCTCCTGCTG	60
TTATTTAGGT ATACTAGGC A TTTCCTGTT TAGGGCCTT GTACCTCCAG TTCCCTCTGT	120
TTGGAATGCT TTTCCCCAGA TAGCCCTGTG GTTAAATCTC TTACTTCCTT TGGGTCTGTG	180
CTCAGATGTT ACTTCTCA G AGGGTCCCC AAGCCCCCAT GCACTCGAG	229

(2) INFORMATION FOR SEQ ID NO:440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

GAATTCTGGCC TTCATGGCCT AGAGTCTATT AACTATTTT CTGTTATAACC CTGCCAGAAA	60
AGAATTTAA AAGTTAGTTT ATGTTTGTG TAACCATGTT CTTCAGAATG CAGGTATGTG	120
AGCATCATGG TTTCTGGTA ATTCTGCTGC TCCTGTCTT GAAAATGGAG ATACCACTTG	180
CAGCTTATCC CACTGCTGAG TATTCCAGCA TTGGTAGTGG TTTCACTCCA TTGCATCCAT	240
CCAGAACATT CACACAGGCC TCCCCATTAC CCAGCATCCT CGAG	284

(2) INFORMATION FOR SEQ ID NO:441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

GAATTCTGGCC TTCATGGCCT AATAAAATAA AAATTGGAAG AATGGCATT TATTACAGTA	60
TAGTTAAGAG ATTGGCTAAG GCAGTAAATA AAACCTAGAA ATGCTCAAAT TTATTGTAAA	120
TTGCTTTTAT AATCATTGAT ATATAAAGCA TGCTACTGCT AATCAATTAG TTTTATGTAT	180
TAAGACCTAT CAGCATGTCT TTTTTTTAGT ATCTGGTTGA CTTAAACATG ATGTTCTCTG	240
TACCATTTAA CATTTCAG ACATATTCTC CCCAAACTCG AG	282

(2) INFORMATION FOR SEQ ID NO:442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

GAATTGGCC TTCATGGCCT ACTCACCTGC AATCTATTGT TTATATTGTT GCTATGTATC	60
TCTATTCTTT CTGCATCAAA TAATGAATAG CTCATTTGT GTTGCTTCA AGTATGACAA	120
ATTCCCTTCC AAATGTGATT CCAGACAGTA TATCCAAACA TGTCTTCTT TTCCCATTC	180
TGATCATCCT ACATGTCAAG CACTGCCAAC GTTTACTCAA GAAAGCTTGG TTAGAACCCA	240
G	241

(2) INFORMATION FOR SEQ ID NO:443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

GCAAGCACAA ATCTAACCAT GAGCTTCAGC AATCAGCTCA ATACAGTGCA CAATCAGGCC	60
AGTGTTCTAG CTTCCAGTTC TACTGCAGCA GCTGCTACTC TTTCTCTGGC TAATTCAAGAT	120
GTCTCACTAC TAAACTACCA GTCAAGCTTTC TACCCATCAT CTGCTGCACC AGTTCTGGGA	180
GTTGCCAGC AGGGTGTTC CTTGCAGCCT GGAACCACCC AGATTIGCAC TCAGACAGAT	240
CCTCTCGAG	249

(2) INFORMATION FOR SEQ ID NO:444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

GAATTGGCC TTCATGGCCT AGGGATTTTT TTTCTTTTTT TTCTCATAT GTGAAGTAAT	60
AGTCTCTTCA CAACAGAAGA AGCCACAAAA CTAAACTTAT TGTCACTGA ATTTCTTCA	120
AGGTTACGTA CCTCTTTGGT ATTTAAATC TAGATTATGT TGATTITAT ATTTTGTTC	180
TCATTTTCT ATTTCTTGT TTCTTTACT GCAAATGGC TCGAG	225

(2) INFORMATION FOR SEQ ID NO:445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

GAATTCCGCC	TTCATGGCCT	AGTTTGAG	AGCTCTACCT	ACTAGCTGGT	TATTCTTAC	60
ATTAATTAA	TACCTTAAA	AAGTATTATG	AAAATAACAC	ACTCAGTAA	AGAAATTAA	120
AAAAACAAAT	GCAATAAAA	TGTGTTCTT	TTAACCTTT	GAATTGTCAC	TTCCCTCAGC	180
TTTCCCTTA	TTAACTGTG	AGAGGTATT	TCTATTAGCA	GTTACTTATC	CCCTTCCTCA	240
					AACTCGAG	248

(2) INFORMATION FOR SEQ ID NO:446:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 256 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

GGATTGAATT	CTAGACCTGC	CTCGAGCGAC	CTCTAGAAC	CTACATTG	AATATTCTGG	60
CAGTGAGGTG	TTCATCCTAA	CTCAGTCAGG	TAGCTGTGGA	CAGCCTTCAC	CTGTTAGGAG	120
CTCCCTAGAA	ATAAATTCTG	AATACCTTG	GTTTCTTTT	ATCCTCCAGA	GGAATTCCA	180
CTATCTCCGA	AGCTGTTCT	TGTTCCACTG	ACAATTGCT	TAGTTAATGT	TCTTTTTAG	240
	CCTGTACTAT	CTCGAG				256

(2) INFORMATION FOR SEQ ID NO:447:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 250 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

GAAGGCAAGA	AAATCTATGG	AAAGAGAAGG	CTACGAGTCC	TCGGGCAATG	ATGACTACAG	60
GGGTAGTTAC	AACACCGTGC	TCTCACAGCC	TTTATTGAA	AAGCAGGACA	GAGAAGGTCC	120
AGCCTCCACG	GGAAGCAAAC	TCACCATTCA	GGAACATCTG	TACCCCGCGC	CTTCATCACC	180
TGAGAAAGAA	CAGCTGCTGG	ACCGCAGACC	CACTGAATGT	ATGATGTCGC	GATCAGTAGA	240
TCACCTCGAG						250

(2) INFORMATION FOR SEQ ID NO:448:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 198 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

GAATTCCGCC	TTCATGGCCT	AGCTGGGGGG	AATAGGTTAT	GTGATAAGGA	GTCAGTCGGA	60
CAGAGTGGGG	TGAAAGATGT	TCAGACAGGG	AAACACACAT	GCAANAGAGG	GAAGGTGGGA	120
CACAGCATAT	GCNTCCAACA	TTTGGTAGGG	CCGAGGCCCC	ACATGGGAGC	AGTGAGAGGT	180
TACCGATCGA	CGCTCGAG					198

(2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

GAATTTCTT TACCAGGAAA ATTCAATGCTT TACAATTGT CAGAGGTGCA CATTACTAAT	60
TACAATAGGT CACACTTTT CTATGCGCTT CATTATAATA TTGGCAACTT TATTATGCC	120
CATTACATAC TGTATTATGC TCTTACTTTA TATGCATTT GAG	163

(2) INFORMATION FOR SEQ ID NO:450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

GAATTGCTGA TATCTTATAA AGGGGACCTT TTTTCTTTAC ATTTCTGACG GTTTTTATCA	60
GAATGTATGT ATTAATGCTA TTTGTCTTG TATATTATT TTATTTCCAG CCACCTCTCG	120
AG	122

(2) INFORMATION FOR SEQ ID NO:451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

GAATTCGGCC TTCATAGCCT AACTCAAGAT CTCCCATCTA TTAAAGCAGA GGAATAACTT	60
TTGTAGGCTT AATACTGCTT TCTCACTTAG GAAAAGTTGA AATTAAGAAC ACACAGGAAG	120
GGATCATTC CTAAGGTTA TGCTCTCAAC ATCAAATTGA GTTGAAACTT GACTACAGGC	180
CATCTGCICA TTCAAGCAT TACAATAAT CTGCTCTATT GATGATCAAA ATGAGAGCTG	240
AATTGGATGC AGGATTGGAC ATTGCAAGCT GTTCTCCAA GTGGGATGGA AAGGTGCTCG	300
AG	302

(2) INFORMATION FOR SEQ ID NO:452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

GAATTGGCC	TTCATGGCCT	ACAAAAATAT	TTATTTGACT	GAATGATTTA	ATATGCAGTT	60
ATGGTGTAA	ATATATCATG	TGTTTATTGT	TTGTTTAAAT	ACAGACATAA	CCCACAGTTA	120
TCTTGACAA	GAAACTACGG	GGATAAATAA	AAGTACCGAG	CCAGATGAGC	AACTGACTAT	180
GAATTCTGAG	AAAAGTATGC	ATCGGAAATC	CACTGAATT	GTAAATGAAA	TAACATGTGA	240
GAACACAGAA	TGGCCCGAC	TCGAG				265

(2) INFORMATION FOR SEQ ID NO:453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

GAATTGGCC	TTCATGGCCT	ACTTTAATT	CTCTGAGCAG	TATTTACAG	TTTGATGTA	60
TAAACCTGGC	ACAGATTATG	TTCAGTTAT	TTCTAAAGTT	AAGTCATGTT	TTGAATGTT	120
ATTTAAAGG	ATTTTTCTT	TTTAAAGAA	TCTACAATGT	TTATTTATT	ATTATTATTT	180
TTAACCTCGC	TTCATCACCA	AGGCTGGAGT	AAAGTGACCC	GACCTCAGCT	CGAG	234

(2) INFORMATION FOR SEQ ID NO:454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

GAATTGGCC	TTCATGGCCT	ACGCACATCC	GCAGTCAGCC	ACCTCGCGCG	CGCCCTCCAGG	60
AGCAAGGATG	GAGAGGCTGG	TGATCAGGAT	GCCCTTCTGT	CATCTGTCTA	CCTACAGCCT	120
GGTTTGGGTC	ATGCCAGCAG	TGGTGCTGTG	CACAGCACAA	GTGCAAGTGG	TGACCCAGGA	180
TGAAAGAGAG	CAGCTGTACA	CACCTGCTTC	CTTAAATGC	TCTCTGAAA	ATGCCAGGA	240
AGCCCTCATT	GTGACATGGC	AGAAAAAGAA	AGCTGTAAGC	CCAGAAAACA	TGGTACCTT	300
CAGCGAGAAC	CATGGGGTGG	TGATCCAGCC	TGCCTATAAG	GACAAGATAA	ACATTACCCA	360
GCTGGGACTC	CAAAGACTCAA	CCCTCGAG				388

(2) INFORMATION FOR SEQ ID NO:455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

GAATTCCGCC TTCATGGCCT AGCTGATATT ATTTCTGAGT TTTTGCTTAT TTGCTTTCTA	60
CATAGAACATCA ATAATGAA CAACTAGCAT TGCCTATATA TGCAAGGTGTG ATACTATTCA	120
GGGTACTAGT ATATTGGCCA CTCATTATGA AACTTCAGG TCCTCATATA TTTCTTTTA	180
TTACAATGAT CTACTTATTG CTGATAAATA TTGGATTCA AGAGGCTAAA GGGCTGGAA	240
AGGAAAACAT TCGTGAACAT TTACAACCAC TTGATACGAG TTGTGTCAAT ACAGACCTCA	300
CACAGCAGCA CCTCGAG	317

(2) INFORMATION FOR SEQ ID NO:456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

GAATTCCGCC TTCATGGCCC ACAAAATGGT AATACAAATA AACCAACTACT TACTGCTTT	60
AATGGTAGTT TGTTTTTTT TTTTGAGAC AGAGTCTCGC TGTGTCGCC AGGCTGGAGT	120
GCAGTGGCGC GATCTGGCT CACTGCAAGC TCCGCCTTTC GGGTCACAC CATTTCCTG	180
CCTCAGCCTC CCGAGTAGCT GGGACTGCAG GCGCCCGACT CCCGGGTTCA CACCATTC	240
CTCCCTCAGA CTCGAG	256

(2) INFORMATION FOR SEQ ID NO:457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

GAATTCCGCC TTCATGGCCT AGGAGAACCG TGAGACCTCT ATTTCCATAT CTTTTTCTAC	60
TACTGGAATT TTTATTTTTA CCATACCCAT AAATTACTTT CTATTTTAAG AAGCAAATAT	120
ATAATTCCCTC AGTTAGTAA AAAGTTCTCA CTTGAAAAGC TGGTATATGA ACTTTAGAGG	180
GCAGATTAAAT CAACTGCTAA ATATTATTA TCTTTCTTCT TGGAACTTC CAACACAAAA	240
GACAGTTAT AGAAAACAAA GTCAAGTGTG AAAACAGCTG AATGAACTAT CTTTTGATAT	300
TTTATTTGTT TTGTTTTGTG TTGTTTTGTG TGAGACAGAG TCTTGCTCTG TTGTCAGGC	360
TGGAGAGTAA TGGCACGATG ACTGCAACCT CTGCCTCCCC GGCTCAAGTG ATTCTCCTGC	420
CTCAGTCCTCT CGAG	434

(2) INFORMATION FOR SEQ ID NO:458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

GAATTCCGGCT TCATGGACGA GGAGATCGTG TCCGAGAAGC AAGCCGAGGA GAGCCACCGG	60
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CAGGACAGCG CCAACCTGCT CATCTTCATC CTGCTGCTCA CCCTCACCAT TCTCACAAATC	120
TGGCTCTTCA AGCACCGCCG GGCCCCTTC CTGCACGAAA CGGGCCTGGC TATGATTTAT	180
GGTCTTTGG TGGGCCTTGT GCTTCGGTAT GGCATTCATG TTCCGAGTGA TGTAAATAAT	240
GTGACCCCTGA GCTGTGAAGT GCAGTCAGT CCAACTACCT TACTGGTAAA TGTTAGTGGA	300
AAATTTATG AGTATATGCT GAAAGGAGAG ATACTCGAG	339

(2) INFORMATION FOR SEQ ID NO:459:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 256 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

GAATTCGGCC TTCATGGCCT ACTTATTTTT GTTTCTGTGT GTTTGTTTA AATGTGTGTG	60
CGCTCATGTG AGTTTGAAGG GAGTTAGATG CAACAGCAGG AGCTGTGCTC AGGGCAGTGG	120
TGTTAATTAT GGAGGGCGTG GGAAGGGCTG GGAAGAGGAG GGGGTTGTAA GACTCCCCTT	180
TTCCCTCGCA TGAAACAGA TGCTGGTGAC TGAAAGTCTG TCTGCGGTTA TTGGCAAGAG	240
TGACGGAAAG CTCGAG	256

(2) INFORMATION FOR SEQ ID NO:460:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 320 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

GAATTCGGCC TTCATGGCCT AATTGAAAA TTCATAAGTT TCTACCAATA CTTCCAATT	60
CAATCCAACA TCTGAGGATC TCCCTAGATT TCCTATTTC ATGATTATAA CTCTTGTACC	120
AGATGATAAG AAACATGGAT CTGACTATAC TCAATTATTAC CACATATTTT CTCAGTGAAC	180
TAACTTATTG GCTGAATATA ACCAGTCCCC AGCCTTCCAA CTGCCTCTCT CACTGCCAC	240
CTCTGCATCT TCCCCCACTG TCTTCCTCAG CAATCAGACT GCCTCTTGCC AAGTCATCAC	300
CACAGCACCC CACTCTCGAG	320

(2) INFORMATION FOR SEQ ID NO:461:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 307 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

GAATTCGGCC TTCATGGCCT ACCCTCTACT ATTTTGAAC CAAATCAACA ACAACCTATT	60
TAGCTGTCC CCAACCTTT CCTCCGACCC CCTAACAAACC CCCCTCTAA TACTAACTAC	120
CTGACTCCTA CCCCTCACAA TCATGGCAAG CCAACGCCAC TTATCCAGTG AACCACTATC	180
ACGAAAAAAA CTCTACCTCT CTATACTAAT CTCCCTACAA ATCTCCTTAA TTATAACATT	240

CACAGCCACA GAACTAATCA TATTTTATAT CTTCTTCGAA ACCACACTTA TCCCCACCCA	300
TCTCGAG	307

(2) INFORMATION FOR SEQ ID NO:462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

GAATTCTGGCC TTCATGGCCT AGTACAATTT AATATAATTT CTTACAAGTT TATTACCTAA	60
AACTTTGCAA ATAATGAAAG TTAGAAGCTT TGGATTTGT TTTTAGAGCT TAATCCTTTT	120
CTGTAAGTGG AAATCCTTTC CACTGGTTA TTTCCCTTT GATTTTATTT TACTTTGACA	180
CCCTAAAGGT TTAGTGTTC TGTTTTAAA TCTACTGATC GTTTCTTATG AGATTCCCTTA	240
GAGTACCCCT CGAG	254

(2) INFORMATION FOR SEQ ID NO:463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

GAATTCTAGA CCTGCCTCGA GAGGACGCCG GAGAGAAATG AGTAGCAACA AAGAGCAGCG	60
GTCAGCAGTG TTCGTGATCC TCTTTGCCCT CATCACCATC CTCATCCTCT ACAGCTCCAA	120
CAGTGCAAT GAGGTCTTCC ATTACGGCTC CCTGCGGGGC CGTAGCCGCC GACCTGTCAA	180
CCTCAAGAAC TGGAGCATCA CTGACGGCTA TGTCCCCATT CTCGGCAACA AGGTAGCGCA	240
GCTGCTTGG GGAGCTCCTC CCTACTGCC AGCAAAACTC GAG	283

(2) INFORMATION FOR SEQ ID NO:464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

GAATTCTGGCC TTCATGGCCT AAAAAGTGGT TCCTATTTC CTGGTTAAC CTTGAGTGAT	60
ACACCCAGTA TTGTACCAACC CAATTAGTAG ACATTATTTC TTCTTAGGTC ATATTATTCT	120
CAGCTTATAG AGCAAGAAGT TGAAGCTAA AGGGTTAGAT TACTTGCCCA AGGTAATACA	180
GCAAGAAC TATTTCATCC AACCTAGAGT GAATATTCC CCCACATCTC GAG	233

(2) INFORMATION FOR SEQ ID NO:465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

GAATTCCGGCC	TTCATGGCCT	ACTGATGTTG	AAGACGACAC	CACGGCTTTG	ATGGAATATC	60
AGATATTGAA	AATGTCTCTC	TGCCGTTC	TCCCTCTT	TCTCACACCT	GGTATTTAT	120
GCATTTGTCC	TCTCCAATGT	ATATGCACAG	AGAGGCACAG	GCATGTGGAC	TGTTCAAGGCA	180
GAAACTTGTG	TACATTACCA	TCTGGACTGC	AAGAGAAATAT	TATACATTAA	AACCTGTC	240
ATAACCACCT	TACTGATCTG	CATAACCCAGT	TAACCCAAATA	TACCAATCTG	AGGACCCCTGG	300
ACATTTCAAA	CAACAGGCTT	GAAGGCTGC	CTGCTCACTT	ACCTCGGTCT	CTGTGGAACA	360
TGTCTGCTG	TAACACAAC	ATTAACCTTC	TTGACAAATC	TGATACTGCT	TATCAGTGGA	420
ATCTTAAATA	TCTGGATGTT	TCTAAGAAC	TGCTGGAAA	GGTTGTCTC	ATTAAAAATA	480
CACTAAGAAC	TCTCGAG					497

(2) INFORMATION FOR SEQ ID NO:466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

GAATTCCGGCC	TTCATGGCCT	AGCCCCGACT	AGCTTGCCC	TAACTCCTTC	ATCAAAAGAC	60
CCCCCGCCAG	CTTCCACAC	CTCATACGCA	GCCACATCTG	CCCTATTCTC	CATGCTTCC	120
AGCTTGCTG	CCCTTCCCTA	TCTCTCCCTG	CCTGTGCAGA	CCTCCACCC	TCTTCCCTCC	180
ACCCCTCCAT	CCCCAATGC	TTGTAGACCT	TCCATTCA	CCGTCTCATC	GTGCGTGGTC	240
TCTGATGTC	CATCACCTGA	CCTCGAG				267

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

GTTCACATCAA	ATATTATACT	AGCATTAC	ATCTCACTTC	TAGGAATACT	AGTATATCGC	60
TCACACCTCA	TATCCTCCCT	ACTATGCCTA	GAAGGAATAA	TACTATCGCT	GTTCATTATA	120
GCTACTCTCA	TAACCCCTCAA	CACCCACTCG	AG			152

(2) INFORMATION FOR SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

CAATATTCA AGCTATAACCA AGCATAACAAT CAACTCCAAG CTCGGAATT TAACTTCATG	60
GCAAACAGAA AAGCTAGACT GAGTTATCG AGTGTGAGA GGAATATTG GCCCAACAAG	120
AGTTGGGGG GTGGGAGGAG GGAGAGACAA AAGGAAAGGA CTGCCAGCTC TCAGAGGGTG	180
GAGATGGGG ACCTCGAG	198

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

GAATTCGGCC TTCATGGCCT ACTGCTATAT TCAAGTTCT CCCACTACTG TGGTTTCTTT	60
TTTTTTTTT TTTTTTTTTT TTTTGAGACA GGGTCTTGCT CTGTCACCCA GGCTGGGTG	120
CAGTGGTGCCT ATCTCGGCTC ACTGCAAATT ACACCTCCTG GATTCGAGCA ATTCTCATGC	180
CTCAGCTTCC TGAGTAGCTG GGATAAACAGG TATGCACCCAC CACCCCTGGC TAATTTTGT	240
GTTCAGTA GAGACAAGTT CTCACCATGT TGTCCAAGCC ACCTCGAG	288

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

GAATTCGGCC TTCATGGCCT AAAAGAAGAA TACTAATTAG AATTTGAGTT CTAGGGTTT	60
TTCCTAGGTT TTTCATTCTA GACTTAGCTT TTATTCAAAC CTGTTGATCC TGCATAGGGG	120
TAGTCTAGCT TAAAAAAAATA AAACAATAAA CATAAAATGAG CCTATTGAGT TCAATCAGAG	180
TAGGGACGAG TTTTATTGAA CAGCACATT TCAAATTCTT CAGTTGTGTT TTGTTTTCA	240
GCTACGTGTC TCTCTGTGAT AATGAAAAGA CAGGTTGCAA AGCCCGGGAA CTAAAATCAG	300
TTTATGTGGA TGCAGTAGGA CTCGAG	326

(2) INFORMATION FOR SEQ ID NO:471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

GAATTCCGCC	TTCATGGCCT	AGTCTAAACT	CTTTTGAC	AGTGCCAGA	AATTGCA	60
ATTTAATGGT	CCTTCCTCCT	TATTTATTTT	TATTACTGT	TTTGT	TTGAGACAGT	120
GTCTTGCTCT	GTCGCCAGG	CTGGAGAGCA	GTGATATTAT	CGTGACTCAC	GGCAGCCTCG	180
ACCTCCAGA	CTCAGGTGAT	CCCTTCACCT	CAGCCTCCA	GGCAGCTGGG	ACCATAGCTA	240
TGAACAAACA	CGTCAGCTA	TGTTTTGTAT	TTTTGTGAA	GACGGAGTCT	CACCATGTTG	300
CCCAGGTGA	TCTCCA	ACTC	CTCGAG			326

(2) INFORMATION FOR SEQ ID NO:472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

GGAAAGGTGT	TGTCCCTTGT	AACATTTGG	TTGGCTATAA	AGCTGTATAT	CGTTTGTGCT	60
TTGGTTTGGC	TATGTTCTAT	CTTCTTCTCT	CTTTACTAAT	GATCAAAGTG	AAGAGTAGCA	120
GTGATCCTAG	AGCTGCAGTG	CACAATGGAT	TTTGGTTCTT	TAAATTGCT	GCAGCAATTG	180
CAATTATTAT	TGGGGCATTTC	TTCATTCCAG	AAGGAACCTT	TACAACGTG	TGGTTTTATG	240
TAGGCAACCT	CGAG					254

(2) INFORMATION FOR SEQ ID NO:473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

GAATTCCGCC	TTCATGGCCT	ACAGAAATCT	AATTCTGGT	GCTATTGCA	ACTACATATA	60
TTTAAATAC	AAGGAGATAA	ATACCCAGAA	CACATTAAGC	CTACTGATTT	AAACAGAACAA	120
TTTCAAGACT	GCTACACAGA	AAGGGAAGGA	AGCTGTTAAC	CCAGCACAGC	AGCACACCTC	180
ACATATTAC	GTCTCAGAGA	TTAAATGCAA	AGAAAGGATC	AATCAAACACC	TTTAATGCTC	240
AGTTTCACA	AACACAGTCA	AGTCTATCAA	ATTTCCAGAT	TTACAG		286

(2) INFORMATION FOR SEQ ID NO:474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

GAATTCCGCC	TTCATGGCCT	ACAATTAAAA	GGTTCTGTTA	AATTACGTCT	TTCAAGTCTGA	60
AATTACTCTG	AGAATTACT	TAAAATTTT	CCATTTAAA	ACAGGTATAA	AATTAATTGC	120
TAGTTCCAT	AATCACCCAG	TATAAAGATA	AAAAGACCT	GTAAGACAAC	TGTGTGGTTA	180

AATACATGAT AACACATTTA CGTGCCTTT ATAGAAATCC ACTTATTATG TACATACTGG	240
CTTGTTCCTT TTCCCACCTC TCCAGTACAC TATTCAGGC ACAGGCTCAA AATTGAACC	300
CAAATGGTCT GTTAGGTCTC TTGACTTTT CAGTTCAAAG CTCTGCTAAT CTGCTAAACC	360
TAGCCCCAAA CCCACTCGAG	380

(2) INFORMATION FOR SEQ ID NO:475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

GAATTCTAGA CCTGCCCGGA GCCCTGACCT AGTCCGGCGT GGAGAGAGGA ATGGAAAGCA	60
GTGTCCCTTT TGAGAAGGCA AATTACAGC TGGCTTTGT AATCCTAGCT ATTTTTGTT	120
TGTTTGCTAA GTCTTGATA CTCCCCAGTG TGGTTTGTCT CCCAGTGATC TCAGCACCAC	180
CAGAGAGCTT GTTAGAAATG CGGCATCCCA ACCCCACCAC AGCCCTCCCA AGTCAGATAC	240
TCCCCCCCTCT CGAG	254

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

GAATTCGCTG TGGAGCTGGG CGTGTGTTG GTCCGGCCCC GGCCCGAAC CGGGCTGGGT	60
AGAGTGATGC GGACCCCTCT GCTGGTCTG TGGCTGGCGA CGCGCGGAAG CGCGCTCTAC	120
TTTCACATCG GAGAGACGGA GAAGAAGTGC TTTATTGAGG AGATCCCGGA CGAGACCATG	180
GTCATAGGAA ACTACCGGAC GCACGTGTAT GACAAGCAGC GGGAGGAGTA CCAGCCGGCC	240
ACCCCGGGGC TTGGCATGTT TGTGGAGGTG AAGCACCCAG AGGACAAGGT CATCCTGGCC	300
CGGCAGTATG GTTCCGAGGG CAGGTTCACT TTCANTCCCC ATACCCNTGT GTGAGCACCA	360
GATCTGTTT CANTCCAATT CCACTCGAG	389

(2) INFORMATION FOR SEQ ID NO:477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

GAATTCGGCC TTCATGGCCT AGAAGGAAAT AAAGGCCCG ATTCTGGAG TTCTGAGCCT	60
ACTTTTTTG GGTGCATTTT GAAACATACG GATTTTACCG CTAGTATATT CAGTGAGGAA	120
GGAAGGCTTC TGAAGGATTG ATGATCCCCA AACTGGATTA TGTGTTCATG ATAATGGTGT	180
ATTTGGTGGC CTAGCATAGT GAGGTGAGGT AGGTCTTTAA AATGGCTCAT TATAAACATC	240

ATTGTTCCCTG AGCTCACTTG CCCTTGCATC TCCTGCCAGA GTGCTTSTA CATAGTAGGC	300
CCTCATCAAT GCTTGTAGAT TTTAAATTGG GAGGCACACT TGGAAGACAA TGTTGGCTGG	360
TAAATTAATT ATCAGGGTTA GCAACTTCAT TTCTGCTNAC GCTTAAAAG TGCTCGCGA	420
GGAAAATCGA G	431

(2) INFORMATION FOR SEQ ID NO:478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

GCCTCTGNTT TTAATTCAATT GGCAACTGTT ACGATGGAAG ACCTGATTG ACCTTGGTTC	60
CCTGAGTTCT CTGAAGCCCG GGCATCATG CTTTCCAGAG GCCTTGCCTT TGGCTATGGG	120
CTGCTTTCTC TAGGAATGCC CTATAATTCC TCCCAGATGG GACCTGTCGCT GCAGGCAGCA	180
ATCAGCATCT TTGGCATGGT TGGGGGACCC CTGCTGGAC TCTTCTGCCT TGGAAATGTT	240
TTTCCATGTG CTAACCCCTCC TGGTGCTGTT GTGGCTGGCT CGTCATGCC	300
TTCTGGATTC GCATCGGGAG CATCGTGACC AGCATGGGCT TCAGCATGCC ACCCTCTCCC	360
TCTAATGGGT CCAGCTTCTC CCTGCCACC AATCTAACCG TTGCCACTGT GACCACACTT	420
CTCGAG	426

(2) INFORMATION FOR SEQ ID NO:479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:

GAATTCCGCC TTCATGGCCT AAATTTTCAG GCAGTTGAA GTATCTGGCA GAAAAAGTAA	60
ATTGAAATCA TTGGGACGTT GATTTTTAAA TTACCTAGAA GCAATCCCAA TGCTTATGT	120
AATACTAAA TTTCTCCTCT CTCTTTCTT TATCTCTCTC TCCCCCTGAAA ATAATCATT	180
TTTTTCCAGT GCCAGTCAG ATCTGGCAA CAGTTGTTT GAAAAAGTAC CTGAACAAAA	240
TACATTTAT AAAGTAAAGT ATTCAAGAAC TGACAGAACT GGAGAAGAAT ATATTTATGT	300
TACAGAAGTC ATGGACAACC TCGAG	325

(2) INFORMATION FOR SEQ ID NO:480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:

GGCAAGTAAC AGTTGCAAG AATTGGAGGC AGAGCAACAG CAGATCCAAG AAGAAAGAGA	60
ATTACTGTCC AGACAAAAGG AAGCTATGAA AGCAGAGGCA GGCCCAGTTG AACACAATT	120

ACTACAGGAG ACAGACAAAT TAATGAAGGA AAAACTAGAA GTACAATGTC AAGCTGAAAA	180
AGTACGTGAT GACCTCAAA ACAACTGAA AGCTCTAGAA ATAGATGTGG AAGAACAACT	240
CAGTAGGTTT ATAGAGCTGG ACAAGAAAA AAATACTGAA CTAATGGATT TAACAGACCA	300
AAACCAAGCA TTGGAAAAGC AGTTAGAAAA AATGAGAAAA TTTTTAGATG AGCAAGCCAT	360
TGACAGAGAA CATGAGAGAG ATGTATTCCA ACAGGAAATA CTCGAG	406

(2) INFORMATION FOR SEQ ID NO:481:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 357 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:

GAATTCGGCC AAAGAGGCCT AGTCGGTGCC TCATTGGTAT AAATGTTATG TCTGCATGGG	60
TTTTTCTAC AATTCTTTC TAAGATTATT TCTCCCCAA GCTCAGCACT TTTGGAATT	120
TTCATTCTCA TCCAAAATG GAAGCAATT TATGTAATG TCTCTGGAA GCAGTGTGG	180
AATTCAATT TTGGTAGCA GAAGCAGTAG TTACAAAGGT AGTGGTGTCT TTTGTGGTGG	240
TGGTGGCACC TGCTGCAGTT GTTCATATTT GGGGTGCAGG AGTAGGGAGG GTAGGATCAG	300
TTGGAGAATT TACAGGGAAA AATGGAGGT CAGGTGGATA GGGTCTAGAA TTCAATC	357

(2) INFORMATION FOR SEQ ID NO:482:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 303 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:

GAATTCGGCC AAAGAGGCCT AAGTGACTCC AGAGCCTCCT GCAAGATGCT GTTGATTCTG	60
CTGTCAGTGG CCTTGCTGGC CCTGAGCTCA GCTCAGAACT TAAATGAAGA TGTCAGCCAG	120
GAAGAACCTC CCTCCCTAAT AGCAGGAAT CCACAAGGAG CACCCCCACA AGGAGGCAAC	180
AAACCTCAAG GTCCCCCATC TCTCTCAGGA AAGCCACAAG GACCACCCCC ACAAGGAGGC	240
AACCAGCCTC AAGGTCCCCC ACCTCCTCCA GGAAAACCAC AAGGACCACC CCCTATTCTC	300
GAG	303

(2) INFORMATION FOR SEQ ID NO:483:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 469 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:

GAATTCGGCC AAAGAGGCCT AAGCAGACAC AATGGTAAGA ATGGTGCCTG TCCTGCTGTC	60
TCTGCTGCTG CTTCTGGTC CTGCTGTCCC CCAGGAGAAC CAAGATGGTC GTTACTCTCT	120
GACCTATATC TACACTGGGC TGTCCAAGCA TGTTGAAGAC GTCCCCCGGT TTCAGGCCCT	180

TGGCTCACTC AATGACCTCC AGTTCTTAG ATACAACAGT AAAGACAGGA AGTCTCAGCC	240
CATGGGACTC TCGAGACAGG TGGAGGAAT GGAGGATTGG AACCGAGACA GCCAACTTCA	300
GAAGGCCAGG GAGGCACATCT TTATGGAGAC CCTGAAAGAC ATCGTGGAGT ATTACAACGA	360
CAGTAACGGG TCTCACGTAT TGCAGGGAG GTTGGTTGT GAGATCGAGA ATAACAGAAG	420
CAGCGGAGCA TTCTGAAAT ATTACTATGA TCGAAAGGAC AAACTCGAG	469

(2) INFORMATION FOR SEQ ID NO:484:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 516 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

GAATTCGGCC AAAGAGGCCT ACTACTTCTG TAGTCTCATC TTGAGTAAAA GAGAACCCAG	60
CCAACTATGA AGTTCTTGT CTTGCTTC ATCTTGGCTC TCATGGTTTC CATGATTGGA	120
GCTGATTCTAT CTGAAGAGTA TGGGTATGGC CCTTATCAGC CAGTCCAGA ACAACCCACTA	180
TACCCACAAAC CATAACCAACC ACAATACCAA CCTGCCTCAA GGTCTCCAC CTCCCTCAGG	240
AAAGCCACAA GGACCACCCCC CACAAGGAGG CAACAAACCT CAAGGTCCCC CACCTCCAGG	300
AAAGCCACAA CGACCACCCCC CACAAGGAGG CACAAGTCC CGAAGTCTC GATCTCC	360
AGGAAAGCCA CAAGGACCAC CCCACAAGG AGGAACAAA CCTCAAGGTC CCCCACCTCC	420
AGGAAAGCCA CAAGGACCAC CCCACAAGG AGGCAGCAAG TCCCGAAGTG CCCGATCTCC	480
TCCAGGAAAG CCACAAAGGAC CATCCACAA CTCGAG	516

(2) INFORMATION FOR SEQ ID NO:485:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 357 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

GAATTCGGCC AAAGAGGCCT ACTTCACCTTC AGCTTCACGT ACTTCCTGAC TCTCCTCTTG	60
AGTAAAAGGA CTCAGCCAAC TATGAAGTTT TTGCTTTG CTTTAGTCTT GGCTCTCATG	120
ATTTCCATGA TTAGCGCTGA TTCACATGAA AAGAGACATC ATGGGTATAG AAGAAAATTTC	180
CATGAAAAGC ATCATTCACA TCGAGAATT CCATTTATG GGGACTGTGG ATCAAATTAT	240
CTATATGACA ATTGATATCC TTAGTAATCA TGGGGCATGA TTATAGAGGT TTGACTGGCA	300
AATTCACTTT TACTCATTCA TTCTCATTCA TCACACCGCA AGTCTAGGCC TCTCGAG	357

(2) INFORMATION FOR SEQ ID NO:486:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 643 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:

GGTTACCATC	CTCAAAGGAT	TGGCTAAAAG	CAAGCAACTG	GATTGAACAC	CCTAAGAAGA	60
AAGATTACA	CTGCACCAGG	AGACATCAGA	AAGAATGAAA	ACTCTGCCGC	IGTTTGTGTG	120
CATCTGTCA	CTGAGTGCTT	GCTTCTCGTT	CACTGAAGGT	CGAGAAAGGG	ATCATGAACT	180
ACGTCACAGG	AAGGCATCAT	CACCAATCAC	CCAAATCTCA	CTTTGAATTA	CCACATTATC	240
CTGGACTGCT	AGCTCACCA	AAGCCGTTCA	TTAGAAAGTC	CTATAAAATGT	CTGCACAAAC	300
GCTGTTAGGC	CTAACGCTTCC	ACCTTCACCT	AATAACCCCC	CCAAATTCCC	AAATCCTCAC	360
CAGCCACCTA	AACATCCAGA	TAAAAATAGC	AGTGTGGTCA	ACCCCTACCT	AGTGCTACA	420
ACCCAAATTC	CATCTGTGAC	TTTCCCACATCA	GCTTCCACCA	AAATTACTAC	CCTTCCAAT	480
GTGACTTTTC	TTCCCCAGAA	TGCCACCAAC	ATATCTTCAA	GAGAAAATGT	TAACACAAGC	540
TCTTCTGTAG	CTACATTAGC	ACCCAGTGA	TTCCCCAGCT	CCACAAAGACA	CCACAGCTGC	600
CCCCACCCACA	CCTTCTGCAA	CTACACCAGC	TCCACCCCTC	GAG		643

(2) INFORMATION FOR SEQ ID NO:487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:

GAATTCCGCC	AAAGAGGCCT	ACAAGATGCT	GCTGGTCCTG	CTCTCAGTGG	TCCTTCTGGC	60
TCTGAGCTCA	GCTCAGAGCA	CAGATAATGA	TGTGAACATAT	GAAGACTTTA	CTTTCACCAT	120
ACCAGATGTA	GAGGACTCAA	GTCAAGAGACC	AGATCAGGG	CCCCAGAGAC	CTCCCTCTGA	180
AGGACTCCTA	CCTAGACCCC	CTGGTGTAG	TGGTAACCAA	GATGATGGTC	CTCAGCAGAG	240
ACCACCAAAA	CCAGGAGGCC	ATCACCGCCA	TCTCCCTTCA	CCTCCCTTTC	AAAATCAGCA	300
ACGACCACCC	CAACGAGGAC	ACCGTTCATC	TCGAG			335

(2) INFORMATION FOR SEQ ID NO:488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:

GAATTCCGCC	AAAGAGGCCT	AGACACATTG	CCTCTGTTT	TCTCCAGCAT	GCGCTTGCTC	60
CAGCTCTGT	TCAGGGCCAG	CCCTGCCACC	CTGCTCTGG	TTCTCTGCCT	GCAGTTGGGG	120
GCCAACAAAG	CTCAGGACAA	CACTCGGAAG	ATCATAATAA	AGAATTGAGA	CATTCCCAAG	180
TCAGTACGTC	CAAATGACGA	AGTCACTGCA	GTGCTTGAG	TTCAAACAGA	ATTGAAAGAA	240
TGCACTGGTG	TTAAAACCTA	CCTCATTAGC	AGCATCCCT	CTACAAGGTG	CATTAACTA	300
TAAGTATAAC	TGCCAACCTC	GAG				323

(2) INFORMATION FOR SEQ ID NO:489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:

GAATTCTGGCC AAAGAGGCCT AGTGACACCA GAGCCTCCTG CAAGATGCTT CTGATTCTGC	60
TGTCAGTGGC CCTGCTGGCC TTCAGCTAG CTCAGGATT AAATGAAGAT GTCAGCCAGG	120
AAGATGTT	128

(2) INFORMATION FOR SEQ ID NO:490:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

GAATTCTGGCC AAAGAGGCCT AATTTGACC AGCAGATTAA TCAACTGTAA GACGGATCCT	60
CACACAAAGA GGCAACTGAA AGGATGAAAT CACTGACTTG GATCTTGGGC CTTTGGGCTC	120
TTGCAGCGTG TTTCACACCT GTGTGAGAGTC AAAGAGGCC CAGGGGACCA TATCCACCTG	180
GACCGCTGGC TCCTCCTCAA CCTTTGGCC CAGGAGTTGT TCCACCCACT CCTCCTCCAC	240
CCTATGGTCC AGGGAGAACCC ACACCTCCCTC CTCTGCAGAG AAAACCTTG AAGAAAAGCA	300
GGAACAGAGA TCGATGGCGA TCTATTCCCC TGTACTATAC TGGAGAGAAA GGTCAAAATC	360
GTGAG	366

(2) INFORMATION FOR SEQ ID NO:491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:

GGTTTCCCGT TTGTCCTTCC TTCAAGGTTT TTTTCAGCAG CTGCAGCACCG CGCTGCCCA	60
CCTATTGAG CTGAGCCTGC TGAGCTGCA CCTCTTACAG CCACACCTGT AGCAGCTGAG	120
CCTGCTGCAG GGGCCCTGT TGAGCTGAG CCTCTGAG AGGCACCTGT TGGAGCTGAG	180
CCTGCTGCAG AGGCACCTGT TGAGCTGAG CCTGCTGAG AGGCACCTGT TGGAGCTGAG	240
CCAGCTGCAG AGGAACCTTC ACCAGCTGAG CCTGCTACAG CCAAGCTAG GCCTCT	296

(2) INFORMATION FOR SEQ ID NO:492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 535 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

CTCGAGTCCT TGTGGCTTC CTGGAGGTGG GGGACCTGAA GGTTTGTGCTCCTTGTGG	60
GGGTGGTCTTCT TGTGGCTTC CTGGAGGAGG TGAAGGACCT TGAGGCTGGT TGCCTCCTTG	120

TGGGGGTGGT CCTTGTCGAGG AGATCGGGGA	CTTCGGGGAC TTGTCCTC	180
CTGGGGGTGG TCCCTGTCGAG GTGGGGAC	TTGAGGTTG TTGCCCTC	240
CTGGGGGTGG TCCTTGTCGAG GAGGTGGGG	ACCTTGAGGC TGTTGCTC	300
CTTGTTGGGG TGGCCTTGT GGCTTCTCTG	GAGGAGATGG GGGACCTGTA	360
CTCCTTGTGG GGGTGCCTCT TGTGGATTTC	GGTGTGTC CTGCTATTAG	420
TGACATCTTC ATTTAAGTTC TGAGCTGAGC	TCAGGGCCAG CAGGGCCACT	480
TCAACAGCAT CTTGAGGAG GCTCTGGAGT	GACAGCAGAA CACTTAGGCC	535

(2) INFORMATION FOR SEQ ID NO:493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

GAATTGGCC AAAGAGGCCT AGTCGGAAT CACAACAAAC	ACGGAGCAAT CTCAATGCTG	60
TTTATCCGGA GGACAGTCTG CGGGTCGTG ACGATTCTT	TCTTCTTGAA GTTTTCCTT	120
TTCCTGAATC TCATAATGAT TCTTGCCTAT GATTCTGTCT	TTTCAATGAC TGTGGCTCT	180
ACTCGAACAA GATCCTTCC GAGGAGTGGC TTGCCAAGCA	GCGTGAAGTT GTCTGCCCA	240
ACCAGCAGGA CCTCTCCAG TCGAATTCTC TCTCCACACG	CAAGGTCTAG TTCATTTCCA	300
ATTAAGATCA GGTCTTCAGA G		321

(2) INFORMATION FOR SEQ ID NO:494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

GAATTGGCC AAAGAGGCCT AACCTGCCTT GGTTCTTGCT CCTCTTTCCA CGTTGGATAAA	60
CAATTTTTG GTTGTGTTGT TTAAGTTGGT GCTCTGAAGC TTAATCTCAG TACCCCTTAC	120
TCTGAATTGT CAAATTTGA TAAAACGTGC CATTTCTTT GGTAAGAGAA AGCAGGTCTT	180
AATGTCTGCC AGAACACAAT TTATATGCC TATTGGCTTC ATTAAACTTT TAGAAAAC	240
TAGCATTTGT TACTTTTTTC CATTGCAATT ACTTTCAAT GCACCTAATG AATTGTCAC	300
CCAGTCGCAA CTTTCCCCTT CTCTGTCCC TTGCTTTCTC CTTTCCCCAA CGCAGCTCGA	360
G	361

(2) INFORMATION FOR SEQ ID NO:495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

GAATTCTGGCC	AAAGAGGCCT	AAAGCGACCA	AGATAAAAAGT	GGACAGAAGA	ATAACCGAGA	60
CTTTTTATCC	ATGAAACAGT	CTCTGCCCT	CGCTCCGGAA	GAGCGCTACC	CCAAAGCCGG	120
GTCCCCAAAG	CCGGTCTTGA	GAGCTGATGA	CAATAACATG	GGCAATGGCT	GCTCTCAGAA	180
GCTGGCACT	GCTAACCTCC	TCCGGTTCT	ATTGCTGGTC	CTGATTCCAT	GTATCTGTGC	240
TCTCGTTCTC	TTGCTGGTGA	TCCCTGTTTC	CTATGTTGGA	ACATTACAAA	AGGTCTATTT	300
TAATCAAAT	GGGAGTGAAC	CTTGTTGAC	TGATGGTGA	ATCCAAGGGT	CCGATGTTAT	360
TCTTACAAAT	ACAATTATA	ACCAAGAC	TGTGGTGTCT	ACTGCACATC	CCGACCAACT	420
AGGCCTCTT	GGCCG					435

(2) INFORMATION FOR SEQ ID NO:496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

GAATTCTGGCC	AAAGAGGCCT	AGAAATATAT	TTTCTAGTGA	ATTCTTATTG	GAAGCCAGGT	60
CTCTCCTCTC	ATTAGATCAA	AAGGGACTTA	TGTACATACA	ACAATTGAAA	GTGTTACTCG	120
AG						122

(2) INFORMATION FOR SEQ ID NO:497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

GAATTCTGGCC	AAAGAGGCCT	AAGAAAATCA	GCCTGTCTGC	TCTCTCCTTG	GCTCAACAAG	60
GCCTCTAAC	ATCTCTGTC	CTCTATTCTG	CACACGGCAT	ATTGGGAAC	GAGAAACAAA	120
AGTTTTCCA	AATGAAGAGA	ACTCACTTGT	TTATTGTGGG	GATTATTTT	CTGTCCTCTT	180
GCAGGGCAGA	AGAGGGCTT	AATTCCCCA	CATATGATGG	GAAGGACCGA	GTGGTAAGTC	240
TTTCCGAGAA	GACCCTCGAG					260

(2) INFORMATION FOR SEQ ID NO:498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:

GAAAGAGGCC TACCAACATG CCAGAGGCCG TACCCATATC CGCAGCAG

48

(2) INFORMATION FOR SEQ ID NO:499:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 276 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:

GAATTCTGGCC	TTCATGGCCT	ACCCGTCAA	AATTTGCC	CCTGTTGATT	TTCAATATAT	60
ATATATTTT	TTGCTTACT	CTGTTGCCA	GGCTAGAGTG	CAGTGACGTG	ACCTTGGCTC	120
ACTGCAACCT	CTGCCTCCCTG	GGCTCAAGCA	ATCCCTCCAC	CTCAGCCCTC	TCAGTAGCTG	180
GGACCACAGG	CATATGCTAC	AAAGCCCAGA	TTATTTTTT	ATAGAACAG	GGTTTCACCA	240
TGTTGCCAG	GCTTGCTCG	AACCCCATGAA	CTCGAG			276

(2) INFORMATION FOR SEQ ID NO:500:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 301 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:

GAATTCTGGCC	TTCATGGCCT	ACAAATGCC	ATCAAAGACT	GGATAAAGAA	AATGTAGTAT	60
ATATATATAT	ACCATGGAAT	ACTGTGCAGC	CATAAAAAG	GAATGAGATC	ATGTGTTCA	120
CAGGGATGTG	GATGAAGCTG	GAAGCCATCA	TCCCCAGCAG	ACTAACACAG	GAACAGAAAA	180
CCAAACACTG	CATGTTCTCA	CTCATAACTG	GGAGCTAAC	AATGAGAAC	GGTGGGCACA	240
GGGACGGGAA	CAACACACAC	CAGGGCCTGT	TGTGTGGTGG	GGGTGAGGGT	TGGAACCTCA	300
G						301

(2) INFORMATION FOR SEQ ID NO:501:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:

GCGAGGCAGG	AAAACACT	TCACGTCTCT	TTCTTGTAG	AGCATCATGC	TTATTTCTGG	60
CTCACTACA	TCTTGTCTC	GGGAGTTCTC	TGCCGAGCCA	TTGCCCTCTA	CACCGAGAG	120
CACAGCTGGC	TGCACTAGTG	CTGAAGGAGC	CAGCCCCAGA	GCAGGGCATT	TCCAGGGGCT	180
CTTGTCCCTAG	AGCGGCAGGC	GTGTGTGCA	GAGAACGCC	CTCCCACGCA	GCACAGAGAA	240
CGCGGGGTGG	GTGTGTGGCT	CCGGCCCTGT	GGGGCTTAGG	CTGCCTGAAC	CACCGCCGAC	300
TGGCACCATG	ACTCGGCATT	CCTGGAAGTG	CCTTACCAAG	TTGTTGTTGT	TGTTTGTG	360
TTTTTAAGA	GACGGGCTTG	CTCTATCATC	CAGGCTCGAG			400

(2) INFORMATION FOR SEQ ID NO:502:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 286 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:

- GAGATAAAACA AAATTGATTG CCCCATTCTC TCACTTCCCC ATCTTGTCTT CCTAGACCCC	60
ACAGAGTAA AACTTGGAT TCCCCTGGCC CCCCCAGAAC ACTTGTATAT TGTGTTGTTG	120
AGGTTCTGTC CGCAGTAACA GACACAGTAT TTAATTGAC ATACAGATGT TTGCTGGGTA	180
TATTCACTGT AAATTTTATT TAATCTGTTT TTTGTTGTTGT TTGGGGGTTA TTTGGGGGGA	240
GGTTGGTTTT GTTTTAAAT ATAAAAAAA AAATCTGTCA CTCGAG	286

(2) INFORMATION FOR SEQ ID NO:503:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:

GGCCTCACCT TACCCAGGA CTCCGCTATG ACACCGCTC TGCCCCTACA AGACACAGAT	60
CTCTCGTCAG CCTCAAAGCC TGTGGCTGCA GCCACGCCG TGTCGGAGCA GGCTGAAGAG	120
GGCCTCACCT TACCCAGGA CTCCGCTATG ACAGCACCTC TGCCCTGCA AGACACAGGC	180
CCCACCTCAG GTCCAGAGCC TCTGGCTGTG GCCACCCCTC AAACCTTGCA GGCAAGAGCA	240
GGCTGTGCC CAGGGACAGA GCCTGTGGCC ATACTCGAG	279

(2) INFORMATION FOR SEQ ID NO:504:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:

GCAATGGCAG GAATTCGAAA TATTGGATA TGGTTCTTT GGATTAGATT ATATAAAATC	60
AGAAGAGGTA GAACCAGGCC CCAAGCACTC CTTTTCTCT GCATGATACT TCTGCTTATT	120
GTCCTTCACA CTAGCTACAT GATTTATAGT CTTGCTCCC AATATGTTAT GTATGGAAGC	180
CAAAATTACT TAATAGAGAC TAATATAACT TCTGATAATC ATAAAGGCAA TTCAACCCCT	240
TCTGTGCCAA AGAGATGTGA TGCAGAAGCT CCTGAAGATC AGTGTACTGT TACCCGGACG	300
CTCGAG	306

(2) INFORMATION FOR SEQ ID NO:505:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:

GAATTCCGGCC	TTCATGGCCT	AAGGAGAATG	GCGTGCACCC	GGGAGGCCGA	GCTTGCAGTG	60
AGCCAACATC	ACGCCACTGC	ACTCCAGCCC	GGCGACTGA	GCGAGACTCT	CTCTCNAAAA	120
AAAAAAAAAA	AAAGAAAAG	AAAAAGAAAA	AGAAAAAGAA	AAGAAAATAT	ATANATACAC	180
ACAGAGACTG	AGAGAGAGAG	AGAGAGAGAG	ACCAGAAAAA	GAGAGAACGA	GAAAGAGAGA	240
ATGAAAAAAC	CAAGAGGANA	GAATGATCCA	CTCTCCAAC	AGAAAGGTAG	CTCTCAATCT	300
GAAAAGTCAC	TTGATTACTT	TGTCTATTTT	GCTTATCTGC	TACATCAATG	GTTCCCTCGA	360
G						361

(2) INFORMATION FOR SEQ ID NO:506:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:

GAATTCCGGCC	TTCATGGCCT	AGGCCTTTTC	TTTTTAAAGG	AATTCAAGCA	GGATACTTT	60
TTCTGTTGGG	CATTGACTAG	ATTGTTGCA	AAAGTTTCGC	ATCAAAAACA	ACAACAAACAA	120
AAAACCAAAC	AACTCTCCCT	GATCTATACT	TTGAGAATTG	TTGATTTCCT	TTTTTTATTG	180
TGACTTTAA	AAACAACATT	TTTTTCACT	TTTTTAAAAA	ATGCACTACT	GTGTGCTGAG	240
CGCTTTCTG	ATCCTGCATC	TGGTCACGGT	CGCGCTCAGC	CTGTCTACCC	GCAGCACACT	300
CGAG						304

(2) INFORMATION FOR SEQ ID NO:507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:

GGGGCTGCGG	GGATTGACCT	CCTCACTTCT	GGGTTGCCAC	TCGAAGCTTG	CTCCGGCAA	60
CGACCCCTGCT	GCTTCCCAGA	GGGAAACTGT	AGCCCCACAGA	CCAGGAGAGA	AGCCAAAGCA	120
CCTGCTCCAC	GTCCACATCA	CCCCAGGCTT	CTAGCCCCCA	GGGGCTTCAT	CAGTGTCTCA	180
GCGCTCTCTC	CCATCCCCCA	CTCCCCATGT	CCCTCGTGAT	CCGAACTCCT	AGGGCTCCGT	240
GTCCCCACAGG	TCACCACTTC	CGGCTGTCTC	GAG			273

(2) INFORMATION FOR SEQ ID NO:508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:

GAATTCTGGCC	TTCATGGCCT	ACATCAATAA	AATAACATTCT	ACACAGAATA	CGCCAACCAT	60
ACACTACTCT	TTTTTGATAA	AAAAAAATGT	ATTTACTGAG	CCAGTTGTGG	TGGCTCGCGC	120
CTATAATCCC	AGCACCTTGG	AAGGCCAATG	GGAGTGGATC	GGTTGAGGCC	AGGAGTTTGA	180
GACCGGCCCTG	CCAACATGG	TGGAATGCCG	TCTCTACTGA	GAATGCAGAA	ATGAGCCGGG	240
CACGGTGGCA	CGCACCTGTA	GTCCCAGGT	CTCCGATTCC	TCTCGAG		287

(2) INFORMATION FOR SEQ ID NO:509:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:

AAGAGGGCAT	GGCGGGCATG	GCATCTCTCG	GCGCCCTGGC	GCTGCTCCTG	CTGTCAGGCC	60
TCTCCCGCTG	CTCAGCCGAG	GCCTGCCTGG	AGCCCCAGAT	CACCCCTTCC	TACTACACCA	120
CTTCTGACCC	TGTCATTTC	ACTGAGACCG	TCTTCATTGT	GGAGATCTCC	CTGACATGCA	180
AGAACAGGGT	CCAGAACATG	GCTCTATG	CTGACGTCGG	TGGAAAACAA	TTCCCTTGTC	240
CACTCGAG						288

(2) INFORMATION FOR SEQ ID NO:510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:

GGCGATGATT	AGGCCAGACC	CTCCCCATCC	TCGTGAGGGC	CAGAAGCTGT	TGCTACACTG	60
TGAGGGTCGC	GGCAATCCAG	TCCCCCAGCA	GTACCTATGG	GAGAAGGAGG	GCAGTGTGCC	120
ACCCCTGAAG	ATGACCCAGG	AGAGTGCCT	GATCTTCCCT	TTCCTCAACA	AGAGTGACAG	180
TGGCACCTAC	GGCTGCACAG	CCACCAAGAA	CATGGGCAGC	TACAAGGCCT	ACTACACCCCT	240
CAATGTTAAT	GACCCCGACTC	CGGTGCCCCCTC	CTCCTCCAGC	ACCTACCACG	CCATCATCGG	300
TGGGATCGTG	GCTTTCATTG	TCTTCTGCT	GCTCATGATG	CTCATCTTCC	TCGGCCACTA	360
CTTGATCCGG	CACAAAGGAA	CCTACCCCTAC	ACTCGAG			397

(2) INFORMATION FOR SEQ ID NO:511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:

GCCTGCCTCC AGGCCTTGC TCCCACGTGTT GCCTCCACTT AGAATAACAT TCCACCCCAT	60
CTCTATAAAT ATCCTACAGA CAAATACTAC CTTCCCTTA AGGCCAGTTC TAACCTAAC	120
TGACACACAA TCATCTCAC ATGATCTTT CTTCTGGGA ATGCCTGAG CACTGTTAA	180
TCCTGCCCA CCACCATCCC CTCAACCCAGC ACCCTCTCCC AGACCAGACA GGGTGGCTCA	240
TGCCTGCAAT CCCAGCACCT TGGGAGGCTG AGGCAGGAGG ATTGCTCGAG	290

(2) INFORMATION FOR SEQ ID NO:512:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 304 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:

GAATTCCGCC TTCATGGCCT ACTATGCCGT CATGATAGAG AAGATGATCC TGAGAGACCT	60
GTGCGGTTTC ATGTTTGCT ACCTCGTCTT CTTGTTGGG TTTTCCACAG CGGTGGTGAC	120
GCTGATTGAA GACGGGAAGA ATGACTCCCT GCGTCTGAG TCCACGTCGC ACAGGTGGCG	180
GGGGCCTGCC TGCAGGCC CGCAGTAGCTC CTACAACAGC CTGTACTCCA CCTGCCTGGA	240
GCTGTTCAAG TTCACCATCG GCATGGCGA CCTGGAGTTC ACTGAGAACC ATGAACCTCT	300
CGAG	304

(2) INFORMATION FOR SEQ ID NO:513:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 314 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

GAATTCCGCC TTCATGGCCT AGGAACCTGG ACCGGGGCGG CGCCGGGTTT CCCTCATGAT	60
CCGGGGCGGG CGCGCGCGGC GGAGAGGCG GCGGGAGGAT GACCTCTTAC CGGGAGCGGA	120
GTGCGGACCT GGGCGTTTC TACACTGTCA CCGAGCCCCA GCGACACCCG AGGGGCTACA	180
CAGTATATAA GGTCAACGCC CGGGTTGTTT CACGAAGAAA TCCAGAGGAT GTCCAGGAGG	240
GAGAATCTG AACCAACCTA TCCATGAACA TACTCTCTGC CATTTCCTTA GTCCCTTTTT	300
CGGAAAAACT CGAG	314

(2) INFORMATION FOR SEQ ID NO:514:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 529 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:

GAATTCCGCC TTCATGGCCT ACAGAACTTAA GAAAATGAGA CTGAGCAATC TCATGGTTCT	60
TGGACAGTTA GTCTATGGCC AATTGATGGA ACCAGTAAAT CGAGAGAACT TTACGCAGAC	120
CTTGCCCAAATGCCAATTCA ATTCTCATGC ACAGCCCCA GATGCCAGGG AAGAGGATAT	180

CATACTTGAA GGTCAACAGA GCCTGCCATC CCAGGCTTCA GATTGGAGCC GATACTCAAG	240
CAGCTTACTG GAATCCGCT CTGTTCCCTGG AACACTAAAT GAGGCTGTTG TAATGACTCC	300
ATTTTCATCG GAACTTCAAG GAATTCAGA ACAGACCCCTC CTGGAGCTGT CCAAAGGAAA	360
GCCCCTCCCCG CATCCCATGAG CCTGGTTTGT GTCTCTTGAT GGAAAGCCAG TTGCACAAGT	420
GAGGCACCTCC TTTATAGACC TGAAAAAGGG CAAGAGAAC CAGAGCAATG ACACCAAGTCT	480
GGACTCTGGG GTGGACATGA ATGAGCTTCA CTCAGTAGA AAGCTCGAG	529

(2) INFORMATION FOR SEQ ID NO:515:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 352 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:

GGAGATGAAA CTTAAAAGTG AAAACCTTAA AGAGGAGCCT CAGTCCTCTG AAGAAGAATC	60
TATGTCCTCT GTGGAAACCA GGACACTAAT AAAATCTGAG CCTGTAAGTC CAAAGAATGG	120
TGTTTTACCA CAGGCTACTG GAGACCAAGA ATCTGGTGGAA AAATGTGAAA CAGACAGACG	180
CATGGTTGCA GCCAGAACAG AACCCCTAAC TCCAAACCCCA GCTTCTAAGA AACCAAGAGT	240
CCACAAAAGG CGATCAGAAT CTAGTTCTGA TTCTGACTCA GATTCTGAGA GATCATCTTG	300
TTCTTCCAGA TCATCTTCTT CCTCATCATC CTCTTCTTGT CCCACTCTCG AG	352

(2) INFORMATION FOR SEQ ID NO:516:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 500 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:

GTCTACACCN TTCCGAGTTG GCTGCAGATT TGTGGTGCCT TCTGAGCCGT CTGTCCTGCG	60
CCAAGATGCT TCAAACTATT ATTAAAAACA TATGGATCCC CATGAAGCCC TACTACACCA	120
AACTTTACCA GGAGATTTGG ATAGGAATGG GGCTGATGGG CTTCATCGTT TATAAAATCC	180
GGGCTGCTGA TAAAAGAAAGT AAGGCTTTGA AAGCTTCAGC GCCTGCTCT GGTCACTCACT	240
AACCAGATTT ACTTGGAGTA CATGTGAAAG AAAACGTCAG TCTGCCCTGTA AATTTCAGCA	300
AGCCGTGTTA GATGGGGAGC GTGGAACGTC ACTGTACACT TGTATAAGTA CCGTTTACTT	360
CATGGCATGTA ATAATGGAT CTGAGATG CACTGCTACCG TGGTACTGCT TTCAGTGTGT	420
TCCCCCTCAG CCCCTCCGGC GTGTCAGGCA TACTCTGAGT AGATAATTG TCATGCAGCG	480
CATGCAATCA GAATCTCGAG	500

(2) INFORMATION FOR SEQ ID NO:517:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 427 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:

GAATTCTGGCC	TTCATGGCCT	AGATGCTCAA	CACCTCCTCC	TTGGTGGAGC	AGCTGAACGA	60
GCAGTTAAC	TGGGTGTC	CCC	GGCTGGCAAA	CCTCACGCAA	GGCGAACACC	120
GGGGGTCA	ACGGTGGCTT	CCC	ACACTTC	TGACTCGGAC	GTCCTCCG	180
GGTGGTCTG	AAGCTCTTG	ACTCTGATCC	CATCACTGTG	ACCGTCCCTG	TAGAAGTCTC	240
CAGGAAGAAC	CCTAAATTAA	TGGAGACCGT	GGCGGAGAAA	GCNCTGCAGG	AATACCGCAA	300
AAAGCACCGG	GAGGAGTGT	ATGTGGATGT	TGCTTTGCA	CCTACGGGG	CATCTGAGTC	360
CAGCTCCCCC	CAAGATGAGC	TGCAGCCCCC	CAGAGAGAGC	TCTGCACGTC	ACCAAGTAAC	420
					TCTCGAG	427

(2) INFORMATION FOR SEQ ID NO:518:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 399 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:

GAATTCTGGCC	TTCATGGCCT	AATCTTAAGG	GACCTTCCT	TACTACAGAT	TCAAATGCGA	60
GATCTTGAGG	GTTACAGGGA	AAAGGAGGTAT	CAGTTACTTC	AGCTTCGACC	TGCGCAGAGA	120
GCATCATGGA	TTGGTTATGC	TATTGCTTAC	CATTATTAG	AAGATTATGA	AATGGCAGCA	180
AAGATTTAG	AAGAATTTAG	GAAACACAA	CACAGATCCC	CTGACAAGGT	GGATTATGAA	240
TATAGTGAAC	TACTCTTATA	TCAGAATCAA	GTTCTTCGGG	AAGCAGGTCT	CTATAGAGAA	300
GCTTGGAAC	ATCTTGTAC	CTATGAAAAG	CAGATTTGTG	ATAAACTGC	TGTAGAAGAA	360
ACCAAAGGGG	ACTCTGTT	GCAACTATGT	CGTTTGAA			399

(2) INFORMATION FOR SEQ ID NO:519:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 399 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

GAATTCTGGCC	TTCATGGCCT	ACTTATCTTA	ATCCAATGGG	TGACATCTTC	AACAACCTG	60
TTCCAATAA	GGCTGCATTC	AAACACTAG	GGATTAAGAC	ATCAACATGT	GAATTTGGA	120
GGAATGTAGT	TCTAACCTATA	ACAGCAGTGA	ATGAGATGAC	AGACTATTGC	TCTCAAAAGA	180
TAGCCAGTT	TCTAGTTCC	TTAGGCATT	TCTGGAGGTT	TGCGAGCAGT	TCATTATTAT	240
CTTAAAAATA	TTATCCAGAG	CTGTGGTCTA	TCAGCAGCTC	ATTACCAAGAC	TGGCAGATAC	300
ATTTAACATCG	CAAAGAGATT	GTTCCTGTGA	TTAGCATCTC	CCTGGTTTCC	CAGCTCAAGA	360
GTTCTTCTGA	GTAATAGTAA	TCCTTCCCCC	ATGCTCGAG			399

(2) INFORMATION FOR SEQ ID NO:520:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 273 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:

GCTGAAGTGG TGACTTTGA GAGAGGACAC AAAATTATCA TCAGCTCCAG TCGGAGAAC	60
CAGAAAGGAG AAGAGGTAAG AGTGTGAGAG ATTGCATCTG CCATGTTGTT CAGATCCTGG	120
GCGAATAGTT CCCTCTTCAC ACAGGTCACT TACTCACTTG TTTCCAATT CTTTGTGTTG	180
ATAAAAACTC TGTCCATAAT AGGCCAGATG TTCCCACCT GCAGTATCTC ACCCTTCAGG	240
CACTCCAGTT CACCTTCCTC CACATCCCTC GAG	273

(2) INFORMATION FOR SEQ ID NO:521:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:

GCTTTAAGAA TTAACGAAAG CAGTGTCAAG ACAGTAAGGA TTCAAACCAT TTGCCAAAAA	60
TGACTCTAAAG TGCATTTACT CTCTTCCTGG CATTGATTGG TGGTACCACT GGCCACTACT	120
ATGATTATGA TTTTCCCTA TCAATTATG GGCAATCATC ACCAAACTGT GCACCAGAAAT	180
GTAACTGCC CGAAAGCTAC CCAAGTGCCA TGTACTGTGA TGAGCTGAAA TTGAAAAGTG	240
TACCAATGGT GCCTCTGGA ATCAAGTATC TTTACCTTAG GAATAACCAG ATTGACCATA	300
TTGATGAAAA GGCCCCACTC GAG	323

(2) INFORMATION FOR SEQ ID NO:522:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:

GGAAAAAGAA GAGAAAGCCA AGGAAGACAA GGGCAAACAA AAGTTGAGGC AGCTTCACAC	60
ACACAGATAC GGAGAACCGAG AAGTGCAGA GTCAGCATTC TGGAAAGAAAA TCATAGCATA	120
TCAACAGAAA CTTCTAAACT ATTTTGCTCG CAACTTTTAC AACATGAGAA TGTTAGCCTT	180
ATTTGTCGCA TTTGCTATCA ATTTCATCTT GCTCTTTAT AAGGTCTCCA CTTCTCTGT	240
GGTTGAAGGA AAGGAGCTCC CCACGAGGCT CGAG	274

(2) INFORMATION FOR SEQ ID NO:523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:

GCCCCAGTCC AGATCCAGGA CTGAGATCCC AGAACCATGA ACCTGGCCAT CAGCATCGCT	60
CTCCTGCTAA CAGCTTGCA GGTCTCCCGA GGGCAGAAGG TGACCCAGCT AACGGCCTGC	120
CTAGTGGACC AGAGCCTTCG TCTGGACTGC CGCCATGAGA ATACCAGCAG TTCACCCATC	180

CAGTACGAGT TCAGCCTGAC CCGTGAGACA AAGAAGCAGG TGCTCTTGG CACTGTGGGG	240
GTGCCTGAGC ACACATACCG CTCCCTCCTC GAG	273

(2) INFORMATION FOR SEQ ID NO:524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:

GAATTCCGCC TTCATGGCCT ACTCTCCTAT AAAGCAGACG CCGCGCCCGCG CTGCGACGCT	60
GTAGTGGCTT CGTCTCGGT TTTCTCTTC CTTCGCTAAC GCCTCCCGCG TCTCGTCAGC	120
CTCCCCGCCGG CGTCTCCTT AACACCGAAC ACCATGCCTT CAATTAAGTT GCAGAGTTCT	180
GATGGAGAGA TATTTGAAGT TGATGTGGAA ATTGCCAAAC AATCTGTGAC TATTAAGACC	240
ATGTTGAAAG ATTTGGAAT GGATGATGAA GGAGATGATG ACCCAGTTC TATAACCAAT	300
GTGAATGCAG CAATATTAAA AAAGGTCAATT CAGTGGTGCAC CCCACCAAA GGATGACCCCT	360
CCTCCTCCTG AAGATGATGA GAACAAAGAA AAGCGAACAG ATGATATCCC TGTTGGGAC	420
CAAGAATTC TGAAAGTTGA CTAAGGAACA CTCGAG	456

(2) INFORMATION FOR SEQ ID NO:525:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:

GAATTCCGCC TTCATGGCCT AATGGGACAA CTCCCTGCCCT TCTACCTGTC CCCTCCCCCT	60
TTGGTTGTAT GATTTCTTC TTTTTTAAGA ACCCTGGAA GCAGCGCTC CTTCAGGGTT	120
GGCTGGGAGC TCGGCCCATC CACCTCTTGG GGTACCTGCC TCTCTCTCTC CTGTGGTGT	180
CCTTCCCTCT CCCATGTGCT CGGTGTTCAAG TGGTGTATAT TTCTTCTCCC AGACATGGG	240
CACACGCCCA AAGGGACATG ATCCCTCTCCT TAGTCTTAGC TCATGGGCT CTTTATAAGG	300
AGTTGGGGGG TAGAGGCAGG AAATGGGAAC CGAGCTGAAG CAGAGGCTGA GTTAGGGG	360
TAGAGGACAG TGCTCTGGC CACCCAGCCT CTGCTGAGAA CCATTCTGG GATTAGAGCT	420
GCCTTCTCCA GGGAAAAAGT GTCCGACTCG AG	452

(2) INFORMATION FOR SEQ ID NO:526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:

GCGATTGAAT TCTAGACCAAG ACTCGTCTCA GGCCAGTTGC AGCCTTCTCA GCCAAACGCC	60
GACCAAGGAA AACTCACTAC CATGAGAATT GCAGTGATTT GCTTTGCT CCTAGGCATC	120

ACCTGTGCCA TACCAGTTAA ACAGGCTGAT TCTGGAAGTT CTGAGGAAAA SCAGCTTAC	180
AACAAATACC CAGATGCTGT GGCCACATGG CTAAACCTG ACCCATCTCA GAAGCAGAAT	240
CTCCTAGCCC CACAGACCC TCCAAGTAAG TCCAACGAAA GCCATGACCA CATGGATGAT	300
ATGGATGATG AAGATGATGA TGACCATGTC GACAGCCAGG ACTCCATTGA CTCGAATCGA	360
CTCGAG	366

(2) INFORMATION FOR SEQ ID NO:527:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 408 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:

GCCCCAGTCC AGATCCAGGA CTGAGATCCC AGAACCATGAA ACCTGGCCAT CAGCATCGCT	60
CTCCTGCTAA CAGTCTTGCA GGTCTCCCGA GGGCAGAAGG TGACCAGCCT AACGGCCTGC	120
CTAGTGGACC AGAGCCTTCG TCTGGACTGC CGCCATGAGA ATACCAGCAG TTCACCCATC	180
CAGTACGAGT TCAGCCTGAC CGTGAGACA AAGAAGCAGC TGCTTTGG CACTGTGGGG	240
GTGCCTGAGC ACACATACCG CTCCCGAACC AACTTCACCA GCAAATACAA CATGAAGGTC	300
CTCTACTTAT CGCCCTTCAC TAGCAAGGAC GAGGGCACCT ACACGTGTGC ACTCCACCAC	360
TCTGGCCATT CCCCACCCAT CTCCCTCCAG AACGTTACAG TGCTCGAG	408

(2) INFORMATION FOR SEQ ID NO:528:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 403 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:

GTAGGTCA CA GCAGAACGAG CCAAAATGGA TCCCCACTGC ACTATGGGAC TGAGTAACAT	60
TCTCTTG TG ATGGCCTTCC TGCTCTCTGG TGCTGCTCCT CTGAAGATT AAGCTTATTT	120
CAATGAGACT GCAGACCTGC CATGCCAATT TGCAAACCTCT CAAAACCAAA GCCTGAGTGA	180
GCTAGTAGTA TTTGGCAGG ACCAGGAAAA CTTGGTTCTG AATGAGGTTAT ACTTAGGCAA	240
AGAGAAATTT GACAGTGTTC ATTCAAGTA TATGGGCGC ACAAGTTTG ATTGGACAG	300
TGGACCTG AGACTTCACA ATCTTCAGAT CAAGGACAAG GGCTTGATC AATGTATCAT	360
CCATCACAAA AAGCCACAG GAATGATTG CATCCACCTC GAG	403

(2) INFORMATION FOR SEQ ID NO:529:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 475 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:

GAATTCCCTCT TCTTTACCCCT CGTCCTGCCG GGCACCTTCC TTAGGTTGG TTTCATCTAC	60
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AGCTTCTATG TTCTCTTCAG CTTGGCTGCT CTCCCCAGTC TCCGTTGGAG GCTGGGCTGT	120
TGCCTTGCGA GCAGCATCCT CTGCGGCAGG GGTGGTGGCA GCAGCAGCAG TGACAGCAGC	180
AGGCACATCG GCTTGTCTAG GCTCCTCCCT GGCTGGGGCA TCTTCAGCCT TGAGGACGG	240
CGAGCTTATCA GTGGAAGCTT TAGTGGCACT TTCTGTCTA CCTGAGGCCG CCTTCTCCCTC	300
TGAGGATGCA GGAGCTGGG GGGCTACCTG CTCTGTGGCA GCATCACCCCT CCCCCCTTTT	360
CTCCTCGAA GGAGTTTCTC CTGCTTGC GGCTTGAGC CAGTGGCTGG	420
GGCTGCTTCG GCAGTAGTGG TGCTTCTCC CCTCTTCTCC ACCCCATCGC TCGAG	475

(2) INFORMATION FOR SEQ ID NO:530:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:

GTGCTGGCGG ACATGGACGT GGTGAATCAG CTGGTGGCTG GGGGTCAGTT CCGGGTGGTC	60
AAGGAGCCCC TCGGCTTTGT GAAGGTGCTG CAATGGGTCT TCGCCATCTT CGCCTTGC	120
ACATGCGCGA GCTACAGTGG GGAGCTCCAG CTGAGCGTGG ATTGTGCAA AAAGACCGAG	180
AGTGACCTCA GCATCGAGGT CGAGTTGAG TACCCCTTCAG GGCTGACCA AGTGTACTTT	240
GATGCACCCA CCTGCGGAGG GGGCACCAC AAGGTCTTCT TAGTTGGGA CTACTCCTCG	300
TCAGCCGAAT TCTTTGTCA CGTGGCCGTG TTGCGCTTC TCTACTCCAT GGGGGCTCTG	360
GCCACCTACA TCTTCTGCA GAACAAGTAC CGAGAGATA ACAAAAGGGCC CATGCTGGAC	420
TTTCTGGCCA CGGCTGTGTT CGCCTTCATG TGCTAGTTA GCTCATGGC ATGGGCAAG	480
GGGCTGTCAG ATGTGAAGAT GGCCACAGAC CCAGATGAAC TCGAG	525

(2) INFORMATION FOR SEQ ID NO:531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:

GCAAACAGAC AAGGCTTACA GGTTAGTTCA GGATCTGCGC CTTATCAAGC AAATTGTTT	60
GCCTATCCAA CCTGCGGTGC CAAACCCATA TACTCTCTA TCCTCAATAC CTCCCTCCAC	120
AACCCCTCCA TAACCCATTA TTGGTTCTG GATCTAAAC ATGCTTTCTT TGCTATTCCCT	180
TTGCATCCTT CATCCCAGCC TCTCTTGCT TTCACTTGGG CTGGCCCTGA CACCCATCAG	240
CCTCAGCAAC TTACCTGGGC TGTACTGCCA CAAGCCTCA CGGACAGCCC CCATTACTTC	300
AGTAGCCCTC GAG	313

(2) INFORMATION FOR SEQ ID NO:532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:

GAGACTATCG CCTATACTTT ATTTGGGTAA ATGGTTTGGT TAAGGTTGTT TGGTGGTAGC	60
TGGTTGGTT GCTGGGGCTC GGTGTTGTA GTCGCGATGT TCTTCTCCGA GCCCAGAGCC	120
AGGTCGCCGA CGTGGGAAGC CAGTCCTCG GAACACAGGA AGTGGGTGGA AGTATTAAA	180
GCATGTGATG AAGATCACAA AGGATATCTC AGCAGAGAGG ACTTTAAAC TGCTGTTGTA	240
ATGCTGTTTG GGTACAAGCC CTCCAAGATA GAAGTGGATT CTGTGATGTC TTCAATAAAT	300
CCAAATACTT CTGGTATATT ACTCGAG	327

(2) INFORMATION FOR SEQ ID NO:533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:

GCCTGCCCTT ACCTTACAGG TCTGGATGTT ACCTTCCAT CTGTTGCTGC TTTCTTCTAT	60
GGGCCCCCTGC CCTCACTCTC AAGAACCTCA ACTACTCCGT GCCGGAGGAG CAAGGGCCG	120
GCACGGTGAT CGGGAACATC GGCAAGGGATG CTGCACTGCA GCCTGGGCTT CCGCTGCAG	180
AGCGCGGGCGG CGGAGGGCGC ACCAAGTCGG GTAGCTACCG GGTGCTGGAG AACTCCGCAC	240
CGCACCTGCT GGACGTGGAC GCAGACAGCG GGCTCCTCTA CACCAAGCAG CGCATCGACC	300
GCGAGTCCTT GTGCCGCCAC AATGCCAAGT GCCAGCTGTC CCTCGAG	347

(2) INFORMATION FOR SEQ ID NO:534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534:

GGTAGGACCG GCGAGGAATA GGAATCATGG CGGCTGCGCT GTTCGTGCTG CTGGGATTG	60
CGCTGCTGGG CACCCACCGA GCCTCCGGG CTGCGGCAC ATTCTTCACT ACCGTAGAAG	120
ACCTTGGCTC CAAGATACTC CTCACCTGCT CCTTGAATGCA CAGCGCCACA GAGGTACAG	180
GGCACCGCTG GCTGAAGGGG GGCCTGGTGC TGAAGGAGGA CGCGCTGCC GGCCAGAAAA	240
CGGAGTTCAA GGTGGACTCC GACGACCAGT GGGGAGAGTA CTCCCTGCGTC TTCCCTCCCCG	300
AGCCCATGGG CACGGCCAAC ATCCAGCTCC ACAGGGCCTCC CAGAGTGAAG GCTGTGAAGT	360
CGTCAGAAACA CATCNACGAG GGGGAGACGG CCATGCTGGT CTGCAAGTCA GAGTCCGTGC	420
CACCTGTCAC TGACTGGGCC TGGTACAAGA TCACTGACTC TGAGGACAAG GCCCTCATGA	480
ACGGCTCCGA GAGCAGAGTT CTCGAG	506

(2) INFORMATION FOR SEQ ID NO:535:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535:

GAATTCCCTCT	TCTTTACCCCT	CGTCCTGCCG	GGCACTTTCC	TTAGGTTTGG	TTTCATCTAC	60
AGCTTCTATG	TTCTCTTCAG	CTTGGCTGCT	CTCCCCAGTC	TCCGTTGGAG	GCTGGGCTGT	120
TGCCTTGCA	GCAGCATCCT	CTGCGGCAGG	GGTGGTGGCA	GCAGCAGCAG	TGACAGCAGC	180
AGGCACATCG	GCTTGTAG	GCTCCTCCTT	GGCTGGGGCA	TCTTCAGGCT	TGGAGGACGG	240
CGAGTTATCA	GTGGAAGCTT	TAGTGGCACT	TTCTGTCTCA	GCTGAGCCGG	CCTTCTCCTC	300
TGAGGATGCA	GGAGCCTGGG	GGCTGCCCTG	CTCTGTGGCA	GCATCACCCCT	CCCCCTTCTT	360
CTCCTCGGAA	GGAGTTTCTC	CTGCTTGC	GGGCTCATCA	GGCTGGAGC	CACTGGCTGG	420
GGCTGCTTCG	GCAGTAGTGG	TGCCTTCTCC	CTTCTTCTCC	ACCCCATCGC	TCGAG	475

(2) INFORMATION FOR SEQ ID NO:536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:536:

GAATTCGCCT	TCATGGCCTA	CAAGCTCTAG	CCTAGACCTT	TAGTGTGCCA	TGCAGTCACA	60
GGTCTGAAAA	GCAGCATCAT	CCAAACCTTA	CTTAATCTCT	AAAATCTAG	CTGGTGGACA	120
GCTCATGATT	AGTTCAGCCC	ACTTCCTCCC	CCTTAGTTGA	GTTTGCAGCA	GGACGCCAGGA	180
GATAAGCACT	TCCAAGCAAG	TCTGATTTAT	ATATCAAAC	CGGTCTCCAT	CCCAGGCCAG	240
CTGACCCTCA	GAGCCAGCAA	TGCTCTGTGC	TTCCTCCCTG	CGTCACGGCT	TGGCAAGAGC	300
TGCCTCTGCT	GAGCAGTGTG	TGTGATGGAG	ACGGAGGCCG	CTGAAGGCCG	AGTGCTTGCA	360
GGCTTGAA	CTGCCATCGA	ACACAATCCA	AACTCTGGAA	ATGTTCTGA	CCACCTAACG	420
CCTCAACAAAC	GTAAATGCCG	TATGTGCTNT	TTNTCAGTAA	ACTCCTTGCT	CATGTCNATA	480
AAGTATCCCT	GAACACTCGA	G				501

(2) INFORMATION FOR SEQ ID NO:537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:537:

GCGGGCACCA	TTTCCAGTAT	GTACCAAACC	AAAGCCGTCA	TCATTGCAAT	GATCATCACT	60
GCGGTGGTAT	CCATTTCAGT	CACCATCTTC	TGCTTTCAGA	CCAAGGTGGA	CTTCACCTCG	120
TGCACAGGCC	TCTTCTGTGT	CCTGGGAATT	GTGCTCTGG	TGACTGGGAT	TGTCACTAGC	180
ATTGTGCTCT	ACTTCCAATA	CGTTTACTGG	CTCCACATGC	TCTATGCTGC	TCTGGGGGCC	240
ATTTGTTCA	CCCTGTTCCCT	GGCTTACGAC	ACACAGCTGG	TCCCAGGAA	CCTCGAG	297

(2) INFORMATION FOR SEQ ID NO:538:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:538:

GCTCCACCAAG CTACTGAGAA AATGGCCTGT AAAGATCCAG AAAAACCAT GGAGGCCTGT	60
GCCTCAGCAC ATGTGCAACC CAAGCCTGCC CCTGAAGCCA GTAGCCTAGA GGAGCCCCAT	120
AGCCCAGAAA CAGGGGAGAA GGTAGTAGCA GGAGAGGTAA ACCCACCAA TGCCCCCTGT	180
GGGGACCCAC TGAGCCTCTT GTTGGGGAT GTGACATCCC TGAAAAGCTT TGATTCTTG	240
ACAGGTTGTG GTGACATAAT AGCAGAACAA CTCGAG	276

(2) INFORMATION FOR SEQ ID NO:539:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:

GAATTCGGCC TTCATGGCCT AGCCAGACAA CTTGACTGA TCTTCTTTG CTTGCCTAC	60
TAATCACACA CACCCCTCTCT TCTAGCCTGT GAAGACTTAA CTGATTTCT ACGGATGAAG	120
GTTCAGTGT CCCAAGGCC CATACCGTAT CTGATTTAC TTATTTTG TTGTTAACG	180
CTAACAGCTT CTGAGGAGCC ACCTAGAGCT CAAGAACAA AAGCTACTGA GAGTAGATGC	240
TATGTAAACT GCACAAAGACG TCTCGAG	267

(2) INFORMATION FOR SEQ ID NO:540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:540:

GAATTCGGCC TTCATGGCCT ACAAAAAGAT GCTGGACAAG GCGTTTGCAG AGCGGATCAT	60
CCATGACTAC AAGGATATTT TCAAACAAAGC AACTGAAGAC AGGCTCACCA GTGCCAAGGA	120
ACTGCCCTAT TTGAGGTG ATTCTGGCC CAATGTGTTA GAAGAGAGCA TTAAGGAAC	180
AGAACAAAGAA GAAGAGGAGA GAAAAAAGGA AGAGAGCACT GCAGCCAGTG AAACCACTGA	240
GGCAGTCAG GGCAGACAGCA AGAATGCCNA GAAGAAGAAC NACNAGAAAA CCAACAAGAA	300
CAAAGCAGC ATCAGCCCGC CCAACAGAA GAAGCCCAGC ATGCCAAGC TGTCCAATGA	360
CCTGTCCAG AAACTCGAG	379

(2) INFORMATION FOR SEQ ID NO:541:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541:

GAATTCGGCC	TTCATGGCCT	ACATAATTG	AATCAACACA	ACCACCCACA	GCCTAATTAT	60
TAGCATCATC	CCTCTACTAT	TTTTAACCA	AATCAACAAAC	AACCTATTTA	GCTGCTCCCC	120
AACCTTTCC	TCCGACCCCC	TAACAACCCC	CCTCTAATA	CTAACTACCT	GACTCCTACC	180
CCTCACAAATC	ATGGCAAGCC	AACGCCACTT	ATCCAGTGAA	CCACTATCAC	GAAAAAAACT	240
CTACCTCTCT	ATACTAATCT	CCNNACAAAT	CTCCTTAATT	ATAACATTCA	CAGCCACAGA	300
					TCTCGAG	307

(2) INFORMATION FOR SEQ ID NO:542:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:542:

GGATGGCGCC	GCGGAGGGTC	AGGTGGTTTC	TGCGGGGCT	CCCGCCGCTG	CTACTGCTGC	60
TGCTCTTCT	CGGGCCCTGG	CCCGCTGCGA	GCCACGGCGG	CAAGTACTCG	CGGGAGAAAGA	120
ACCAGCCCAA	GCCGCTCCCCG	AAACCGCGAGT	CCGGAGAGGA	GTTCCGCGATG	GAGAAGTTGA	180
ACCAAGCTGTG	GGAGAAGGCC	CAGCGACTGC	ATCTTCCCTCC	CGTGAGGCTG	GCCGAGCTCC	240
ACGCTGATCT	GAAGATACAG	GAGAGGGACG	AACTCGGCTG	GAAGAAAATA	AAGCTTGACG	300
GCTGGACGA	AGATGGGGAG	AAGGAAGCGA	GACTCATACG	CAACACACTC	GAG	353

(2) INFORMATION FOR SEQ ID NO:543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:543:

GGATACCTA	AAAAAAACAAT	CTATGTCAGA	GGCTTCACTG	GAGGTTACGT	CACGTTATCG	60
TATTAATTAA	GAAGATGAGA	CACAGGATT	AAAGAAAGAAA	TTAGGTCAAA	TCAGAAATCA	120
ATTGCAAGAA	GCACAGGATC	GACATACAGA	AGCTGTCAGA	TGTGCTGAGA	AGATGCAAGA	180
TCACAAGCAA	AAGCTTGAAA	AAGATAATGC	CAAGTTAAA	GTTACAGTCA	AAAAGCAAAT	240
GGACAAAATT	GAGGAGCTTC	AGAAAAACCT	GTTAAATGCA	AATTGTCTG	AAGATGAAAA	300
					GGAACCTCGAG	310

(2) INFORMATION FOR SEQ ID NO:544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:544:

GTGGGATGA	TTGGTGGCGT	GTACGCAGCT	GCTATGGCCT	GGGCCATCAT	CCCCCACTAT	60
GGGTGGAGTT	TTCAGATGGG	TTCTGCCTAC	CAGTTCCACA	GCTGGAGGGT	CTTCGTCCTC	120

GTCTGCGCCT	TTCCTTCTGT	GTTGCCATT	GGGGCTCTGA	CCACGCAGCC	TGAGAGCCCC	180
CGTTTCTCC	TAGAGAATGG	AAAGCATGAT	GAGGCCTGGA	TGGTGCTGAA	GCAGGTCCAT	240
GATACCAACA	TGCGAGCCAA	AGGACATCCT	GAGCGACTCG	AG	282	

(2) INFORMATION FOR SEQ ID NO:545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:545:

GAATTTCGCC	TTCATGGCCT	AGAACCTTGT	ACACCATGGA	ATGTTCTACT	TATTATTTG	60
TGCTACAATA	TGTGCTGTTT	CTTTTGTGTT	AATTGCGAGAT	TGTCTACTAT	GAAGCAGGGGA	120
TTATTCTATG	CTGTGCTCTG	GGGCTGCTGT	TTATTATTCT	GATGCCCTTG	GTGGGGTATT	180
TCTTTTGAT	GTGTCGTTG	TGTAACAAAT	GTGGTGGAGA	AATGCACCAAG	CGACAGAAGG	240
AAAATGGCC	CTTCCTGAGG	AAATGCTTGT	CAATCTCCCT	GTTGGTGATT	TGTATAATAA	300
TAAGCATTGG	CATCTCTAT	GGTTTGTGG	CAAATCACCA	GGTAAGAACCC	CGGATCCTCG	360
AG						362

(2) INFORMATION FOR SEQ ID NO:546:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:546:

TCGAGGGACA	TGAGGCTGAG	CTGGTCCAG	CTCCTGACAG	TACTGTCAT	CTGCCTGAGC	60
GCCGTGGCCA	CGGCCACGGG	GGCCGAGGGC	AAAAGGAAGC	TGCAGATCGG	GGTCAAGAAAG	120
CGGGTGGACC	ACTGTCCTAT	CAAATCGCGC	AAAGGGGATG	TCCTGCACAT	GCACTACACG	180
GGGAAGCTGG	AAGATGGGAC	AGAGTTTGAC	AGCAGCCTGC	CCCAGAACCA	GCCCTTGTC	240
TTCTCCCTTG	GCACAGGCCA	GGTCATCAAG	GGCTGGACC	AGGGGCTGCT	GGGGATGTGT	300
GAGGGGGACC	TCGAG					315

(2) INFORMATION FOR SEQ ID NO:547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:547:

GAATTTTAAT	TAAGAATTG	GCCTTCATGG	CCTAACGAG	GAGAACGGAG	ACCAAACCTG	60
TGATAACCTG	TCTCAAAACC	CTCCCTCATCA	TCTACTCCTT	CGTCTTCTGG	ATCACTGGGG	120
TGATCCTGCT	GGCTGTTGGA	GTCTGGGGCA	AACTTACTCT	GGGCACCTAT	ATCTCCCTTA	180
TTGCCGAGAA	CTCCACAAAT	GCTCCCTATG	TGCTCATCGG	AACTGGCACC	ACTATTGTTG	240

TCTTTGGCCT	GTTTGGATGC	TTTGCTACAT	GTCGTGGTAG	CCCATGGATG	CTGAAACTGT	300
ATGCCATGTT	TCTGTCCTG	GTGTTCTGG	CTGAGCTCST	AGCTGGCATT	TCAGGGTTG	360
TGTTTCGTCA	TGAGATCAAG	GACACCTTC	TGAGGACTTA	CACGGACGCT	ATGCAGACTT	420
ACAATGGCAA	TGATGAGAGA	ATGCTCGAG				449

(2) INFORMATION FOR SEQ ID NO:548:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 374 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:548:

GGGCTTTAAA	GGCAGACATT	GATGCTACAT	TATATGAACA	AGTCATCCTG	GAAAAAGAAA	60
TGGGAACTTA	TTTGGCACC	TTTGATGATT	ACTTGGAGTT	ATTCTGCAG	TTTGGTTATG	120
TGAGCCTTT	CTCCTGTGTT	TACCCATTAG	CAGCTGCCTT	TGCTGTGTTA	AATAACTCA	180
CTGAAGTAAA	TTCAGATGCC	TTAAAAATGT	GCAGGGTCTT	CAAACGTCCA	TTCTCAGAAC	240
CTTCAGCCAA	TATTGGTGTG	TGGCAGTTGG	CTTTGAAAC	GATGAGTGTGTT	ATATCTGTGG	300
TCACTAACCTG	TGCGCTGATT	GGAAATGTCAC	CACAAGTGAA	TGCACTCTT	CCAGAATCAA	360
AGGCAGACCT	CGAG					374

(2) INFORMATION FOR SEQ ID NO:549:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 294 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:549:

GTACAATCTG	AATCCAGGTC	TGACAGCTGG	CCATACAAAG	TCATACTTTC	CCCACATCCC	60
TCCCTTTGA	TAGGCATTGT	CATCTAGAGC	AATAGCCTG	AAATAGACTG	AACACCGTGG	120
CCCATAGCTT	AACTCCGTTTC	CACCTCTATT	TCAAAGTAAA	CTTGGGCTGG	GATTACAGGC	180
ATGAGTATGT	TTTCATTTGT	ACATAAAAGAC	TTTATACAAA	TGCTCTCCCT	AATATTTGCT	240
ACTTATTTC	GCATTAGTTC	AAATTCTTG	TCCTGTCATC	CCAAAACCTCT	CGAG	294

(2) INFORMATION FOR SEQ ID NO:550:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 303 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:550:

GAATTCCGCC	TTCATGGCCT	ACACTGCAAG	GGGAACCCCC	GAACCATCAT	CGTGCCACCC	60
CTGAAAACCC	AGGCCAGCGA	AGTATTGGTG	GAGTGTGATA	GCCTGGTGCC	AGTCAACACC	120
AGTCACCACT	CGTCCTCTTA	CAAGTCCAAG	TCCCTCCAGCA	ACGTGACCTC	CACCAAGGGT	180
CACTCTTCAG	GGAGCTCATC	TGGAGCCATC	ACCTACCGGC	AGCAGCGGCC	GGCCCCCAC	240

TTCCAGCAGC AGCAGCCACT CAATCTCAGC CAGGCTCAGC AGCACATCAC CACGCCGTC GAG	300 303
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(2) INFORMATION FOR SEQ ID NO:551:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551:

GCCACAAGCC TGTCAAGCAAG TGGGGCTACT TGGGTCTCG GGCCTCAATC CACTCCTGGC CAGAGACAAC TTCCCTCTCCC ATGGGAAAGG CTAACGCATG CCCATAAATT AAGACATTG CTCTCCCTCC AAGCCCTGGA AACCTGGAC TCTCTAACAT CTACCTCTGT TTTCTTGGC TGCATTCAAC TTTCTTGCAA TTAGTCAGGC CCTGGGGCAG CAGTTAGACG ACAGATGAGT CAGAGGATTG CAGAACTAA TCCAGAAGGA AGAGTTTATC CAAATGTTGG TGGCCTTCT CTTTTGGCGC ATTCTCTTCT GTTCTGTCT TTTCTCAGGA GTCCCTTGAG CTTCCATGTA CCGGGCCCCC TCGAG	60 120 180 240 300 360 375
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(2) INFORMATION FOR SEQ ID NO:552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552:

GCAAGGGCAG GCGGGTCCCC CAGTCCCGCC ATTACGGGTT GTCAGACCGT CTGCGTGTGG CAGGGCTCCC AAGGGCAGGC GGGTCCCCCA GTCCCGCCAT TACGGGTTGT CAGACCGTCT GCGTGTGGCA TTTTTGGCT TATAAGCTTC ACCCACTCAC CCCCAACCCA CACCCCACAT CCCCCTGCCG GCAGCCCCCTC AACCTAAGAA GGCCAGAGCA TATTTATTTT CCGAGGGAGC AGATTACTTC TCCCAGAGAA AGGAAAATCT TGGAAAAGAT TTAAAAAACAC AAATCTAAGC CTTGACCGTT TTTTTTCTCCTT TTTGACCCCC CTTCCCATTT TTTCAGNATT TATTCCCATG GCTTTTTTTT TTCTTGTGCG TGGTCTCGAG	60 120 180 240 300 360 390
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(2) INFORMATION FOR SEQ ID NO:553:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:553:

GAATTCCGCC AAAGAGGCCT AAGCAGGCCG GAGGCCGGGG CAGCGAGCCG GGTCCCACCA TGGCCGCCAA TTATTCCAGT ACCAGTACCC GGAGAGAACAA TGTCAAAGTT AAAACCAGCT CCCAGCCAGG CTTCTGGAA CGGCTGAGCG AGACCTCGGG TGGGATGTTT GTGGGGCTCA TGGCCTTCCT GCTCTCCTTC TACCTAATT TCACCAATGA GGGCCCGCA TTGAAGACGG	60 120 180 240
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CAACCTCATT GGCTGAGGGG CTCTCGCTTG TGGTGTCTCC CGACAGCATC CACAGTGTGG	300
CTCCGGAGAA TGAAAGGAAGC TGGTGCACAT CATTGGCCCG TTACGGACAT CCAAGCTTTT	360
GTCTGATCCA AACTATGGGG TCCATCTTCC GGCTGTGAAA CTGCGGAGGC ACGTGGAGAT	420
GTACCAATGG GTAGAAAATG AGGAGTCCAG GGAGTACACC GAGGATGGGC AGGTGAAGAA	480
GGASACGAGG TATTCCTACA ACACTGAATG GAGGTCAAGAA ATCATCAACA GCAAAAACTT	540
CGACCGAGAG ATTGGACACA AAAACCCCAG TGCCATGGCA GTGGAGTCAT TCATGGCAC	600
AGCCCCCTTT GTTCCTCGAG	620

(2) INFORMATION FOR SEQ ID NO:554:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:554:

GAATTGGGCC AAAGAGGCCT AGGACTTGTT TCGGAAGGAG CTGACTGGCC AATCACAATT	60
GCGAAGATGA AGGCTCTGTG GGGCGTGTG TTGGTCACAT TGCTGACAGG ATGCTAGCC	120
GAGGGAGAGC CGGAGGTGAC AGATCAGCTC GAGTGGCAA GCAACCAACC CTGGGAGCAG	180
GCCCTGAACC GCTTCTGGGA TTACCTGGCG TGGGTGAGA CGCTGTCTGA CCAGGTCCAG	240
GAAGAGCTGC AGAGCTCCA AGTCACACAA GAACTGACGG CACTGATGGA GGACACTATG	300
ACGGAATGAA AGGCTTACAA AAAGGAGCTG GAGGAACAGC TGGGTCCAGT GGCGGAGGAG	360
ACACGGGCCA GGCTGGCAA AGAGGTGCG AGGGCACAGG CCCGACTCGG AGCCGACATG	420
GAGGATCTAC GCAACCGACT CGGGCACTAC CGCAACGAGG TGACACCCAT GCTGGGCCAG	480
AGCACAGAGG AGATACTGGC GCGGCTCTCC ACACACCTGC GCAAGATGCG CAAGCGTTG	540
ATGCGGGATG CCGAGGATCT GCAGAACGCG CTAGCTGT ACAAGGCAGG GGCAGTCGAG	600

(2) INFORMATION FOR SEQ ID NO:555:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:555:

GAATTGGGCC TTCATGGCCT AGTATTTCT TATCACAGAT TTTGGGAGCA ACAGTGTGTTT	60
CCCATCTGGA GGAGGCTGAG TTAATTCTGT GGAACACCCA TTTGGTTGGA AATAAAAACA	120
CAGCATGGAT TTAATTCTATG CCACTTATTT ATTTTTATTA GGACTTGAGC TTCTTTGTAT	180
TTTTTTGCT TTGCTTCCAC TCAAAACCAAG ATTTGGTGGT TGCTGTGAA ACAGTGAAT	240
ACAAACACAGG CCAGGACTCC AG	262

(2) INFORMATION FOR SEQ ID NO:556:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:556:

GAATTGGGCC AAGAGGCCTA GTATTCTTTC GTTTCTCTCT AAAAGAAGAA AAATATAATT	60
TAGAAATACA TTGCGTATT TCTAAAACAA TAAATTTATA GTGTTAATAT TCATAGGTC	120
AATCAAAATG AAGCTTCTCC TTTGGGCTG CATTGTATGT GTTGCTTTG CAAGGAAGAG	180
ACGGTCCCCC TTCATTGGTG AGGATGACAA TGACGATGGT CACCCACTTC ATCCATCTCT	240
GAATATTCT TATGGCATAC GGAATTTAC ACCTCCTCTT TATTATCGCC CAGTGAATAC	300
AGTCCCAGT TACCCGGGA ATACTTACAC TGACACAGGG TTACCTTCGT ATCCCTGGAT	360
TCTAACCTCT CCTGGATTCC CCTATGTCTA TCACATCCGT GGTTTCCCT TAGCTACTCA	420
GTTGAATGTT CCTCCTCTCC CTCCTAGGGG TTTCGGTTT GTCCCTCGAG	470

(2) INFORMATION FOR SEQ ID NO:557:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:557:

GAATTGGGCC AAAGAGGCCT ATGCAGATTC TGTGGTTATA CTCACTCCTC ATCCCAAAGA	60
ATGAAATTAA CCACTCTCCT CTTCCTGGCA GCTGTAGCAG GGGCCCTGGT CTATGCTGAA	120
GATGCCCTCT CTGACTCGAC GGGTCTGTAT CCTGCCAGG AAGCTGGAC CTCTAAGCCT	180
AATGAAGAGA TCTCAGSTCC AGCAGAACCA GCTTCACCCC CAGAGACAAAC CACAACAGCC	240
CAGGAGAGTT CGGGCCAGC AGTTCAAGGG ACAGCCAAGG TCACGTCAG CAGGCAGGAA	300
CTAAACCCCC TGAATCCAT AGTGGAGAAA AGTATCTTAC TAACAGAACCA AGCCCTTGCA	360
AAAGCAGGAA AAGGAATGCA CGGAGGCCTG CCAGGTGGAA AACAAATTAT CGAAAATGGA	420
AGTTCCCTCG AG	432

(2) INFORMATION FOR SEQ ID NO:558:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:558:

GAATTGGGCC AAAGAGGCCT AAAAAGTATA TACATTTTAG TACTGCTTTG ATTTGTTTA	60
CATACTGAAA AATGTATCTG AAAATGAGTT ATTTGGACT CGAG	104

(2) INFORMATION FOR SEQ ID NO:559:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:559:

GAATTGGGCC AAAGAGGCCT ATTCACTTCA GCTTCAGTGA CTTCTGGATT CTCCTCTTGA	60
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GTAAAAGGAC TCAGCCAAT ATGAAGTTT TTGTTTTGC TTTAATCTTG GCTCTCATGC	120
TTTCCATGAC TGGAGCTGAT TCACATGCAA AGAGACATCA TGGGTATAAA AGAAAATTCC	180
ATGAAAAGCA ACATGATCTC GAG	203

(2) INFORMATION FOR SEQ ID NO:560:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:560:

GAATTCCGCC ACAGAGGCCT AGCCCAGTCT CGGGTATGTC TTTATCAGCA GCATGAAAAT	60
GGACTAATAC AGTTGCTATG ATTATTAGTT TTTTGCTACT GAGTTGTAGG AGTATCTGAT	120
ATATATTTTG GTAACAATC CCTTATAAAA TATATTGTTT CCAAATATTT TTTTCCATT	180
CCATAGGCTG CCTTTTCATT CTGTTGTTTC CTTTGCTTC GGTAAGGGAT TCTGAAACAA	240
CTATTTGGC AGCAGAACAG CTTCTTTTGT TTGCTTTCTC ATTGTCACT GTGTTCTGCA	300
TAAATAAGGT TATGAATTAG CTGTTGTTCA TATGGGTGAA AGATTTGCAT CTGTGGACGC	360
TTAGATAAGCA CATATGGTAA ACCATAGAAC TTCACCATT ATAACCTTTG AACAACTGAT	420
ACACTTAGAA AAGCAGTTT TGCGTGGCG CGGTGGCTCA TGCCCTAAT CCCTAGGCCT	480
CGAG	484

(2) INFORMATION FOR SEQ ID NO:561:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561:

GAATTCCGCC AAAGAGGCCT ATTGAATTCT AGACCTGCCT CGAGCTGACA ACTATGAAGT	60
TTTTGTTTT TGCTTTAAC TGGCTCTCA TGCTTTCCAT GACTGGAGCT GATTACATG	120
CAAAGAGACA TCATGGGTAT AAAAGAAAAT TCCATGAAAA GCATCAAGGA CTCGAG	176

(2) INFORMATION FOR SEQ ID NO:562:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:562:

GAATTCCGCC AAAGGGCTA ATTTTATTAA TAACATTTA AAAACAACAA TTATGAAAAA	60
GCAATTGGT TTACCGCTGA TGCTTGCGTC AGCCCTGCC TTCTCTGCTT GTAGCTCTGA	120
TGATGTGGCC GAGAATGGCC CAAAGGACAT CGCAGCTCTT ACAGATGGTG GTTACTTGAA	180
GATGCTATC AATCTTCCTT CCCGTGCTGC TAATGGTGGC TTCAGAGCTA CGGAACAAAGA	240
CGGTTATGTT AACTTGGAAAG ATGGATTGCC AAAAGACTAC AATGTAAGG ATGCTATCCT	300

CGTCCTTTTC CAAGGTGATA ATGAAGCAGA TGCCAAGTTC CATTCTGCAT ATGAACCTAC	360
TACATCAATG CAGAAGGATG GCTCTACGCA AATCACTTCC ACAACGAAAC TTGTTAAGAA	420
TGTGAATATT GGTGGTCAGG GAAATCCTCT TAAACCTGCT GATGTTAACG TCGAG	475

(2) INFORMATION FOR SEQ ID NO:563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:563:

GAATTCCGCC AAAGAGGCCT ACAATTATGG GGCTTATGGG GAACATGCTC ATTGTGTTT	60
ACCAATCAGG ACATGGAACT TAAACAATAT TTGTTGACTT ATAGTGAAAC CTGGCTAATT	120
AGGACTCTTA ACCAGCACTC TTAATTAACT GACTTATTTC TCTCTGTGTC CACCCCTCTT	180
AAAGAAAAAG AAGCGAAACT CGAG	204

(2) INFORMATION FOR SEQ ID NO:564:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:564:

GAATTCCGCC AAAGAGGCCT ATAGGCCCTCT TTGGCCGTAG GCCTTTGG CCGATTGAAT	60
TCTAGACGCG GCTCGAGGCC GGTCTAGGCC TCTTTGGCCG AA	102

(2) INFORMATION FOR SEQ ID NO:565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:565:

GAATTCCGCC AAAGAGGCCT ACTCAATTGT TCCTTTCTTC CATCACCAACC CTTTGAAGGT	60
CTCTTTGCCT ACTTGTAGAT TTAGGGGAC ATAACATTGA GACTGAGCAG TTTCTTGAAC	120
CTCTCCCTCTC AGCAGGCCACC AGCCTGGCTT TCGCAGACCA CTGGAAAGTA TCCCAGCTCA	180
TTAGCTTTG GAAATGACGGG AAGCCTTTTG ATGTTNGACG TCTTAATCTC AACTCTCAA	240
CTTAGCTCAT TCTGGAGCAG TCACGGCGATG ACAGATGAGC TCGAG	285

(2) INFORMATION FOR SEQ ID NO:566:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:566:

GATAACTTGA GATCAAATCA GTCATATTG ACTCTTCTCT TTTTCACTCC TTTTATATCT	60
GATCAGTCAG CAGTTTTTG AAACCCCTGTT CGAAGCAGTT CTCAACACTT GTGCACCCAT	120
TCTTTCTCCT ACACCACTCA ATCTAGACCC TCACATGTGG CTGTCCGTGCT TTCCCTCTCT	180
CCTACTCTCA AGCTATTCTG TGGAGAGATG TCAAAGTAAT CTTCACAAAA AATCTGATTG	240
CATCACTTCA CATCTCGAG	259

(2) INFORMATION FOR SEQ ID NO:567:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 374 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:567:

GGGCTTTAAA GGCAGACATT GATGCTACAT TATATGAACA AGTCATCCTG GAAAAAGAAA	60
TGGGAACCTTA TTTGGGCACC TTGATGATT ACTTGGAGTT ATTCCCTGCAG TTTGGTTATG	120
TGAGCCTTT CTCCGTGTT TACCCATTAG CAGCTGCCCT TGCTGTGTTA AATAACTTCA	180
CTGAAGTAA TTCAGATGCC TTAAAAATGT GCAGGGTCTT CAAACGTCCA TTCTCAGAAC	240
CTTCAGCCAA TATTGGTGTG TGCCAGTTGG CTTTGAAAC GATGAGTGTT ATATCTGTGG	300
TCACTAATG TGCGCTGATT GGAATGTCAC CACAAGTGAA TGCAGTCTT CCAGAATCAA	360
AGGCAGACCT CGAG	374

(2) INFORMATION FOR SEQ ID NO:568:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 250 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:568:

GAATTCCGCC TTCATGGCCT AGATAAGTAA ATAGACTTAC AGAGGGAAAG TAACTTGGCT	60
AAGGTGAAGT TGAACCAAGA TGACTGACTC CAGAGCTTCC ATTTTTCTTT TCTTTCTTT	120
TTTTTTTTTT NGGAGACAGA GTCTCACTCT GTGCCCCAGG CTGGAGTGCA ACGGCGCGGT	180
CTCCACTCAC TGCAGCCTCC AGCTCCTGGG CTCAAGTGAT CCTCCCACCT CAGCACCCCC	240
ACGTCTCGAG	250

(2) INFORMATION FOR SEQ ID NO:569:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 367 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569:

GAATTCCGGCC	TTCATGGCCT	ACAGGGAGGG	AGGGGTTCTG	AGAGCCTCAG	ACCACAGGGC	60
CTGAGGCCCA	CAGTGGCCCA	GAGTCCATCT	GGCAGCCCC	GCTCTGCTGG	CCCAGGGGGC	120
TCTCCCGAGG	GTGGAGTAGG	CAGGGGAGGG	TCGCTGGTCC	CCAGTCCCAG	CCTTCGAGAG	180
GTGGGGCCAG	ACAGCAGGGC	ACCCGTACCC	GAGACCACAG	TGCTCCCCAA	GGCCAGCTCT	240
CTCCCCAGTG	AGGTCACTCC	TACCTCCGGG	GCCATTGAGG	GCGGGGGATC	CTGTAGATCT	300
CTGACTCTGC	GGCCCTTAT	CTTGATGGCC	TGGCNCAAGA	AGGGAGGGCG	CTGCCCACTT	360
CCTCGAG						367

(2) INFORMATION FOR SEQ ID NO:570:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:570:

TTTTGACTGA	CTCTTTAAAT	TAGTACAATT	TTTCTACTTG	TCATATAACT	CCTGGAACAA	60
TAGTACGGGA	AGCCGTGATC	CTTTTCCCTG	ACTCATGATT	TTAGTCTTTT	TCCAAATCGC	120
TGTTTTTTTT	TGGTTTTTTT	TTTTTTGCT	GCTCCAACGA	CCAGCATGTG	TTGGAGCAGA	180
TCTCCATGGT	AAGCCAAAAG	TGGACTTGTC	AGCCTATAAC	TACTCTGCAG	CTGCCACTAA	240
CTCTACAGGC	ACAGAGCTCG	AG				262

(2) INFORMATION FOR SEQ ID NO:571:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:571:

CAGAAACTCT	TGGACTCAA	AGAGAAAGAA	AAAAGTCAAG	CCAAGGAAG	CACAAGAGGT	60
AAGACAGGCC	TAGTGATCTC	AGCAGGCAGA	ATTTATGGAC	ATATTITGCA	GGCAAGTGGT	120
TCTCAATCAG	GGGTGATTTT	TGGCTTGAA	GGACATTAG	CAATATCTGG	ACACATTTTT	180
TGGTTGTCGT	AAGTGGATGG	GGGTTGCTGC	TATCATCCTA	CAATGCATAG	GTGCATTAGT	240
CTGTTTTCAT	GCTGCTGATA	AAGACATACC	GGAGACTGGG	CAATTGCAA	ATGAGAGATG	300
GCTCGAG						307

(2) INFORMATION FOR SEQ ID NO:572:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:572:

GAATTCCGCC	TTCATGCCTA	CAGCCATATT	AAAACTAAGT	AAACTCGTCC	CTGGGAACTA	60
CACTTTCA	GTGACTGTAG	TAGACTCTGA	TGGAGCTACC	AACTCTACTA	CTGCAAACCT	120
GACAGTGAAC	AAAGCTGTGG	ATTACCCCCC	TGTGGCCAAC	GCAGGGCCCCA	ACCAAGTGAT	180
CACCCCTGCC	CAAAACTCCA	TCACCCCTTT	TGGGAACCA	AGCACTGATG	ATCATGGCAT	240
CACCAAGCTAT	GAGTGGTCAC	TCAGCCCAAG	CAGCAAAGGG	AAAGTGGTGG	AGATGCAGGN	300
TGTTAGAAC	CCAACCTTAC	AGCTCTCTGC	GATGCAAGAA	GGAGACTACA	CTTACCAAGCT	360
CACAGTGA	GACACAATAG	GACAGCAGGC	CACTGCTAA	GTGACTGTTA	TTGTGCAACC	420
TGAAAACAAT	AAGCCTCATC	AGGCAAGATGC	AGGCCCAGAT	AAAGAGCTGA	CCCTTCCTGT	480
GGATAGCACA	ACCCCTGGATG	GCAGCAAGAG	CTCAGATGAT	CAGAAAATTA	TCTCATATCT	540
CTGGGAAAAA	CACAGGGACC	TGATGGGTGC	AGCTCGAG			578

(2) INFORMATION FOR SEQ ID NO:573:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 623 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:573:

GAATTCCGCC	TTCATGGCCT	AACTTTGTGT	GATCAGAGTT	TATGGGTTGG	GCTGCCAG	60
GCTTGGATAA	CTTAAAGGCT	TGATGAGGTC	ATCAATTAT	GCTTGGCTAC	CCATGGCACA	120
GAAGCATAGC	CCCACGTG	TGGCTGGGGT	GGCTCCGGGC	ATCCTGGGCA	GTCAGGAGGA	180
AACTCCATGA	AGGAAGGAGC	TAACCTTTCT	GGGGGTACCC	CTATCCCAGC	ACAGACTTCC	240
TCATCTCATT	GGTCAGAACT	GGGTACATG	AAACATGCCTC	AGCCTATCAC	AGGCACAGGG	300
AATGAGACCA	TCATGGACCA	ATCAGGATTC	ACCACTCAAG	GTGGGGCTG	CCATCCGGAT	360
GGATGCTCTC	CGCCACAGGG	AGGTGGGGGA	CCCAGAAAGCT	GTGGGCAATG	GCCATGTGCA	420
CACTAGGACT	GAGGCACTCA	GTCCCGTAGC	TGACCTACCT	GGGACAGGCC	TGGAGGCTGA	480
CTTAGGGTGTG	AGGGCCAGAG	AGATTACTGT	GCACAGACCG	CTGTGTGACC	CCAGATCTAG	540
GTGGGATCCC	GGTGTGCCCC	ATCTGCCTGG	CTTACCCCAA	CCCCCTGGA	ACCTGAACCA	600
TTGAATTCTA	GACCTGCCTC	GAG				623

(2) INFORMATION FOR SEQ ID NO:574:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:574:

GAATTCCGCC	TTCATGGCCT	ACTCCAGAAT	GAAGATCTTC	TTGCCAGTGC	TGCTGGCTGC	60
CCTTCTGGGT	GTGGAGCGAG	CCAGCTCGCT	GATGTGCTTC	TCCTGCTTGA	ACCAGAAAGAG	120
CAATCTGTAC	TGCCCTGAAGC	CGACCATCTG	CTCCGACCA	GACAACACT	GCGTGACTGT	180
GTCTGCTAGT	GCCGGCATTG	GGAACTCTCGT	GACATTGGC	CACAGCCTGA	GCAAGACCTG	240
TTCCCCGGCC	TGCCCCATCC	CAGAAGGCCT	GCTCGAG			277

(2) INFORMATION FOR SEQ ID NO:575:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:575:

GAATTCGGCC TTCATGGCCT AAGCTTTGCG TTTTTAATA ACTTGTATAG CTAAAACCTT	60
GACGGTGAA AGCTCTCAGA TCAAAGCTGA TCCTTCTGTC AGTAATGATT CTAAAATAA	120
GCAAGATTT AATGGGAAAT ATATTTTATT TCATTCCTAT CTCAAACCTA GGTACTGTGG	180
TCGTTTGAG TTCATTTCGA GGCAATTCTCA ATGTGCCTCA GCCCACATCC AACCTCTCCC	240
CAGAACTCGA G	251

(2) INFORMATION FOR SEQ ID NO:576:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 261 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:576:

GAATTCGGCC TTCATGGCCT ACAGTCTAAG ACATTTCTA TTCTGCCTTC TTGTCTTCCT	60
CCCTCTCTTC CACATTGGTC AGACTTACAT CTTGGACAGC TCTCCCAGCC ATCTTCTACT	120
GCCTCCCTAT TTTTCCCTCC CAGACTTTTC CCCGCAAAAC ATCTGTTGCA GGTGGTATTA	180
ATTTCTATC ACGGCTGTGA CAAATTACCA CAAACTCAGT GGCTTAAAC AATGCACATT	240
TATTATCTGA CAGTTCTCGA G	261

(2) INFORMATION FOR SEQ ID NO:577:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 216 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:577:

GAATTCGGCT TCATGGCCTA GCAAGACTCC ATCTCAAAA AAGAAAGAAA GAAAAAGAAA	60
AGTACAAGTT TATAAAGTAT TATAGTGAAA AATTTCGATT CTGGCTGATT TTAAGCCATT	120
TAAAATTAT ATAAAACAAC CTTCCATAAA AATTGACAG GTGCCAGAT GTTGCCTTCT	180
CCATTTATTT TTTGTTTTTT TTTAATCACA CTCGAG	216

(2) INFORMATION FOR SEQ ID NO:578:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 294 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:

GGCATTGAAT TCTAGACCTG CCTCGAGTAA GTGCCAAAAA CTTCACTGTG CTCATCAAGA	60
ACAAATATCGA CTTCCCGGC CACAACATACA CCACGAGAAA CATCCCTGCCA GGTTTAAACA	120
TCACTTGAC CTTCCACAAG ACTCAGAACATC CACAGTGTCC CATTTCGCA CTAGGAGACA	180
TCTTCGAGA AACAGCCGAT AATTTTCAG ATGTGGCAAT TCAGGTTGGT GGTGCTTGT	240
ACACTGGGAT GTGGGCTGT GTGTCTAGGG ATGGAGGATG TCAAACAACT CGAG	294

(2) INFORMATION FOR SEQ ID NO:579:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 229 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:

GAATTCCGCC TTCATGGCCT ACCTTCACAG AAAATGCAT AGCTGGATGC TGCAGACTCT	60
AGCCTTTGCT GTAACATCTC TCGTCCTTTC GTGTGCAGAA ACCATCGATT ATTATGGGA	120
AATCTGTGAC AATGCATGTC CTTGTGAGGA AAAGGACGGC ATTTTAAC TGAGCTGTGA	180
AAACCGGGGG ATCATCAGTC TCTCTGAAAT TAGCCCCCCC GATCTCGAG	229

(2) INFORMATION FOR SEQ ID NO:580:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 205 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:580:

GAATTCCGCC TTCATGGCCT AGCTTACTTT ACAATTCTGC TGTTTGTCAA GTGTTCTAT	60
AGTTTTTTTT AAAGGTATGT TAACTATTTT TCCCTTTGG TTTATATTG TAGGAATCTT	120
TGCCTTAAAG TGTGCCGTG CAGAAGAATT ATTTAACATG TTGCAAGAGA TTATGCAAAA	180
TAATAGTATA AATGTGGAGC TCGAG	205

(2) INFORMATION FOR SEQ ID NO:581:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 200 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:581:

GAAGTGTAAAT GTCAGACACA CAAGAAAAGC AAATCAGTGT TGTAAGCTTA AAGTACAATT	60
TCAAAGGTCA TTACCAACAG CAGGGTTTTT TTTATACCTT AAAAACATTA TGCTACATAT	120
CATTGCCATT TTCATATTTT GGGGTTTGC TACTCTTATA CAATGGAATC AATGGAAATG	180
TCATCCAGCC AGATCTCGAG	200

(2) INFORMATION FOR SEQ ID NO:582:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:582:

GAATTCTGGCC	TTCATGGCCT	ACACAAATGT	TTGTTGAGTG	CTCATTGTAT	GTCTGGAGAC	60
CATTCTGTCT	TCTTCCCTAA	GAGTGTTCAT	GCTGTTGGAC	CAGGTGTTAT	GATTTGGCTC	120
TGGAGAAATAA	GGTATTTCGA	CATGGAGCAT	GTGAAAATA	TAGTGCCTAT	CTCCTGAAAG	180
GTCCAGGTGA	TGCAAAGATG	AATGAGACAT	GATTGGAGGT	TTTCTTCTG	TCTGAAATGC	240
AGACAGTTCT	GGTTGGGCA	GCTCTGTAAG	ATGCTGAACA	TGTGTCCTTC	CAAGAACCAA	300
GGATCAGAAA	GCAGACTCCA	G				321

(2) INFORMATION FOR SEQ ID NO:583:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:583:

GAATTCTGGCC	TTCATGGCCT	ACACCATTGA	CTTCTTCTAC	CGGCCGCATA	CCATCACCC	60
GCTCAGCTTC	ACCATCGTCA	GCCTCATGTA	CTTCGCCCTT	ACCAGGGATG	ACTCTGTTCC	120
AGAAGACAAAC	ATCTGGAGAG	GCATCCTCTC	TGTTATTTC	TTCTTTCTTA	TCATCAGTGT	180
GTTAGCTTTC	CCCAATGGTC	CGTTCACTCG	ACCTCATCCA	GCCTTATGGC	GAATGGTTT	240
TGGACTCACT	GTGCTCTACT	TCTGTTCT	GGTATTCCCA	CTCTTCCGTA	ATTCGAGCA	300
GGTTAAATCT	CTAATGTATT	GGCTAGATCC	AAATCTTCGA	TACGGCCACC	TCGAG	355

(2) INFORMATION FOR SEQ ID NO:584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:584:

GGAAACTTCT	AGAAATAATG	ACAAGGATTC	AAACTTATTG	TCAAATGAGT	CCAATGTCAG	60
ATTTTGGAAC	TCAACCCTAT	GAACAATGGG	CCATTCAAAT	GGAAAAAAAAG	GCTGCAAAG	120
AAGGAAATCG	CAAAGAACGT	GTTTGTGCAG	AACATTGAG	GAAGTACAAT	GAGGCCCTAC	180
AAATTAATGA	CACAATTCGA	ATGATAGATG	CGTATACTCA	TCTGAAACT	TTCTATAATG	240
AAGAGAAAGA	TAAGAAGTTT	GCAGTCATAG	AAGATGATAG	TGATGAGGGT	GGTGATGATG	300
AGTATTGTGA	TGGTGTGAA	GATGAGGATG	ATTTAAAGAA	ACCTTGAAA	CTGGATGAAA	360
CAGATAGACT	CGAG					374

(2) INFORMATION FOR SEQ ID NO:585:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 295 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:585:

GAATTCTGGCC TTCATGGCCT AGAGAAACTG AGAGGAAAGT AAAGATTGTG CTTACAAAGG	60
CTGTGTAGTG ATAAGACCTA AGGTTTCCTC TGAGATTCAA AATGGTATT ATTGTTCTT	120
TAATCCTTCT GATTATTCTT TTGGAAAAAA GGAAAGTAGA GGAAAGGAAG TAGAAAATA	180
ATATTCCTTA TACTTATTAT GTACCAGACA TGGTCTAAG TTCATTTAAA ACACTGCCTC	240
ATTTAATCTT TGCAACCAAT TTATACCCAT ACACATAAGG CCACAAAAGC TCGAG	295

(2) INFORMATION FOR SEQ ID NO:586:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:586:

GAATTCTGGCC TTCATGCCCTA AGGTAAGGGA AAGTGAGAAG CAGCAGGATA GTCAGCCTGA	60
AGAAAGTTATG GATGTCTAG AGATGGTTGA GAATGTCAA CATGTAATTG CTGACCAGGA	120
GGTAATGGAA ACTATCGAG TTGAAAGTGT AGAACCTTC GAAAATGAAG CTAGCAAAGA	180
ATTGGAACCA GAAATGGAAT TTGAAATTGA GCCAGATAAA GAATGTAAT CCCTTTCTCC	240
TGGGAAAGAG AATGTCAGTG CTTAGACAT GGAAAAGGAG TCTGAGGAAA AAGAAGAAAA	300
AGAATCTGAG CCCAACACAC TCGAG	325

(2) INFORMATION FOR SEQ ID NO:587:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 272 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:587:

GAATTCTGGCC TTCATGGCCT ACAAGGACGT TAAAGGCATT TTATTCCAGC GTCTTCTAGA	60
GAGCTTAGTG TATACAGATG AGGGTGTCCG CTGCTGCTT CCTTCGGAAT CCAGTGCTTC	120
CACAGAGATT AGCCTGTAGC TTATATTGAA CATTCTTCAC TGTCTGTTGT ATACCTACCG	180
TAGCTTTTA CCGTTCACTT CCCCTTCCAA CTATGTCCAG ATGTGCAGGC TCCTCCTCTC	240
TGGACTTTCT CCAAAGGCAC TGGACCCCTCG AG	272

(2) INFORMATION FOR SEQ ID NO:588:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 243 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:588:

GAATTCGGCC	TTCATGGCCT	AGCATCCCTG	AAACTGTGTA	ATTTGAGGA	TCCTTCTGGT	60
CTTAAAGCCA	ATTTAGAAGG	TGCTAATCTG	AAAGGTGTGG	ATATGGAAGG	AAGTCAGATG	120
ACAGGAATTA	ACCTGAGAGT	GGCTACCTTA	AAAATGCAA	AGTTGAAGAA	CTGTAACCTC	180
AGAGGAGCAA	CTCTGGCAGG	AACTGATTAA	GAGAATTGTG	ATCTGTCTGG	GTGTTAGCTC	240
GAG						243

(2) INFORMATION FOR SEQ ID NO:589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:589:

GAATTCGGCC	TTCATGGCCT	AAATTATACT	CCAAATGTTT	TATCTAAAAT	GCATTTCTG	60
TCTTTCTT	TTTACTCTTG	TCCTCACTTT	TAATGATCCA	TCGGCTGACA	GTGTCCTTAC	120
ATCCAAAATG	CAAAGCAGAC	AAATGGGCAT	ATCAGGGAAG	AACATGACAA	AAAGCACCAAG	180
CATCAGTGG	GACATGTGCT	CACTGGAGAA	GAATGATGGC	AGCCAGTCTG	ACACTGCAGT	240
GGGCACCTTG	GGCACCAAGTG	GCAGAAAGCG	GCGCTCTAGC	CTTGGTGCCA	AAATGGTAGC	300
TATCGTTGGT	CTGTCACGGA	AAAGTCGAG	TGCTTCTCAG	CTCAGCGGAC	TCGAG	355

(2) INFORMATION FOR SEQ ID NO:590:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:590:

GAATTCAAAT	GTTTCAGGTA	AATGTTGAAG	CTCGGGTGTAC	CGCGGGACAA	ATCCTGAGTC	60
ACCCCTGGGT	GTCAGATGAT	GCCTCCCAGG	AGAATAACAT	GCAAGCTGAG	GTGACAGGTA	120
AACTAAAACA	GCACTTAAC	AATGCGCTCC	CCAAACAGAA	CAGCACTACC	ACCGGGGTCT	180
CCGTCATCAT	GAACACGGCT	CTAGATAAGG	AGGGGCAGAT	TTTCTGCAGC	AAGCACTGTC	240
AAGACAGCGG	CAGGCCCTGGG	ATGGAGCCCA	TCTCTCCAGT	TCCTCCCTCA	GTGGAGGAGA	300
TCCCTGTGCC	TGGGGAAAGCA	GTCCCCGGCCC	CCACCCCTCC	GGAATCTCCC	ACCCCGCTCG	360
AG						362

(2) INFORMATION FOR SEQ ID NO:591:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:591:

GAATTCCGCC	TTCATGGCCT	ACTCAGTCTG	CACAACCTTT	TTGCTGTGTG	TCGGAATATG	60
TATAACTGGC	TACTGCAGAA	TCCCCAAAAT	GTCTGTGTTG	TCCACTGCTT	GGATGGACGG	120
CGGGCATCAT	CAATTCTGGT	TGGTGCATATG	TTCATTTCT	GTAATCTCTA	CTCTACTCCT	180
GGCCCAGCCA	TTCGATTGCT	ATATGCAAAG	CGACCAGGAA	TTGGACTTTC	ACCATCCCAT	240
AGGAGATACC	TGGGCTATAT	GTGTGACCTA	CTGGCAGACA	AGCCCTACCG	CCCTCGAG	298

(2) INFORMATION FOR SEQ ID NO:592:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:592:

GAATTCCGCC	TTCATGGCCT	ACCGTAAGCA	GATGAAGCTG	CTGCTGCTGC	TGCTGCTGCT	60
GAGCTGCGCC	CGCTGGCTCA	CCTACGTGCA	CCTGGGCCTG	GTGCGCCAGG	GACGCGCGCT	120
GCGCCAGGCC	CTGGGCTACG	GGCGAGATGG	TGAGAAGCTG	ACCACTGAGA	CCGACGGCCG	180
GGGGGTCCAC	GCTGCGCCAT	CCACACAGAG	GGCTGAGGAC	TCCAGTGAGA	GCCGTGAAGA	240
GGAGACCAGC	GCAGACATGC	TGGGCCAGA	TCCCAGGGAT	TACCTCGAG		289

(2) INFORMATION FOR SEQ ID NO:593:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:593:

GAGAGATGGT	GACTGAGGCA	GAAGCTAATA	GGGAAGATGA	TAGGAAAGAA	ATTTTACCCA	60
AGGAATTAGA	TTTAGCAAGA	GAGCGAAGGA	AAGCTGAGAG	GCCAAAAACA	TCTCTGAGGA	120
AAACTGACTC	TGAGAGAGAA	GAGGTGACAA	GGGCAAATGC	ACTCAAGGAT	GAAGATGCTT	180
TTAAAGAAGA	GCAAAAACTT	AAAGCGGAAG	AAGGGAAAC	AGAGACAGAA	GTAAGAGCTG	240
AGGAAGAGAC	AAAAGCTCCC	CCAAATGAAA	TGGGATCTGA	TGCTGAGAAC	GAAACACTCG	300
AG						302

(2) INFORMATION FOR SEQ ID NO:594:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:594:

GAATTCCGCC TTCATGGCCT AGGATATTTA AACCTCTATT ATTTAGACA AGACTGTCTA	60
GAACCTTAAGT TTGATCTGTC AGCCAGTACT CCCATTAAT TCAGTGTAGT TTCACCTTGAT	120
AGAACATCGAT ATGTTATCGA AATGTTAGCA GCAGCTTCAT CCTCCTTCTG ATTAAAGTAA	180
GTAGAAATGG GATGTTTGT TTAATAACAG CCATAGTGTG TGTTTAGACC ACAGCGGATG	240
TTGTAGACCA GGACCCCTCGA G	261

(2) INFORMATION FOR SEQ ID NO:595:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595:

GAATTCCGCC TTCATGGCCT AGGGGCTTT GTCAAGATAG AAGGGTATCA ACGGTTCTG	60
TACAGCACAG ATTATGACAG CGTCTTCTT AAGACTTATC ATTTGGAGCA CTGGCTCAGG	120
AGTCGAAATC ACCAATGGCT CATCCATCAA TCAACCAGAA GTGAAGACGA AAGCTCAA	180
GAAGAGAAATG TTTAAATTC ATCAAATGAA ACATATTGAA GAAATACTTG ATAAAATGAG	240
ATGCCTGAGA AAACGTTCTA CAGTGTCTT CTTGGGAGTT CTTGTCTATT TTCTCCTTTT	300
TATGAACCTG TACATTGAAG ATAGCTATGT TCTGGAAGGA GACAAACAAAC TTATAAGGGA	360
AACTCTCGAG	370

(2) INFORMATION FOR SEQ ID NO:596:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:596:

GAATTCCGCC TTCATGGCCT ACTAACGACT CATCTTGTGTT TTTAGTTTTT TTAATTAACA	60
ATCGTTCTGT TCACAATTT TAATTCCTT TCTTCCCCCT TCTCCGCAAA GCACTCAGGC	120
ATCGGACACG CTATGGTAAA CAAACTACAT TGTCTGGTAG ATATCATTCT TATTGTCTCT	180
TTTTTTGGGT TTGCCGTGTG TTGCCCCCTT TTTCCTCTCC AACCCCCCCC ATTCTCGAG	240

(2) INFORMATION FOR SEQ ID NO:597:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:597:

GAATTCCGGCT TCATGGCCTA GTGTATTGGT TGTGTGTGTT TTCTTTTG CATAAGAAAT	60
ATGTCATTT AGTCAGAGG CTCTTGCTTT ATCCGGATGA CGGAGGGTAC ACGGGGCGTC	120
CGCTCTAGTT CCCCCCGAAG GACGTATTGCG CTGAACCTGGG ACGACTCTAC TCCTCCCCCA	180
CAGGAGCCCA CGATTCAAA TCCTCTTGC TGCAACCTCT CGAG	224

(2) INFORMATION FOR SEQ ID NO:598:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:598:

GAATTCGGCC TTCATGGCCT AGATATTTA AAGGAGTGAT GACATCTTT TCCTATCATG	60
TGAAGAGGGG AAAGAGAAAG GAAAGGGCCC ATATTATTGT GTTCCCTGCCT GTGCCAGCTG	120
TTCTATATCT GTTGATCTCA TTTAGTCCTC ATGACAGTTC TATGAGGAGG GCACGTGTCAT	180
CATCACCAATT CCACAGATGC AGAAACTGTG GCTCACAGAG GATAAAGCTA GGTCACTCAC	240
ACAACCCCCCT GACTCCAGAG CCACCACTCG AG	272

(2) INFORMATION FOR SEQ ID NO:599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:599:

GAATTCGGCC TTCATGGCCT AGTAAGGGAG AAACTGAATG GTGATTTCAGA GCATAGAGAT	60
TATGTTTTTT TATGCACAGG GCTTCATCAG AAAATGGAA GGAATTGTCA ATAACAATAA	120
AATGTTCAAGC TAGATCAACT CAGTATATAG TATGTATTAT ACAATTATTC AAAATAGTGT	180
TTAACAGTAC TGATAATAACA TGAATAAAATG TTTTGTATA TTAAGTGAAGA AAGAGCTATA	240
TAAAATTATTC TAAGTTTATG GTATATGTAG ATTGTTGCAA AAATGTCTTC AATTCTTTAT	300
CCCTCCCTGT ATCCACACCT GTATCAGTTT TCTCGGGCA GCTGCCCTCGA G	351

(2) INFORMATION FOR SEQ ID NO:600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:600:

GAATTCGGCC TTCATGGCCT AGAATATTT TATCATCCC AAGCTAAAAC ATTAAAAAAT	60
TTAAAGTTTA TTCTTAGAGA TTGATCCAAC TTGCAATATCT AATCGAG	107

(2) INFORMATION FOR SEQ ID NO:601:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:601:

GGAAAATTAC TTAAACGTTG CACACAACGT TTCACAAAAT	CTTTTGTGAA AGAAGAAAAG	60
GAAATTCACT GTGTGAGTCT CAGCAGGAGT TAAGCTAATG	CAGCTTAACA TCATGCCGAC	120
AAAGAAGCGC TTATCTGCGG GCAGAGTGCC CCTGATTCTC	TTCCTGTGCC AGATGATTAG	180
TGCACTGGAA GTACCTCTTG ATCTGGTACA GCCTCCAACC	ATCACCCCGC TAAATCCCCT	240
AGAAGTCCCA CTCTAAACA CATCCGTATT ACTCGAG		277

(2) INFORMATION FOR SEQ ID NO:602:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:602:

GAATTCAAAT TAACATTTTA CCTTGAAATA GTGGGCTTCA GATTAATATC AACTTAGTTT	60
CAATAGCATA CGAAATTTGC TTCACATATAT TTCCATTTTC TCCCCGTCCT TTGTCCTATT	120
ATTACTATAC CAATTAGATC TCTACACAAT ATAGGCATAT CAACACATTT TGTAATTATT	180
TCCTTATCCA GTGTCCTTTT AATATAGATC TGTGAAGAAA AGTATTACAC AAATAGATCT	240
ATTCTGTTTT TTATAATTAT TTAATTACCT TTGGTGGTGC TGTTTATTT TCATGCATT	300
GAGTTACTGT CTAGTATTCA TTCATTTCTC TCTGAATCAC TCCCCGGTAT TGTCGAG	358

(2) INFORMATION FOR SEQ ID NO:603:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:603:

GAATTCGGCC TTCATGGCCT AGCCATCTTA TTTGAACTAT ATTTTCCTT CAAAGAAGCA	60
ATAGGTCTCA ACATAGTGTG GGTAGCATCA GGTGACAGAAA AGCAATTAT ATTTCAAAT	120
TTAAGTTAAT TATCTCGTG ATCCTATTTA TCCACAATT CTITCAGAAA AGACTGAAAA	180
AACACATTAT ATTCAAGGAGA TATAATGAAA TTATTGGAAG GCATCACTCG AG	232

(2) INFORMATION FOR SEQ ID NO:604:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:604:

GAATTCGGCC	TTCATGGCCT	AAATATTTTC	CATCTTCCTC	TCCAGTAAAC	ATTCTTTGT	60
CATCACAGTC	TGTCTCTGAC	ACCTTCGTTA	AAGAGGTCTT	AAAATGGAAA	TATGAAATGT	120
TTTTGAACTT	TGGTCAGTGT	GGGCCCGCTG	CAAGTCTTTC	TCAGTCCATC	TCAAGACCTG	180
TGCCTGTCAG	ATTCACAAT	TATGGAGATT	ATTTTAATGT	TTTTTCCT	TTGATGGTAT	240
TGAATACTT	TGAAACAGTG	GCACAAGCGG	CTCGAG			276

(2) INFORMATION FOR SEQ ID NO:605:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 450 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:605:

GAATTCGGCC	AAAGAGGCCT	AAAAATATAA	TTTAAAAATA	CATTGCGTAT	TTTCTAAAAC	60
AATAAATTAA	TAGTGTAAAT	ATTCTAGGG	TCAATCAAAA	TGAAGCTTCT	CCTTTGGGCC	120
TGCATTGAT	GTGTTGCTTT	TGCAAGGAAG	AGACGGTTCC	CCTTCATTGG	TGAGGATGAC	180
AATGACGATG	GTCACCCACT	TCATCCATCT	CTGAATATTTC	CTTATGGCAT	ACGGAATTAA	240
CCACCTCTC	TTTATTATCG	CCCAGTGAAT	ACAGTCCCCA	GTTACCTGG	GAATACTTAC	300
ACTGACACAG	GGTTACCTTC	GTATCCCTGG	ATTCTAACTT	CTCCCTGGATT	CCCCATGTC	360
TATCACATCC	GTGGTTTCCC	CTTAGCTACT	CAGTTGAATG	TTCCCTCTCT	CCCTCCTAGG	420
GGTTCCCGT	TTGTCCCTCC	TAATCTCGAG				450

(2) INFORMATION FOR SEQ ID NO:606:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 614 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:606:

GAATTCGGCC	AAAGAGGCCT	ATCAGGTGAT	TTAATAATAA	TTTAAAACCA	CTATAGAAC	60
TCCAGACCAA	AGGAAGTGGC	TTAATGATCC	TGAAGGGATT	TCTTCTGATG	GTAGCTTTG	120
TATTATCAAG	TAAGATTCTA	TTTTCACTG	TGTGTAAGCA	AGTTTTTTT	TAGTGTAGGA	180
GAAATACCTT	TCCATGTTT	AACTGCAAAA	CAAGATGTTA	AGGTATGCTT	CAAAAATTTT	240
GTAAATTGTT	TATTTAAC	TTATCTGTTT	GTAAATTGTA	ACTGATTAAG	AATTGTTGATA	300
GTTCACTTG	AATGCTCTT	AGAGGGTGGG	CTTTGTTGA	TGAGGGAGGG	GAAACTTTTT	360
TTTTTCTAT	AGACTTTTTT	CAGATAACAT	CTTCTGAGTC	ATAACCAGCC	TGGCACTATG	420
ATGGCCTAGA	TGCAAGAGAAA	ACAGCTCCTT	GGTGAATTGA	TAAGTAAAGG	CAGAAAAGAT	480
TATATGTCAT	ACCTCCATTG	GGGAATAAGC	ATAACCTGTA	GATTCTTACT	ACTGATGAGA	540
ACATTATCTG	CATATGCCAA	AAAAATTTA	AGCAAATGAA	AGCTACCAAT	TTAAAGTTAC	600
GGAATCACCT	CGAG					614

(2) INFORMATION FOR SEQ ID NO:607:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 293 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:607:

GCGAAGACCA	TCAAATGAAT	TGTCACAATA	CTCGAATAAT	GCAAGACACA	GAAAAGGATG	60
ATAACAATAA	TGACCAATAT	GACAATTACG	ATGAACGTGGT	GGCCAAGTCA	TTGTTAAACC	120
TCGGCAAAAT	CGCTGAGGAT	GCAGCCTACC	GGGCCAGGAC	TGAGTCAGAA	ATGAACAGCA	180
ATACCTCCAA	TAGTCTGAA	GACGATACTG	ACAAAAACGA	AAACCTGGGT	CGGAAAAGTG	240
AGTTGAGTTT	AGACTTAGAC	AGTGATGTTG	TTAGAGAAAC	AGTGGGGCTC	GAG	293

(2) INFORMATION FOR SEQ ID NO:608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:608:

GAATTCCGCC	TTCATGCTTA	CTCAGAAAGC	CACTGCCCA	AACAAGCCAC	CTGCATTATC	60
AAACACAGAG	AAGAGGAATC	ATTCCGCCCTT	TTGGGGACCA	GAGACTCAAA	TCATTCCTGT	120
GATGCCAGAT	AGTAGTTCCT	CAGGGAAAGAA	CAGAAAAGAG	GAAAGTTATA	TATTTGAGTC	180
AAAGGGTGAT	GGAGGGAGGAG	GGGAACACCC	AGCCCCAGAA	ACAGGTGCAG	TGCTACCCCT	240
GGCGCTGGGT	TTGGCTATCA	CTGCTCTGCT	GCTTCTCATG	GTTGCATGCC	GACTACGACT	300
GGTGATCCTC	GAG					313

(2) INFORMATION FOR SEQ ID NO:609:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:609:

GCCCATTCCG	GCCCCCATCT	CACCCAAGAT	CCCCCAGAGT	CCAGGAGCTG	GACGGGGACA	60
CCCTCAGCCC	TCATAACAGA	TTCCAAGGAG	AGGGCACCT	CTTGTCTTA	TCTTTGCC	120
TTGTGTCTGT	CTCACACACA	TCTGCTCCTC	AGCACGTGG	TGTGGGGAGG	GGATTGCTCC	180
TTAAACCCCA	GGTGGCTGAC	CCTCCCCACC	CAGTCCAGGA	CATTTTAGGA	AAAAAAAAT	240
GAAATGTGGG	GGGCTTCTCA	TCTCCCCAAG	ATCCTCTTCC	GTTCAAGCCAG	ATGTTTCTG	300
TATAAAATGTT	TGGATCTGCC	TGTTTATTTT	GGTGGGTGGT	CTTTCCCTCCC	TCCCCTACCA	360
CCCGTCCTCG	AG					372

(2) INFORMATION FOR SEQ ID NO:610:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:610:

GGAGCTAAAT TTAAGAAAATG CAACTAGCCA GGTGCTAAGA AGCTCAGTTA CACGTTTCTC 60
 AAAAGTTGGC TGTTAGTTCC ATGACTCAGA GTGCACTCAA ATCATTAA TTACTCGAG 119

(2) INFORMATION FOR SEQ ID NO:611:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:611:

GAATTCGGCC TTCATGGCCT AGGTCCGTGTT TGCCATTTG AGCTGCTATT AGTGTGAGAA 60
 GAAACTCAGA TGATACTAGC AGAAAACGAA AGAGGAAGAG GCTACAAGAG ATGGTAGATG 120
 CTGAACTTAA GGCAATTGAT AACCAATGGA TATAGAAAGA AAAGGAAATG AAAGGACAAA 180
 AATGGCTCTA AGTCTTCAAA CTTGACTGAT GAGGAAAATA TTCACATCAA GAATGGACTG 240
 AAGAAATAAG GAGGAGATGC TGGGTTAGGG TGAAAGGAGA TGAGCCCCAT TTTACATTGG 300
 AAAGCTCTAT GGAACAAACGG AAGTAGTGT AGCTTTATAT TCCAGTATGC CAAATTCTCA 360
 GCTCCAAGAC TCCACCACTG TGTGCTCTAC AGTATGTTT GTGATGTGCC TGAGTTTTGG 420
 TTTCTTATT TCAATTAGGG ACTCTTCATA CCAGGGTCAG GGGTTATGCT CGAG 474

(2) INFORMATION FOR SEQ ID NO:612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:612:

GAATTCCGCC TTCATGGCCT AGTTCCGTGCTCTTGAAAG AACAAAGTTGA TGCTTGTAAA 60
 GCTGTTTGA TTATTTTGTAG GCGCATGATA ATGGAGCTTA CAATGAATAA AAAGACATGG 120
 GAACAGATGT TGCAAAACTACTCAGGATA ACAGAACGCTG TCATGCAGAA GCCAAAGGAT 180
 AAACAAATAA AGGACTTGTGTT TGCCCAGAGC TTGGCAGGGT TACTATTTAG GACGCTCATG 240
 GTAGCTTGA TCCGAGCAAA CCTCTGTGTG TACATTTCTC GAG 283

(2) INFORMATION FOR SEQ ID NO:613:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:613:

GAATTCCGCA CGAGGGGCCG CGGTTTTTTT TTTTTTTTTT TTTCAGGTG CACATAAAGT 60
 TAGTTTATTA ATGACTATAT TTGAAAGCCA GCCATTTGT CCAATATTTA AATAACAAGC 120
 TGTTTAATAT TAAAGCAGAA AGTACTGCCA CATTGTGACA GAAGTACAGC TTTATCCATA 180
 AACCCCTCAC ACAATTATAC ATTAAATGCT ATTTTTATTT AAGCAAGGCA CCCCTACTTG 240
 TTCTAAAATA TGGGATGTAC TACACCATGT ATTACTCGAG 280

(2) INFORMATION FOR SEQ ID NO:614:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:614:

GAATTCTGGCC	AAAGAGGCCG	GAATTTGGCC	CTCGAAACCA	AGAATTCTGGC	ACGAGGGAAT	60
GAAATTAGCT	AACAGCCTTC	ACCTACAGAA	ACTTTGGGAT	CCAGACAGCA	TTTGAGCTGA	120
CGCCACGCC	TTCTCAGGCA	GCCCCCACAG	TGAAGGAGGA	GGATCTAGAA	GGGCCTGGCC	180
ATTTTCCTC	AATGTAGGGT	CCCTCTGATG	GGAATTCTTT	GTCTGGAGAC	CCGAGCTGAG	240
ACTTTGTCAG	ATTGGCATCT	CTGTCCTGTC	TCAATGCTGC	TTTCCATGCT	CCCTTTCTA	300
TCACAGACAT	CATAGCCTGA	AATCTTCCA	CACCAATAAC	TGCTTCCTAT	ACCCCTTAGC	360
CTTTCCTGAT	CTCATTGAGG	TTACCATTT	TCCTCCGTG	CTCGAG		406

(2) INFORMATION FOR SEQ ID NO:615:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:615:

GAATTCTGGCC	AAAGAGGCCG	GAATTTGGCC	CTCGAAGCCA	AGAATTCTGGC	ACGAGGCTTT	60
TTTAGGTAAT	TCTTTGTACT	CCTGCTGTCT	ACCTCTCCTC	ACACCCCCAGC	ACCCCCCATT	120
TTTCAAAACC	TTGGTATCTG	TTGGGTGAAC	AGTATAATCT	TTTCATCTGC	TTTTAGAATG	180
TGGGATATTT	CCAGTACCTA	CTTTTTTTTT	TTTTTTTTGC	TGAATCCAAA	GATATATAAA	240
TAAAATATAT	ATATTTATA	AAGATCAGAA	TGATATAAAG	GAGATACATG	TTTCTTCCTT	300
TAAAAAAATAA	ACGGAAGTTA	CATTGTTAAT	GTTCATATTA	TGATGCGAAT	TCTCTGGTTC	360
CTCCTCGAG						369

(2) INFORMATION FOR SEQ ID NO:616:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:616:

GAATTCTGGCC	TTCATGGCCT	AGGATGTCTG	AGGTCTTAAC	CTGCCAGTC	CTGAATTCT	60
GGGACTTCAA	CGACTCTCTC	TCTGCCAAT	GATGTGAGTC	TTTGGGATAGA	TTTATAGCGC	120
AAAGGGCTAC	TATCAATGTT	ATTAAGCATA	AATTATGACT	AGAGCCACAG	AATGATTTC	180
TCATTAATCC	AAAAAA	AAAAAGCAA	CCACTCTTT	ACTTTATGAT	GAGCACATAA	240
ACAGTTTTT	TTTCTTTTTA	TTTATCTACT	TTTACTTACT	TAAATTTAG	AGATGGGTC	300
TTGCTATGTT	GCCCAGACTA	GACTCAAAC	CCTGGGCTCA	AGTGATCCTC	TAGCCTCAGC	360
CTCCCAACTA	GCTGGGACTA	CAGGAAGGAG	CTACTGCACC	TGACTCAATT	TTTTTTTTTT	420

CTGAGATGGA GTCTCACTCT GTGACCCAGG CTTGTCTCGA G

461

(2) INFORMATION FOR SEQ ID NO:617:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 391 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:617:

GAATTCCGGCC TTCATGGCCT ACATCAATAA CAGCCAACT GAGACACATA ATGTTTCTA	60
CGTCCAAGAG GCTAAATGTG AGAACAGA ATTGAGAGA AATGTGGAGA ATACATCTTG	120
TTTCATGGTC CCTGGTGTTC TTCCCTGATAC TTTGAACACA GTCAGAATAA GAGTCAAAAC	180
AAATAAAGTTA TGCTATGAGG ATGACAAACT CTGGAGTAAT TGGAGCCAAG AAATGAGTAT	240
AGGTAAGAAG CGCAATTCCA CACTCTACAT ACCATGTTA CTCATTGTC CAGTCATCGT	300
CGCAGGTGCA ATCATAGTAC TCCCTGTTA CCTAAAAAGG CTCAAGATTAA TTATATTCCC	360
TCCAATTCTT GATCCTGGCA AGAATCTCGA G	391

(2) INFORMATION FOR SEQ ID NO:618:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 306 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:618:

GAATTCCGGCC TTCATGGCCT ACGTGAAGAC AAGATGAAGT TCACAATTGT CTTTGCTGGA	60
CTTCTTGGAG TCTTTCTAGC TCCTGCCCTA GCTAACTATA ATATCAACGT CAATGATGAC	120
AACAACAATG CTGGAAGTGC GCAGCAGTC GAGTGTCA ACAATGAACA CAATGTGGCC	180
AATGTTGACA ATAACAACCG ATGGGACTCC TGGAAATTCCA TCTGGGATTA TGGAAATGGC	240
TTTGCTGCAA CCAGACTCTT TCAAAAGAAG ACATGCATTG TGCACAAAAT GAGCAAGGAA	300
CTCGAG	306

(2) INFORMATION FOR SEQ ID NO:619:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 370 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:619:

GAATTCAAGG CCACGCCGGA GCTGTACCTT GGAAGGAGGA GCCAAAAATT ATGCTGAGAG	60
TGATCACAGT GAAGACGAGG ACAATGACAA CAATAGCCCC ACCGAGGAGG AGTCCACGAA	120
GAAGAATAAG AAGAAACCAC CGAAAAAAA GTCTCGTTAT GAAANGACAG ATACCGGTGA	180
GATAACATCC TACATCACTG AAGATGATGT GGTCTACAGA CCAGGAGACT GTGTGTATAT	240
CGAGAGTCGG AGGCCAAACA CACCGTATTG CATCTGTAGC ATTCAAGACT TCAAACCTGGT	300
AAGCGTTTT AATGTGCTGT TCACTCTGCT CTGATTCTC TCTTTTCCA GTTCCATTGG	360

CGCTCTCGAG

370

(2) INFORMATION FOR SEQ ID NO:620:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:620:

GAATTCCGCC TTCATGGCCT AAAAACCTTA CAACTAAAGC AAATAGACTT TTCAAGAATT	60
TAAATAGGAT TCCTTCCTT TAATCAATTA ATTATCCACT TTGTATGGT GTCAACCTGT	120
AATTCATGG TTTTGTGTGT GTGTGTGTGT GTGACAGAAA TTTACAAACA ATGTGATCTC	180
GAG	183

(2) INFORMATION FOR SEQ ID NO:621:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 565 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:621:

GAATTCCGCC TTCATGGCCT ACAACTAATT TGATCATATT AACAAAGAGGT TGGTTTTAA	60
ACCAAGCAGT ATAATATATAA ATACAGCCTT GGGTAGATCA TAGTCAAACT ATCCAAATGC	120
AACCTCAGCT TCAAAGATTG TAAAGTCTT TCTTTCCCCTT TTTCTCCCTT CCTTTTTTTT	180
TCCTCCAAT ATTATATTAC TACCTACCAT GTGCCAGGCA CTGTGATGGG CTATGAGGAT	240
GCAGTGGGGG ATAGGACAGA TGCCATCCCT GCCCTGAGGA GACTTGAGT TTATTGGAAA	300
AGATGGACAT CGTAAAATAT ACAATCATAC AAATAAAAAT TACATAAATA ATTCACTACT	360
TCAACTTGTG GGAGGTACAG CAGTTTATAA TAATAACATC CCTCCCACCT TCTTGAGAGA	420
GTCATTGGTT GCCCCACTTC TCTTCATGAA TGAGAGGACA TGATTAACC TATCATTTCA	480
GGTAGGAGTT TACTGTGGGA TGGAATATCAA TCTTCTATTA ATATGTTGT GCTCATGCTC	540
TCCATTTGC AATGGACGTC TCGAG	565

(2) INFORMATION FOR SEQ ID NO:622:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:622:

GAATTCCGCC TTCATGGCCT AAAATGAAAG CTATGTCTTA GAACCAATGA AAAGTGCAAC	60
CAACAGATAC AAACCTTCC CAGCGAAGAA GCTGAAAGC GTCCGGGGAT CATGTGGATC	120
ACATCACAC ACACCAAACC TCGCTGCAA AAATGTGTTT CCACCAACCT CTCAAGACATG	180
GGCAAGAAGG CATAAAAGAG AGACCCCTCAA GGCAACTAAG TATGTGGAGC TGGTGATCGT	240
GGCAGACAAAC CGAGAGTTTC AGAGGCAAGG AAAAGATCTG GAAAAAGTCT CGAG	294

(2) INFORMATION FOR SEQ ID NO:623:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 492 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:623:

GAATTCCGCC	TTCATGGCCT	AGCTTCTGGT	AATGGCGGAC	TAGATGATTT	AGAGCAACCC	60
ACCCATTGAA	AAGAACTACA	AAACGTCAGA	TCTCTAAAAG	GCTACAAAAT	TAATACAATT	120
GTGAGGAATT	GCTAGGTTAT	ACTACAAAGAG	ACAGAGAACCA	TCCAGAGAGG	TAAGCTAGG	180
ACTTAAAAC	ATATTTTTAT	TGAAGGTATC	TGTGGTTGAG	TAATAAGCCT	GTGCTAAACT	240
CGCTGGAAC	TATGGCACAT	TCAAGGCAC	ATAGTAACAG	AAAGTCAGAGC	CCAAGGCCA	300
TCAAAAGGGG	TGGAGTGT	TTCTGACAAAC	CATCACCCAT	AGTATGCTGG	GAACCGCAA	360
TGTTTATACC	TTCAGGGTAA	TTGTAATCAA	AAAATATACT	AGCCCTTACA	AAAGTCTTGTA	420
GCTTGGCTT	GCATCATCTG	GGTGGACTAG	TGAACGTAA	GTTCTGAACA	AATATTATGG	480
AGGCAACTCG	AG					492

(2) INFORMATION FOR SEQ ID NO:624:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 496 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:624:

GAATTCCGCC	TTCATGGCCT	ACTTCCCTGA	GCTGGGGTTT	CCCTGCTTGT	CCAGTTGTGA	60
GCTGTCCTCG	GTGTTACCGA	GGCTGTGCCT	AGAGAGTGG	GATTTTGAT	GAAAGGTGTG	120
CTCGCTCTCT	GCGTTCTATC	TTCTCTCTCC	TCCTTGTTC	TGCAAACCCAC	AAGATAAAGG	180
TAGTGGTGTG	TCTCGACCCC	ATCAGCCTCT	CACCCACTCC	CAGACACACA	CAAGTCTCA	240
AAAGTTTCAG	CTCCGTGTGT	GAGATGTGCA	GGTTTTTTCT	AGGGGGTAGG	GGGAGACTAA	300
AATCGAATAT	AACTTAAAT	GAAGTATAC	TTTTTATAAT	TTTTCTTTTT	AAAACTTGGT	360
GAATTATTT	CAGATACATA	TTTGTGTGTC	AAGGCAGATT	AGTTATTAG	CCACCAAAAA	420
AAAGTATTGT	GTACAATTG	GGGCCTCAAA	TTTGAATCTG	CCTCAAAAAA	AAGAAATATA	480
TCCTATGCAT	CTCGAG					496

(2) INFORMATION FOR SEQ ID NO:625:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 412 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:625:

GAATTCCGCC	TTCATGGCCT	ACAAAATTGA	TTATGACAAG	ATTGTCTACT	ATGAAGCAGG	60
GATTATTCTA	TGCTGTGTCC	TGGGGCTGCT	GTTTTATTATT	CTGATGCCCTC	TGGTGGGGTA	120
TTTCTTTGT	ATGTGTCGTT	GCTGTAACAA	ATGTGGTGG	GAAATGCACC	AGCGACAGAA	180

GGAAAATGGG CCCTTCCTGA GGAAATGCTT TCGAACATCTCC CTGTTGGTGA TTGTATAAT	240
AATAAGCATT GGCATCTTCT ATGGTTTTGT GGCAATCAC CAGGTAAGAA CCCGGATCAA	300
AAGGAGTCGG AACTGGCAG ATAGCAATT CAAGGACTTG CGAACTCTCT TGAATGAAAC	360
TCCAGAGCAA ATCAAATATA TATTGGCCA GTACAACACT ACCAAGCTCG AG	412

(2) INFORMATION FOR SEQ ID NO:626:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 372 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:626:

GAATTCCGCC TTCATGGCCT AGTTAGGTGG CTTTTAGTGT ATTGACAAAG TTGTGAACCC	60
ATTATCACAA TCTAACTTTA GAACATTTTT ATCAGCCTCC TTGCCCCCTA AAAAAACCCA	120
GTACTTTTA CCAATCCAGT CATTAAAC TTACTACATA TTTAATAGAT CGATAGATAG	180
ACAGGAGGAT GGACAGACTG AAGGAAGAAT GGATGATTAT GTATAAATAA ATGAAAAAAC	240
AAAAACTATC CCCAAATCAT AAGGGTATAC GCAATGCTT CCTGTGGCAA AAGATTCCGA	300
ACATGTACAG CAGATTTTT TTCAAATGTT CATAATTCTA AATTCCAAA ATGGTCTACA	360
CAACTTCTCG AG	372

(2) INFORMATION FOR SEQ ID NO:627:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 575 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:627:

GAATTCCGCC TTCATGGCCT AGGAGAAAGG AAGGAAAGCA TTACTGGGTT ACTATGCACT	60
TGGCAGTGT TTCTTGGCTT TTATCATT TGAACCTTAT GGAATACATC GGCAGCCAAA	120
ACGCCCTCCCG GGGAAAGGCGC CAGCGAAGAA TGCACTCTAA CGTTAGTCGA GGCTGCCAAG	180
GAGGCTGTGC AACATGCTCA GATTACAATG GATGTTTGTG ATGTAAGCCC AGACTATTTT	240
TTGCTCTCGA AAGAATTGGC ATGAAGCAGA TTGGAGTATG TCTCTCTTCA TGTCCAAGTG	300
GATATTATGG AACTCGATAT CCAGATATAA ATAAGTGTAC AAAATGCAA GCTGACTGTG	360
ATACCTGTTT CAACAAAAAT TTCTGCACAA AATGTAAGAG TGGATTTAC TTACACCTTG	420
GAAAGTGCCT TGACAATTGC CCAGAAGGGT TGGAAAGCCAA CAACCATACT ATGGAGTGTG	480
TCAGTATTGT GCACTGTGAG GTCAGTGAAT GGAATCCTTG GAGTCCATGC ACGAAGAAGG	540
GAAAACATG TGGCTTCAAAGAGGGGATC TCGAG	575

(2) INFORMATION FOR SEQ ID NO:628:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 457 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:628:

GAATTCCGCC	TTCATGGCCT	AACAGGGTCT	TGCTCTGTCA	CCCGGGATGG	AGTAGTGTGG	60
CGCAATCACA	GCTCACTGCA	GACTCAGCCT	CCCAGGATCA	AGCAATTCTC	CCACCTCAGC	120
CTCCCAAGTA	GCTGGGACCA	CAGGTGCACA	CCATCATGCC	CAGCTAATT	TTGTATTTT	180
TTGTAAAGAC	AGGTTTCACT	GTGTTACCA	GGCTGATCTC	GAACTCCCCT	ACTCAAGCAA	240
CTCCCCACCT	CAGCCTCCCA	AACTGCTGGG	ATTACAGACG	TGAGCCACAG	CGCCGGCCCC	300
CAAAATCTAT	TTTAAATGTA	AAGAAACCCA	AAAGTAACAG	TTTTGTAAAA	GAAAATTTCAC	360
GTACTGTTT	GTAGTAAATT	CTAAACACTG	TGTATCTTG	TGTCTAGTTA	AATCCTAGGC	420
TTACAGCTAA	AATTCAATGA	GAAGGCAAGT	ACTCGAG			457

(2) INFORMATION FOR SEQ ID NO:629:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:629:

GAATTCCGCC	TTCATGGCCT	AGAAAAGCTAT	CATTTATTGA	GAGTTAATTG	TATATTAAGT	60
ACCATGCTAA	GTGCTTGT	TGTATTATTT	ATCTTATAA	AAATCCTATG	AAATGAATAC	120
TGTTATTTTC	CCCCATTATA	CAGATGAAGA	TAGAGAAAGG	AAGAAAAGGG	AGGGAAAGAG	180
GAATACCATT	TCACTGAGCA	ATTTTACTGA	AATATTTAT	GGGCAATTG	TGGGTTTTGT	240
TTGTTTGCTT	GTTTTGT	TTTGTGTT	TTTTTTTTG	AGACAGAGTC	TCACTTGTC	300
GCCCAAGGCTG	GATCTCGAG					319

(2) INFORMATION FOR SEQ ID NO:630:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 557 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:630:

ACGGTGAAAC	CCTGTCGT	CTAAAAAATAC	AAAAAAATTAG	CGGGGCATGG	TGGTGGGCAA	60
CTGTAGTCCC	AGCTACTCGG	GAGGCTGAGG	CAGGAGAATG	GCATGAACCC	AGGAGGCGGA	120
GCTTGCAGTG	AGCCGAGATC	ACGTCACTAC	ACTCCAGCCT	GGGGCACAGA	GCGAGACTCC	180
GTCTCAAAAAA	AAGAAAAAAC	CAAGACAAAA	CCAAAAATAA	CTTGTCTGT	TAAGTACAAT	240
ATCTGTGTT	CTCAGGGACA	GTTCCTATTG	ACCATTGTT	TTCTTGTGCA	TAGACTATCC	300
TTTCTTTTT	TTGTACATCT	TGTAATT	TTTTTATTAA	AACTGGAATT	TTAAAAATAA	360
TGCACTGTGG	CAA	CTACT	GCTTGATTTG	GCTCAAGGT	ATATTATTAA	420
TAACAAACCA	ATATTTGGGT	TCTCTATTCT	ATAGTTTAG	CATTTGAAT	GCAACAACTG	480
TCTTATTACAC	CATTTAATTC	TCAGTACTAC	CGTTCTAGT	ACACAATATG	CACTTAATGA	540
ATATGAGGGT	CCTCGAG					557

(2) INFORMATION FOR SEQ ID NO:631:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:631:

GAATTGGCC	TTCATGGCCT	AGACCGTGCC	AGGTATTGAG	ASCGACCCCTC	ACATTCCCTAC	60
AGTGCCTCTG	GTGGCATCTT	AATGAAACTT	TATTCTCTCC	CCTTAAATGA	GAAGAAATAG	120
CTAGTTGTCA	TCCTTCTGA	ACCGATTTG	TCTTCAAAG	GTAGTAGTGT	ACCAGGCCCTG	180
CTATTTGCA	AAACGGTCTC	CACCAAAATC	GAATTACCTG	CCTCGCGGGG	CAGGCGTGT	240
GACCAAGGTGG	ACTCTAGAAG	TAGGTGGTTT	GCTTGGTTTC	TTTTCTTTT	AAAGTTCCC	300
TTTCTCTTC	TCTTTCTG	TGTTTTTTT	TTTTTTTTT	TTTTTCAAT	ATAGAAACTG	360
TCCCTAACAGAG	AGGAAACCTT	TCTGGCCATG	TTATTCAGG	AATCTTTGT	CCCCTAACAGTT	420
TGACCTTGTT	CTTCTGTC	CCCTTTACTC	TTGCATCTCG	AG		462

(2) INFORMATION FOR SEQ ID NO:632:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:632:

GAATTGGCC	TTCATGGCCT	ACATAAAATC	AGTTGACTAT	TGTGCAACAT	AGAATTATTG	60
TTTGTGTGAA	ATTACCGCTG	AAGGACCTTG	CCTACATTCA	AGGGTCTATT	TTTATTTTTC	120
CAGGTATTCT	TTCACATTAG	TGACATTATA	GTCTAGTACA	ACTGCTTGAT	AATTTGGAGA	180
AACTAACATT	AATTTAGAT	ACTGATTGAT	AAAATTGGC	CTGCCAAATG	CATTTAAAAA	240
ATAATTCTAG	GATTTATCTA	TGCTCATTTC	TAGTATACTT	CATGATATAT	AAGACATCTT	300
TCTTTGTCA	TATCAGTTCT	TCAGATACTA	AGACAGAGGT	CCTCGAG		347

(2) INFORMATION FOR SEQ ID NO:633:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:633:

GAATTGGCC	TTCATGGCCT	AGGTGGTGCA	ATAATTATAA	ATGTTGCCAG	TCAATGCCAA	60
CCAGTGTCTG	ATTGGCTTCC	TGTGCATGTC	CAATTCCCTC	TGTGACACTG	TGTTGGTGCC	120
AGAGCTTCTG	AATCTTCTT	AATCGCTCTT	TGCTATAATG	TAAGGATTT	CCCCGTCTGA	180
GTCCCTGGTC	GGTCTCCCCA	TAATCATCAA	GGTAAGGAGG	AGAATAAAAA	CAGCCTTTGG	240
TTTTGCCAGC	TAAAAATAGC	ACCTGACATT	CCCGTACTCT	CAGGAAGATG	CCCACTCCAG	300
AGCCACAGGA	GTAGGTGTGA	GCTGTGCAGG	CTCCTACATC	CTCCCTTCC	AGTTCACTCT	360
GGCAGCAGTA	ACTCTGGGAG	CACAGCAGAG	ATCCGCACAC	AAGGCACAGA	GTTGGGGCTC	420
TGCTCTTATC	ACCACCTGAT	TTCGGGCACC	TCGAG			455

(2) INFORMATION FOR SEQ ID NO:634:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:

GCATGAAGGC CGGCCTTCAT GGCCTACAGG CTATGTACTG TATGATTCCA AATATGACAT	60
TCTGGAAAAG GCAAAACCAG GGACACAGTG AAAAGATCAG GGTTTGAGAG GGGAAAAAAG	120
GAGGGATGAG TAATCAGAAC ATACAAGATT TTCTTAAGGC AGTGGAAACCG CTCTGTATAA	180
TACCATATA GTGGATACTGT GTCATTATGC ATTCACTCCAA ACTCTTAGAA TGTAACAGCAC	240
AAATAGTGA CTGTAATGTA AATGCAGTGT GTAGGTGTTT ATACAAAAAA ACAGATGGAA	300
AGATTTGTA CATACTCTA TGTGAAAATG TATTTTTTA TTAAGAGCAA AAATATGCTT	360
ATTCAAAATT TCCACGTACG ACTTTTCAA AAAGACACGA TCCACTGAAA TAACCCCTCCA	420
AAAGAATTTC TATAATCTAT AGCAGGTGTA CATGTTGTTA ATCAAGTGCT TAATGTTACT	480
CGAG	484

(2) INFORMATION FOR SEQ ID NO:635:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:635:

GAATTCCGCC TTCATGGCCT ACCCCCACCAAG AGGACAGACG TTGAAAGATA CCACGTCCAG	60
TTCTTCAGCA GACTCAACTA TCATGGACAT TCAGGTCCCG ACACGAGCCC CAGATGCAGT	120
CTACACAGAA CTCCAGCCCC CCTCTCCAAC CCCAACCTGG CCTGCTGATG AAACACCCACA	180
ACCCCCAGACC CAGACCCAGC AACTGGAAGG AACGGATGGG CCTCTAGTGA CAGATCCAGA	240
GACACACAAG AGCACCAAG CAGCTCATCC CACTGATGAC ACCACGACGC TCTCTGAGAG	300
ACCATCCCCA AGCACAGACG TCCAGACAGA CCCCCAGACC CTCAAGCCAT CTGGTTTCA	360
TGAGGATGAC CCCTTCCTCT ATGATGAACA CACCCCTCCGG AAACGGGGGC TGTTGGTCGC	420
AGCTGTGCTG TTCATCACAG GCATCATCAT CCTCACCACT GGCAAGTGCA GGCAGCAGTC	480
TCTCGAG	487

(2) INFORMATION FOR SEQ ID NO:636:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:636:

GAATTCCGCC TTCATGGCCT AATTTTATTT AAATTTTAT ATTATATATAT TTTATTTAAA	60
ATTTTCATGA AATGGCCAAG CAGGGTTAA TATAAAATGG AAACAGGGTT TATCTCAGAA	120
ATTTGGTGGC TAAATTCCCT GTATCCCGTC TTATCTAGGG ATGGTGTGTTG TTTCAAGGTT	180
CTACCTTGAG AGGAGCCTGT CATTTCCTTT TTGTTGTGCT GCTTGCCTA GTTGACATCT	240
TGGCTTATG TGCTCCTGTT GAATGCATTG GGAAATTTTC TTCTTCTTT CTATGTCCTG	300
AAATAGCTTA TATAAGAGGG AAACTCTCGA G	331

(2) INFORMATION FOR SEQ ID NO:637:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 625 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:637:

GAATTGGCC	TTCATGGCCT	ACAAAATAC	TTTCATTGT	TTTGCTATT	CTAGTTCTC	60
ATTTTTATT	GCACTTGCAA	TCATTTAGG	AATATCCTCA	AAATATGCTC	CAGATGAAAA	120
TTGCCAGAT	CAAAATCCTC	GTCTCAGGAA	TTGGGATCCA	GGACAAGATT	CTGCAAAGCA	180
AGTTGTTATC	AAGGAGGGGG	ATATGCTCCG	TCTGACCTCA	GACGCCACCG	TGCAATTCTAT	240
AGTCATTCA	GATGGAGGAC	TGCTTGTATT	TGGGGACAAT	AAAGATGGAT	CCAGAAATAT	300
TACTTTGAGG	ACTCATTACA	TCCTGATCCA	GGATGGTGGG	GCGCTTCATA	TTGGACCAGA	360
AAAATGCCG	TATAAATCCA	AAGCAGACAAT	TACCTGTAT	GGCAAGTCAG	ATGAAGGTGA	420
AAGTATGCCA	ACATTTGGCA	AAAAGTTAT	TGGTGTGAA	GCTGGCGGG	CACTGGAGTT	480
ACATGGGGCA	CGGAAGGCAT	CGTGGACGT	GTTGGCAAGG	ACCCCTGAATT	CCTCAGGCTT	540
GCCGTTGGG	TCTCTATACCT	TTGAAAAGGA	CTTTTCCCGG	GGCCTCAATG	TGAGGGTCAT	600
TGACCAAGAC	ACGGACGCTC	TCGAG				625

(2) INFORMATION FOR SEQ ID NO:638:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:638:

GAATTGGCC	TTCATGGCCT	AGAGAACTTT	TTGAGGGCTT	TTTTTTTTCC	CCTTTTAAGC	60
TATTTTGAT	GTAGACTTAA	TTTTTCTAAT	TTTGCCACTT	CTGGCAATCT	GAATCATTA	120
AAAAGGACAC	AATTCAAATT	TATGTTAAAG	GTCATAAATT	TTGCCAGGA	CTCAATATTT	180
TCTCATT	CCCCAAAATAA	AATCTTATT	ATGCATTATA	GCGACTTGGT	TTTCACTTA	240
TCTTGATT	TAGCTTTAA	GAGGCAGAAA	GAATCCTTT	TATAAGGACA	GTCCTCAAGTG	300
TACACACAGA	TTAAATATTA	CAAAATATAG	TTGCAAAATAA	AACTTCAAA	ATGTGGGATT	360
ATAGGAAGCA	AAAGAGAAC	AACCAAAGCA	TCAACAAATT	TACCTTTTG	TTTTTTTAA	420
AGATTTTCT	TATTCCTTA	GCTGCTTTG	CATTAGCATT	AAATAACATT	CTTATTGGAG	480
TGGTATGTGC	ATGGCCCAAG	CTCGAG				506

(2) INFORMATION FOR SEQ ID NO:639:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 388 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:639:

GAATTGGCC	TTCATGGCCT	ACTCCAGCTT	TATTATCTCA	GCTACCCTCA	AACTATATTA	60
CATCAAATT	TCATCATTAC	TCTCCTGCAC	AGTAACCTTC	TTTCTGCTCC	ACTAAGAAGC	120
TTACTCCCCT	CCTGTTTATT	CTCTATATCG	TAGCTGGACT	AACTTTTCA	AAAGTCAAAG	180
CCAATCACAA	TACCCACCTGC	TTAAAATCCA	TCAGTGGCTA	ACTTTTCAATT	CTAGGACGAA	240
AAGAAAATTC	TATAACATGA	CTTCAAAGGC	TCTGCATGTC	CTTCTATTTC	TCTTGTCCCTC	300

TCTAGTCTTT TCTTTGATGG TCTCCACTCC AGCCCTACTG GCTTCTTTCT GGAATCAATG	360
TCACCCACAA CCCGTACGC CACTCGAG	393

(2) INFORMATION FOR SEQ ID NO:640:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:640:

GAATTCCGCC TTCATGGCCT ACTCCGCTCT GGCCAGAAG GAGGCCAAGA AGGACGAGCC	60
CAAGAGCGGC GAGGAGGCC TCATCATCCC CCCCGACGCC GTCCGGTGG ACTGCAAGGA	120
CCCAGATGAT GTGGTACAG TTGGCCAAAG AAGAGCCTGG TGTTGGTGCA TGTCCTTGG	180
ACTAGCATTG ATGCTTGAG TGTTATTCT AGGAGGAGCA TACTGTACA AATATTTTGC	240
ACTTCAACCA GATGACGTGT ACTACTGTGG AATAAAGTAC ATCAAAGATG ATGTCATCTT	300
AAATGAGCCC TCTGCAGATG CCCCAGCTGC TCTCTACCAG ACAATTGAAG AAAATATTAA	360
AATCTTGAA GAAGAACAGGC TCGAG	385

(2) INFORMATION FOR SEQ ID NO:641:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:641:

GAATTCCGCC TTCATGGCCT AGCAAGGAGA ACTATTGTCT TATGATCACG TTTGCCATCT	60
TTCTGTCTCT TATCATGTTG GTGGAGGTGG CGCGAGCCAT TGCTGGCTAT GTGTTTAGAG	120
ATAAGGTGAT GTCAGAGTTT AATAACAACT TCCGGCAGCA GATGGAGAAT TACCGAAAA	180
ACAACCACAC TGCTTCGATC CTGGACAGGA TGCAAGCAGA TTTTAAGTGC TGCGGGCTG	240
CTAACTACAC AGATTGGGAG AAAATCCCTT CCATGTCGAA GAACCGAGTC CCCGACTCCT	300
GCTGCATTAA TGTTACTGTG GGCTGTGGGA TTAATTCAA CGAGAAGGCG ATCCATAAGG	360
AGGGCTGTGT GGAGAAGATT GGGGGCTCG AG	392

(2) INFORMATION FOR SEQ ID NO:642:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:642:

GAGTTGAAGT GCCAAAAAA TTATAACACT CTCCACTTT CATATCTTGA TTTTAATTTC	60
TTCCCTTACT TGTATTTAT TTCTGAGTGG CTAATGGATC TTAGTCTAAG AACTGGAGGT	120
GGAGAACTCG AG	132

(2) INFORMATION FOR SEQ ID NO:643:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:643:

GCACAAAGAC GCATTCATC TGAGTTCCC TGAAAGCTAG AATAAGTTG CTGGTGTCA	60
CTGGGATCCT GTCTTCTATA GCTTTGTATC AAGCAAAC TC AGCATTTGTGT CTTGAATGCA	120
TGTCATGTGC AGCCTGCGTT TATGTGCGAC TGAGCACTTG GGTGGGGACA TCTTAAGGCT	180
GTTTATATTG CTTTTTCATG TGTTGTTGTT GTTGTGTTT TTGTTGTTT GGAGAGAGTC	240
TCGCCAAAG CTCGAG	256

(2) INFORMATION FOR SEQ ID NO:644:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:644:

GTGCTCGCAG CCNTGGTGGC CTGGCGCTCG GCGTNCCCTG TCTGCCCTCG TTTCTCCTTG	60
GCCACCCCTGG TCCAGCGAGG ATCTGGGGAC TTTGATGATT TTAACCTGGA GGATGCAGTG	120
AAAGAAAATT CCTCAGTAAA GCAGCCATGG GACCACACCA CCACCAACCA ACCAACATAGG	180
CCAGGAACCA CCAGAGCTCC GGCAAAACCT CCAGGTAGTG GATTGGACTT GGCTGATGCT	240
TTGGATGATC AAAGATGATGG CGCGAGGAAA CGGGGTATAG GAGGAAGAGA GAGATGGAAC	300
CATGTAACCA CCACGACCAA GAGGCCAGTA ACCACCAAGAG CTCCAGCAA TACTTTAGGA	360
AATGATTTG ACTTGGCTGA TGCCCTGGAT GATCGAAATG ATCGAGATGA TGGCCGCAGG	420
AAACCAATTG CTGGAGGATG GCTCGAG	447

(2) INFORMATION FOR SEQ ID NO:645:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:645:

GCTCAGCAAC ATTTAGGAA CAACATTGGT GAGTATATGA GAATAGCCGT GACCTCCATA	60
TTTCATCAGC CGGGTTTCG TATGTATGTC ATGTGCTACC AGAATTGCGAT CTTCACAGCC	120
CTCTTCCACC AGGAGACGCA CCTGTGAAA AATGTTAACT CATTAGATGT CATTGTCCTT	180
TCATTTCGC TTTCAGGAT GCTTCAACT TTTTACTCAT TAACCTATTG TGTTGTCGT	240
AAAGATACTG ACTTCTACTG TGGCGTGTGT ACTGAGAGAC TCGAG	285

(2) INFORMATION FOR SEQ ID NO:646:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 257 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:646:

GGAGATTGAGAAGAATTG AATGAAAGGA TGATTCAAGC AATTGATGGG ATTAATGCAC	60
AGAACATG GCTCAAGTCT GAAGACATTG AGAGAACTC ACTGTTTTC TATAACAAAG	120
TACTAGAAAA AGAGTACCGG GCCACGGCAC TGCCAGCGTT CAAGTATTAT GTGACTTGTC	180
CCTGTCTCAT ATTCTTCTGC ATCTTCATTG TGCAGATTCT CGTGCTGCCA AAAACGTCTG	240
TCCCCGGCTA TCTCGAG	257

(2) INFORMATION FOR SEQ ID NO:647:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 296 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:647:

GGGGCAGCAG TAAAATCCAG GCCCGAATGG AACAGCAGCC CACTCGTCCT CCACAGACGT	60
CACAGCCACC ACCACCTCCA CCACCTATGC CATTCAAGGC TCCAACGAAG CCTCCAGTTG	120
GACCCAAAC TTCTCCCTTG AAAGATAACC CGTCACCTGA ACCTCAGTTG GATGACATCA	180
AAAGAGAGCT GAGGGCTGAA GTTGACATTA TTGAACAAAT GAGCAGCAGC AGTGGGAGCA	240
GCTCTTCAGA CTCTGAGAGC TCTTCGGGAA GTGATGACGA TAGCTCCAGA CTCGAG	296

(2) INFORMATION FOR SEQ ID NO:648:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 324 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:648:

GTGCANATGT ACGGTGACCA CCTGGCCCTT GACCGGGCGG CTCGAACCTG GCGGCCCTGG	60
GACCAAGCGTC TTCTTCCTCA ACAGCCCCTT CCCCAAGATG TCCAGCCACT CTTCTGGGGC	120
CGGGGCTGGG GCGGGCTCGG GCTCCATGGC AGCAAGGAAC TCTCCGGCCA GGGCCCCAGG	180
CTGCTCANCC TCCTCCGCGG GGGTTGTCC CATGTCCTCC AGCGGTGGCA GCTCACTCAG	240
GTCATCCTCT TCCTCCTCTT CCTCCTCCTC TTCCCTCCTCA CCCTCTGCAT CCTCAACCCC	300
ATCCAGTACC TCGAAGTCCT CGAG	324

(2) INFORMATION FOR SEQ ID NO:649:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 309 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:649:

GAATTCGGCC TTCATGGCCT ACTTCCTGAT ACAGATAACAT TTACTACAGA AAATTCCTT	60
TATAGGTGA AATTCTGTT TACAACAGGC GAGTCGAAAA ATAATAAGAA CAAAAGGAAA	120
AAAAGCACTC ATACTTATT TTAGGCAGTT GAGGGTAGC TGAATAAGTT ATCCCTGTGTT	180
GTTTGGTTCT GTTACTTATA GCTCAAAGTC ATCAATATGC CAGGGTGGA TGTTTGGGA	240
TGGTGCATTC TTGTCTTTG CAGTCATTTA TCAGGGTGCG GTTTCCTAAA TTCTAACACA	300
GACCTCGAG	309

(2) INFORMATION FOR SEQ ID NO:650:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:650:

GGTGACGCC GCTTCACATC TCTAATGAAC ACCCTCATGA CGTCGCTACC AGCACTAGTG	60
CAGCAACAGG GAAGGCTGCT TCTGGCTGCT AATGTGGCA CCCTGGGCT CCTCATGGCC	120
CGGCTCTTA GCACCTCTCC AGCTCTTCAG GGAACACCAAG CATCCCGAGG GTTCTTCGCA	180
GCTGCCATCC TCTTCCTATC ACAGTCCCAC GTGGCGGGG CCACCCCGGG CTCAAGACAG	240
GCAGTGCTAG CCCTGTCCCC TGAGTATGAG GGCACTCTGG CCGACCTGCA GGAGCTCTGG	300
TTCCTCGAG	309

(2) INFORMATION FOR SEQ ID NO:651:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:651:

GCAAGGGCAG GCGGGTCCCC CAGTCCCCGCC ATTACGGGTT GTCAGACCGT CTGGGTGTGG	60
CAGGGCTCCC AAGGGCAGGC GGGTCCCCCA GTCCCGCCAT TACGGGTTGT CAGACCGTCT	120
GCGTGTGGCA TTTTTGGCT TATAAGCTTC ACCCACTCAC CCCCAACCCA CACCCACAT	180
CCCCCTGCGC GCAGCCCCCTC AACCTAAGAA GGCCAGAGCA TATTATTTT CGGAGGGAGC	240
AGATTACTTC TCCCAAGAGAA AGGAAAATCT TGGAAAAGAT TTAAAAACAC AAATCTAAGC	300
CTTGACGGTT TTTTTTCCC TTTTGACCC CTTCCCATCT CTTCAAGATT TATTCCCATG	360
GCTTTTTTTT TTCTTGTGCG TGTTCTCGAG	390

(2) INFORMATION FOR SEQ ID NO:652:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:652:

GAATTCGGCC TTCACTGGCCT ACCAAATTCC CTGCCTGTGC CTGCTGGGAC CAGACTCCGC	60
TGTCACTGAGG GTGACATCCG CCACCTGTGC TCTTCTGCTG GCTCTGATCT GCAGCGTCCA	120
GCTGGGGGAT GCCTGCCTGG ATATCGATAA ACTGCTTGCG AATGTTGTGT TTGATGTGTC	180
CCAAGACCTC CTGAAGGAGG AGCTTGCTCC TTACAACCCC AGTCCCTGA CAGAGGAGTC	240
CTTCCTCAAT GTCCAGCAAT GCTTTGCCAA TGTCCCTCGAC	280

(2) INFORMATION FOR SEQ ID NO:653:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:653:

GGTGTGTTGGC CACAGTTCCG GACCTATGGT AGAAAAATAC TCAGTAGCTA CCCAGATTGT	60
AATGGGTGGC GTTACTGGCT GGTGTGCAGG ATTTCTGTC CAGAAAGTTG GAAAACTTGC	120
AGCAACTGCA GTAGGTGGTG GCTTCTTCT TCTTCAGATT GCTAGTCATA GTGGCTATGT	180
GCAGATTGAC TGGAAAGAGAG TTGAAAAGA TGTAAATAAA GCAAAAGAC AGATTAAGAA	240
ACGAGCTCTC GAG	253

(2) INFORMATION FOR SEQ ID NO:654:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:654:

GAATTCGGCC TTCACTGGCCT AATTGAATT TAGACCTGCC TCGGCCTCCC AAAGTGCTGG	60
GATTACAGGG GTGAGCCACC GCACCCAGCC TGTGAATAC TATTTTATG GTAAGCTAGA	120
ATTTTAAAC TATTTCTTGC AAGTTAGGA TTAAATGAAT TACATTATGT AAAATTACAT	180
CTTTGTCTGT ATTACGTATT TGTATACAGT TGAATAGTT TGGAACACG TACCTTAGTG	240
CTTTACATTG ATTGGCTCAT TAATTTATA TTTTGACTAA TAATCATCTA ATTTTATTAT	300
TGTACAATTG AGTCTTAAAT TATGTTATGA TGTGAAATG GTAGCTTCT TGAGTGTATT	360
TATTTTGTGTA GTAGTGGGCA ATGTAATTAT CACACATAAA ATGAACGTG AGACTTTGA	420
GCCTGAAATA TTATTCTAT TATAATGCTC CTCGAG	456

(2) INFORMATION FOR SEQ ID NO:655:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:655:

GAATTCCGCC	TTCATGGCCT	AGTATATACA	TGCATTTAAT	TGTGATTTA	TCACCTTTCC	60
CATTTCTTC	CCCACAAGCT	GGCATTTCA	TAGTTGCTT	TGAATAATGG	TTTGGTTAC	120
CTGGGAAGGC	AGGCCAGAA	CCCATTTCCT	TGACTTGCA	TTCCGGGCTG	TGTTCACATG	180
ACTGCTGTCT	AGCTGATGCA	TTTTACAT	TTGTCAACT	TGGTAGAAA	CAGGCTCTCA	240
GGAGTATTCT	CTAACCTGAT	ATTTCTAAA	AAAGATATGTT	GATTCAACTT	TGTTTAGCAT	300
CCTACTTTCT	AGATTGTGGG	GCTCATTTG	CCAGGGCCAA	GCTACCAGAA	AAGTAGAAGT	360
GGAGATTACC	TGGTATGTAT	CTCTCTGGGT	GCCCCAGTTA	GAGCTGCCAC	ACCTCAGGAA	420
AAAGATGAGG	CATAACGACC	TTGAATGTAA	TTGGAGTAAG	TGACAAAAATA	AGAACTACCC	480
GGGAAACTC	GAG					493

(2) INFORMATION FOR SEQ ID NO:656:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:656:

GAATTCCGCC	TTCATGGCCT	ACTTGGCCTT	TGTTTGTGTT	TGCCTTGTC	AGTCTCCTGC	60
CTCTGGATGG	GTITCTGTT	GTTCACAAAC	TGTCTGGGC	TGTGACCCAT	GGAGACAGTG	120
TCCTGGCTG	CCTCTAGCCT	GATCTGGTTA	GAATAAGCCC	CTCTCCTTG	CATCGCTCTC	180
CAACCTGACA	TTTGGAGCAT	CAAAACAAA	TCATGACATT	CCCAAGTAAA	GATAGAAACC	240
ACCGTCTCCA	CTCCACTCGA	G				261

(2) INFORMATION FOR SEQ ID NO:657:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:657:

GAATTCCGCC	TTCATGGCCT	AGATGGTCTC	TGCTGCTCTT	GCCTCTAGTT	CATGGAGATG	60
TGTCTCTGTT	CAGGCCAAGA	TACAGCCAGC	CAGGCCCTGTC	GTCTGGGACC	CAGGAGGCC	120
CTGATGACCA	AGGGCTTCA	CATCCTAAGT	CATTGGAAG	GAGGCCCTGA	AAACAAAGTC	180
ACCTTGTCA	CTCCCAGTGA	ACTGAATGAG	GAACATGCTG	TCTCCTGTCT	TGGCTCCCC	240
TTTCATGAGA	TACTGGGGAG	AAGAGAACAT	TCCTCCGGC	TTAGTTGTAG	CAGACCCAGA	300
CCTGTGCCA	GCTTTGGTCC	CCCTTCCCAA	CTTCTGAAGC	ACGTGCTGCA	GAGCCACCTT	360
GGTCTGAGCA	CCTGAGGACC	AGCCCCCTCT	CCCTCAGTGC	GGGTCATCTC	TTGGGGGATT	420
TTCTTAAAGT	GAAGAAAGGG	GGTGGGGAAAC	CATATTGCC	CTCCCTCCCC	CATCAAACCTT	480
CCTTCATTTA	ACTTGCTATA	AAATGAGTCA	TATAAAGAAA	CTCTATATGG	GTGAGGTATA	540
TCCCCACTCT	GTGAAAACAT	TACAAATCAA	ACCGCTCTC	TCAGTTTATT	TAAGATGCTT	600
TTGTTGCAAG	CGGTACTCGA	G				621

(2) INFORMATION FOR SEQ ID NO:658:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 567 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:658:

GAAGTCTTGG AGATTTCTAG TTTATTCAATT AACACCGAGAA GGATGGAAGA AAATTCCTCT	60
GGCAATACCA TGTCAGCCTC TTGATGTTT AATACAGAAG AAAGAAAATG TTTGCAGACT	120
CACAGAGTCA CGGTGATGG GGTCCCAGGG CCAGAGCCCT TTACCGTTTT CACTATTAAT	180
GGAGGCCACCA AGGCAAAGCA GCTTCTGCAG CAAATCTGA CAAATGACA AGACATCAAA	240
CCTGTTACCA CAGACTATTT TTGATGGAA GAAAAATATT TTATATCTAA AGAAAAGAAT	300
GAATGTAGGA ACAACCAATT CCAGAGAGCC ATTGGTCCAG AAGAGGAGAT CATGCAAATT	360
TTAACGCAGCT GGTTCCAGA AGAGGGATAC ATGGCAGGA TTGTCTAAA AACCCAGCAG	420
GAAAACCTAG AAGAGAAAAA CATTGTTCAA GATGACAAG AGGTGATCTT GAGCTCAGAG	480
GAGGAGAGTT TCTTGTCCA AGTGATGAT GTTTCTCCAG AGCAACCTCG AACAGTCATC	540
AAAGCACCCCC GCGCCAGCAC ACTCGAG	567

(2) INFORMATION FOR SEQ ID NO:659:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:659:

GAATTGGCC TTCATGGCCT AGGCCCTTG GCCCTGGGT GGGGGTGCTT ACTACATCCC	60
TGGAAGGTGC AGGGAGGCTG ATGGCCTGA TCTCTAACAC AAACAGGAAC CAGCTTCCTC	120
CCTCCCCAC CCTGGGTTCC CAGGGCCTCC GGGTGTGAGA TCCTCCCCA CTGCAGTGCC	180
CCACCCCTC CCCACAGAAG CCCGGAGAGT GGCTCTGTCA CCAGAGGTGT CATTCCCCAG	240
CTGTCTGTGG GAGGTGAGTG AGCAGGAAAT GTGTGTGCTG GGTGTGGAA CTCAGCCCAA	300
TCTAAGAGAA GATACTCTTG GCTTCTCC CCTCAGAGGA GCAGCCCGT CCCTGGCCT	360
TGTGCACTGA CAGTCCCGGA GTCTCGAG	388

(2) INFORMATION FOR SEQ ID NO:660:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:660:

GAATTGGCC TTCATGGCCT AGCCAGGAGT TGAGGTGGAA GTCACCATTG CAGATGCTTA	60
AGTCAACTAT TTTAATAAAAT TGATGACCAAG TTGTTAACCT CTGTTGGTTT TTATTCAGAA	120
TACTGGCAGA TTTAGGAAT ATAAAGGTGT ACTATGAGAC TTCCACTTTT CAGGTGGAAT	180
ATATGGGTAT CTTAGAGTGG TCTATCCTGT TTTCGTTGTC GTTTGAGTC TTTGAAAATC	240
GGATTCGGTT AACTACATAA TATGTGAGAC CTGACTGGTT TTATGGACA CTGGCAGTTT	300
ATAACTTTGG CATACTCTAG ATAAATTCTG ATTGGTATGG GGTGTAAAGG TTTCTGGGGC	360
GTTTGTAAATG CACACCCATG GTTGAGAACC TAGTGCCTA GTAGGCACGT GTAAAAAAGC	420
TAGTAACTAA TATTTTAAA TTAACCAAGT TTAACGTCT TAAAAAAGGA TTAAGTGGCA	480
AGGACCTCGA G	491

(2) INFORMATION FOR SEQ ID NO:661:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:661:

GAATTCCGGCC	TTCATGGCCT	ACCTCAATAT	GCTATCGAGT	TCTGAAAATT	CCCAGCATCT	60
GGAACCTTCAT	GAGCCACCAA	AAGCTGTGGA	TAAGGCAGAA	TCCCCAGGGG	TTGATCCTAA	120
GCAGTTGGCA	GCAGAACTCC	AGAAGGTTTC	ACTACAGCAG	TCACCGCTGG	TTCTGTCATC	180
AGTTGTTGAA	AAAGGATCTC	ATGTTCATTC	AGGTCTTACA	TCAGCAGGAT	CCAGTTCCGT	240
TCCCAGCCCT	GGCAGAACAG	GGTCCCCCTC	AGTGAGCAAA	AAGAAGCAGC	GCAGCAGCAA	300
GCCACTCGAG						310

(2) INFORMATION FOR SEQ ID NO:662:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:662:

GAATTCTTAT	GGCCTACTTC	CGCGCAGAGT	GGCTTCTGAT	AATCATGGCG	CCCTCGGAA	60
CAAATGTATT	GCTGTGGAGC	CTCTTGAGGA	GTTCTCCGGG	CGTGGAACGG	GTCTGTTTCC	120
GGGCTCGAAT	CCAGCCCTGG	CACCGTGGCC	TGCTCCAACC	GCTACCTTGC	TCTTCGAGA	180
TGGGGCTGCC	ACCCCGCCGG	TTCAGCTCCG	AGGCCGAGA	ATCTGGTAGC	CCAGAGACCA	240
AGAAAACCTAC	ATTATGGAT	GAGGAAGTTC	AAAGCATACT	CACGAAAATG	ACAGGCTTGA	300
ACTTGCAGAA	GACTTTAAG	CCAGCTATAC	AAGAACTGAA	GCCACCAACC	TATAAGCTAA	360
TGACTCAGGC	ACAGTTGGAA	GAGGCTACAA	TACAGGCTCT	CGAG		404

(2) INFORMATION FOR SEQ ID NO:663:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:663:

GAATTCCGGCC	TTCATGGCTA	ATTTGTGTA	TGGCCAAAGA	GTTCTTATCA	GAAGTGGCAA	60
AAACTACATA	CAGGTTGGCT	TCCAATAACA	TGAGCCAGGT	ATTTTCAGT	AATATTTGAA	120
AGTGTCTTTT	CTTTCTAGAC	ATGCACATGA	TGGTGTCCAA	GCCAGAACAG	TGGGTAAAGC	180
CAATGGCTGT	AGCAGGAGCC	AATCAGTACA	CCTTTCATCT	CGAG		224

(2) INFORMATION FOR SEQ ID NO:664:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:664:

GAATTCCGCC	TTCATGGCCT	AGGTCTACCA	AAGTGAGGAC	ATTACTGCAG	ATATTCTTCT	60
CCTTTCTCC	TACATTATCA	TTTCTCTTTT	AAACATCAT	TTCTGCAGAT	ATGTAAAAAT	120
ACATCCCATC	TTCAAAAAAGA	AAAACAAAAAA	TCTGACTGTA	CTTCATATCC	CCTTCTAGAC	180
ATTGCCACAT	TTCTCTACTT	CTGTTTACAA	CAAAACTCCT	GGAAAGATT	GTCTATACTG	240
GCTTCTCTA	CTTCTTTTAC	TTCCATTCCCT	TCCTAAACCA	CTCTAAACAT	GCTTGGGTCC	300
CCACCACTGT	AACAAATATA	ATTGTGTCC	AATAACCAGT	GATCTCTGTA	TCACCGGTTC	360
CAAGGGTAG	ATCTCAGACT	TCACCTTCT	GGATTGATTG	ACACATTGGA	CTCAGTTGGT	420
TACTCCTCAC	TTCTGAAAC	TGCTTCACT	GGGCTTTTG	GACTCCATAT	CTCGAG	476

(2) INFORMATION FOR SEQ ID NO:665:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:665:

GAATTCCGCC	TTCATGGCCT	ACTCTCTACT	CCTTTGTGCT	CAATTCCAT	TGTGGAATT	60
TGCATATATG	ATCTGTGGC	ACATTCTAC	ATTTCCCTAG	CCCAGAAGGC	CTTCCCTGTT	120
CACTATCTCC	TTCTTTTAC	TAACTCTTAC	TATATTTCCA	GGCACAGTTC	AGGCATCAGA	180
TAGCCCTATT	TGTTCCA	ACTTTCAC	TTCACCGTAG	GTCAGATTAT	AAGCCTTGCA	238

(2) INFORMATION FOR SEQ ID NO:666:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:666:

GAATTCCGCC	TTCATGGCCT	AGACCATTTC	CATTGTTAT	AGTTTATTT	TTATAAATAG	60
TGCTTCTGG	AATATCCTTA	AATACCTCTA	TCTTTTAAC	ATCCTGTGT	ATACATCTT	120
TCTCACACTT	GGCTTCTCT	TGGAATAGAA	TCTCCTGAA	ATTAGATAGC	TGAGGTAAAA	180
GTCCCTGAAC	CTTTTACAAA	TTGCTACACA	ATAAATACCA	AACTGATT	TAGGAATGTA	240
GTCCCACCAA	CAGTGTGCTT	CTTATCCAT	ATCGTTGCTG	ATCTGAGTT	TGTCAGTCTA	300
TTGATTCCTA	CCAATCTGCC	AGTATCATAG	ATTTAAAAT	ATTTTTGTG	TCCATCTCGA	360
G						361

(2) INFORMATION FOR SEQ ID NO:667:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 343 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:667:

GAATTCCGCC	TTCATGGCCT	ACTCATACAC	AATGAATAACA	AAAACGGAA	CTCTGCAATT	60
TAATACTGTT	TCCAAACTGG	ACACTGGAGA	ATATTCTGT	GAAGCCCGCA	ATTCTGTTGG	120
ATATCGCAGG	TGTCTGGGA	AAAGAATGCA	AGTAGATGAT	CTCAACATAA	GTGGCATCAT	180
AGCAGCCGTA	GTAGTTGTGG	CCTTAGTGAT	TTCCGTTTGT	GGCCTTGGTG	TATGCTATGC	240
TCAGAGGAAA	GCCTACTTTT	CAAAGAAC	CTCCTTCCAG	AAGAGTAATT	CTTCATCTAA	300
AGCCACGACA	ATGAGTCAA	ATGATTTCAA	GCACACCCTC	GAG		343

(2) INFORMATION FOR SEQ ID NO:668:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:668:

GAATTCCGCC	TTATCCTACA	ACTTTGAATA	GACATAAGAG	TGCCTGTCTG	CATAAACCTT	60
CATCAACATT	GGTATTATCT	TTCTTTTCA	TCTTGCTAA	TTGGATAAGT	TTTAAAAAGT	120
GTAACACATT	TTAGTTGCA	TAGCTTGAT	TATAAGTGAG	GTTCGACATT	TTTTTCATT	180
TCTTTACACT	TTAAAAAAATC	TAACCGTGGC	AACGTTGCA	GGTGTGTGTT	CTTCTTATGT	240
TGCTGAGTGT	TATTTACTCC	TGGACC				266

(2) INFORMATION FOR SEQ ID NO:669:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:669:

GAATTCCGGCT	TCATGGCCTA	CAAAAAAGAA	ATTAAGAAC	TCCTAAAGAC	GCAAAGAAAT	60
CATCTACTCC	TCTGTCTGA	CAAAAAAAAC	CAGCTGCTT	AAAACAAAAA	GTACCCAAGA	120
AGGAAGAGTC	TGTCAGAAA	GATTCTGTTG	CTGCCGGAA	GCCAAAGGAG	AAGGGGAAAA	180
TAAAAGTCAT	TAAGAAGGAA	GGCAAGGCGC	CAGAGGTGT	CGCTGCAGCT	GTGGCACTG	240
GAGCCACAC	AGCAGCTGTC	ATGGCGGAG	CTGGAATACC	AGCCATTGGC	CCTGCCAAAG	300
AACTCGAACG	TGAGAGGTCC	CTTATGTCA	CTCCTGAGGA	TCTAACCAAG	GACTTTGAAG	360
AGTTAAAGGC	TGAAGAGGTC	GATGTAACAA	AGGACATCAA	GCCTCAGCTG	GAGCTAATCG	420
AAGACGAAGA	GAAACTGAAG	AAAAAAACTCG	AG			452

(2) INFORMATION FOR SEQ ID NO:670:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 284 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:670:

GAATAATTGA CTGAAAGTGT AGTGTGAGT GGTAGAATAA GTGCTGATCC TGGGGTCTTA	60
TACCAATGTT GCTAACTGTG AGCAGCCTT GTCAAATCAC TTGGCTTCAT TTTCACTGGC	120
CTAACAGTAA TAGGTTAAT TATTCACATA ATTCCCTTAA GTTTTACAT TTTCTGAGTT	180
CATCTTTGTG GTTTTCTG GCATTTACT ATTCCCTTT CCTGCTTTG GCTATTTCT	240
CAACAGGTCC ACGACTGGAA TTGAAAGCA AGAACATCT CGAG	284

(2) INFORMATION FOR SEQ ID NO:671:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:671:

GAATTCTGGA AGCACCTAT CATCGCTCCG TCTGCCCTCC ATACACAGCG TTTGTGTGTG	60
TTATGCCAAA CTGCTTGGTG TTTTCAACC GTGGACCATG ATATCTCACT TCCTTAACCT	120
TACCTTCATA TGCTTTCCCT TTGTGTCTTC TTCTGAAATG CTTCTTCCTT TTGTCCAGGC	180
TGACTCCTGT TTGTCTGAGA CATGTGTCTC AGGAAGCCTT TCGTTCCCC TCGAG	235

(2) INFORMATION FOR SEQ ID NO:672:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:672:

GAATTGGCC TTCATGGCCT AGCATTGATG GCCCATGTAG AAGACCTGAT CATTAAAGACT	60
ATAATCTCTG CTGAACCTAGC TATTGCTACT GCCTGTAAAA CCTTTGTTCC TCATCGCAGC	120
AGTTGTTTG AACTCTATGG CTTTGACGTG CTCATAGATT CTACTCTGAA GCCATGTTG	180
TTGGAAGTGA ATCTCTCTCC TTCTTTGGCC TGTGATGGC CTCTGGACCT AAAGATTAAA	240
GCCAGTATGA TTTCAGATAT GTTCACTGTT GTAGGATTG TGTGCCAAGA TCCTGCCAG	300
CGGGCATCAA CTCGGCCAAT TTATCCCACC TTGAGTCTT CCAGGGAAA CCCTTTCCAG	360
AAACCTCGAG	370

(2) INFORMATION FOR SEQ ID NO:673:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:673:

GAATTCCGCC TTCATGGCCT ACACAGACAT CATCATGCAG AAGATGACCA TTTCCAACAT	60
GGAGGGAGAT ATGAATAGAC TCCTCAAGCA ACGGGAGGAA CTCACAAAAA GACCGAGAGAA	120
ACTTTCAAAA AGAAGGGAGA AGATAGSTCAA GGAGAATGGA GAGGGAGATA AAAATGTGGC	180
TAATATCAAT GAAGAGATGG AGTCACTGAC TGCTAATATC GATTACATCA ATGACAGTAT	240
TTCTGATTGT CAGGCCAAC TAATGCAGAT GGAAGAACCA AAGGAAGTAC TCGAG	295

(2) INFORMATION FOR SEQ ID NO:674:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:674:

GAATTCCGCT TCATGGCCTA CCTGCCTCGA GTGATGGTA TCGGGATGGG TATCGGGATG	60
GCCCACGCGG GGATATGGAT CGATATGGTG CCCGGGATCG CTATGATGAC CGAGGCAGCA	120
GAGACTATGA TAGAGGCTAT GACTCCCAGA CTCGAG	156

(2) INFORMATION FOR SEQ ID NO:675:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:675:

GAATTCCGCC TTCATGGCCT AATAATTGT AAGTTAAAAT AAGTAATACA AATTAAATGC	60
AAATCAAATG CCTGAAGAAG AAGCACGAAT ACCTATTG AAATCTGCTG TACCCGAGAC	120
AGCTTCTAAA TCTCCCACCTT GGGTTCTGTT TCTGGAAGGT GTGGGTCTG TGGTAGCTGG	180
AGTGTGGTG GCCATCTTGG TGCTGGCGGT CCTCATGCTG ATGTACTACT GCTGCAGACA	240
GAACAAACAAA CTGGCCAAC TCGAG	265

(2) INFORMATION FOR SEQ ID NO:676:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:676:

GAATTCTGGA TCAAAACAGA GGAAAATGGT GGGATTCTT GTATAGATAC AGTCTAACAT	60
AGAAACCCAT GCCCATCAGC AGTAATTCC AGTCCCCAG TCCTCCAAGC CCTGGTACTC	120
GAG	123

(2) INFORMATION FOR SEQ ID NO:677:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:677:

GAATTTCAGAG ATAAAGCTAA AGTTCCATTT GAGCACCAAGC CCAAATCCTG GACTTCTTTC	60
TGCTCCCTCT CAGAGGTTCT CTGGTTATAA GTTTTATGTG TATCTTGCCA GAATTTTTCC	120
TATGTTATTA ATACAAATAT ATGTAGGCC AGAAATTATA GCGTGTTCATT CAGCCTTTGG	180
TTTTATTTGC ATTGATAGTA TTATGTCCAT ATCACTCTAC AACTTCTTAG GCCATGAAGG	240
CCG	243

(2) INFORMATION FOR SEQ ID NO:678:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:678:

GCGATTGAAT TCTAGACCTG CCTCGAGACC ACCTATGGAA GCCAAGTGTT CCCGGGCCAT	60
GAGACCTGCC CAATCAAGCA GAAACACATT TGGAGAGACA AACAATCACG ACACGCTCGA	120
G	121

(2) INFORMATION FOR SEQ ID NO:679:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:679:

GAATTCTAGA CCTGCCCGA GTACCTGATC TTTTACTGTC TCTATAGTT CATCTTTTC	60
TTCCCTTTGT TAATTCFACT TTTTAGTTT TTTGCTAGAT TTTTCTTGCA ATTGGATAGG	120
CCCATTAAAC CTATTTGCC TCCACTCTAA ATTCACTACT CCAAGAATTG GTTCACTCT	180
TCCAAATTTC GTATATAAGC CAGAGTTCTG CATAAAGGAA AATACTTAAA TTCTTTCTAA	240
TCTAATGTGG TTTCCTGCAT CTTCAGGAA ACTTTCCCTC GAG	283

(2) INFORMATION FOR SEQ ID NO:680:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:680:

GAATTCCGCC	TTCATGGCCT	AGGGTTTGTG	GCTAAAAATT	ATGCTTAAGA	ACACATCTAA	60
CAAACCTAAA	GCTGCAAAAGA	CATAATGTTA	ATGTAGGTGA	AAATTTCACT	TGTGTTTATT	120
CTGATAGACA	AAATTGTATT	TTAGATGAGA	AGCAACAAATT	TTCATGTTGT	ACTGAGATTG	180
TTAGTAATGA	AATACTTCCA	AATATTAGTG	ATGGTAGAAA	TCTAGTGTAG	GGCTCTTGC	240
TGAGAAGGGA	AAAAAGTCAC	ATAAGAAATC	TACTTTCAAG	AAAATGCAA	ATATGTGTGC	300
TTCAACCTAT	AACATATTCT	GTCACTTTGA	GCTTGTACATA	TTGACAGAGA	ATGAAAACCTT	360
GATAAGACTC	GAG					373

(2) INFORMATION FOR SEQ ID NO:681:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:681:

GAATTCCGCC	TTCATGGCCT	AGAGCGACTT	CGACACCATG	CCAGACATTG	AGAGTGATAAA	60
AAACATCATC	CGGACCAAGA	TGTTCCCTTA	CCTGTCAGAT	TTGTCCAGGA	AGGACCCGGAG	120
AATTGTCAGC	AAAAAATATA	AAATTTATTT	TTGGAACATC	ATCACCATTG	CTGTGTTTAA	180
CGCGCTGCC	GTGATCCAGC	TGGTCATTAC	CTATCAGACA	GTAAGTGCTA	AACCTAGCCC	240
CAAACCCCTC	GAG					253

(2) INFORMATION FOR SEQ ID NO:682:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:682:

GAATTCCGCC	TTCATGGCCT	AATCGAGGAG	AATGGAGACC	AAACCTGTGA	TAACCTGTCT	60
CAAACCCCTC	CTCATCATCT	ACTCCTTCGT	CTTCTGGATC	ACTGGGGTGA	TCTGCTGGC	120
TGTTGGAGTC	TGGGGCAAAC	TTACTCTGGG	CACCTATATC	TCCCTTATTG	CCGAGAACTC	180
CACAAATGCT	CCCTATGTGC	TCATCGGAAC	TGGCACCACT	ATTGTTGTCT	TTGGCCTGTT	240
TGGATGCTTT	GCTACATGTC	GTGGTAGCCC	ATGGATGCTG	AAACTGTATG	CCATGTTCT	300
GTCCCTGGTG	TTCCTGGCTG	AGCTCGTAGC	TGGCATTCTA	GGGTTGTGT	TTCGTCATGA	360
GATCAAGGAC	ACCTTCCTGA	GGACTTACAC	GGACGCTATG	CAGACTTACA	ATGGCAATGA	420
TGAGAGAATG	CTCGAG					436

(2) INFORMATION FOR SEQ ID NO:683:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:683:

GAATTGGCC TTCATGGCCT AGTCCCCACT TTATCTTTT AAACGGTTTC TTTTTCTTT	60
TTTTTTTTA GACCTCTAG GGATGAAACA TTTTATTTTT TAAACTAGTT TTTTTTTAA	120
ATAACATTAA CACATGCTGA ATGCTTAAAT CTTTTAGAA TTCAGAAAGG TAAATGAAA	180
GTCACCATTG TCATTCTCAT CATCTTACTC CCAGAGATGA TTGTTATTAA TATTCCAGA	240
AATTTGCTT GTATATGCAA ACAGCAATAT ATTGTAGCTG CTCGAG	286

(2) INFORMATION FOR SEQ ID NO:684:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:684:

GAATTGGCC TTCATGGCCT ACCCTTACCA GATACTGAAT CTGCCAGTGC CTTATTTGG	60
ACTTCTCAGC CTCCCTGGCT GGGTGAGGTG GTTCACTACC AGCCTGGCA CCATAGTGAG	120
ACTCCCATCT CTACAAAAAA AAAAAAAA AAACTTCTG TTGTTGTAA GCTACCCAGT	180
TTATGGTATT TTGTTACAGC AACCCAAACA GTCTGAGACG TTTAGCTTAA CTCCGTATG	240
CACTAGATAC AGTCTGCACT TTGACATCAA TCTCGA	276

(2) INFORMATION FOR SEQ ID NO:685:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:685:

GAATTGGCC TTCATGGCCT ACTAAGAATA GGAAAAAAA TAACACTATG ATACCACAAAC	60
CTTATTACAT CAAACTGCTT TGGGCTTTAT CCTCTTAA GTGTGCTCAG GTGTTCAGCC	120
ACGAGGTTTC TGACAGCCCT CATAAGACCT TCGAG	155

(2) INFORMATION FOR SEQ ID NO:686:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:686:

GAATTGGCC TTCATGGCCT ACTTTGAAGA GTACGATTTC AAAACCAGCA ATTGGTGTGA	60
ATGAAAAAAC ATTTGTTGGC ACCATTATT TAAAAAAA AAAAGCTGTA TGCAAGCAGAA	120

AGCCTTATAC AAGTTGTTT TCTTTTTTC CTTTTCTTT TTTTGATAC CTTCATTTCT	180
GTTACTTTA TATAAAATTC TCTGCAAAGG AAGGCCTCTC TTGGACTAC AATTGGAGG	240
CAGCCACTTG TTGTGCCCTGC TTCTGTTAAA GAATGTGGAT ATCAAGCCCC CCCGACTCGA	300
G	301

(2) INFORMATION FOR SEQ ID NO:687:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 254 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:687:

GAATTCCGCC TTCATGGCCT AATTTTACA GAAATTATTT CCACAATCAG AAGTACTGTA	60
CTGATTGCAT TTCTTTGTCT CAAAAAGTTT TCCTTATGTT TCTCAAAGCA GTATTACAC	120
TAATTATTCA ATTCTTATCT TTCTTCAGT TTCTCCAAT AGACTGTGAG ATCTTTGAGG	180
GCCAGGTTGA CATGCTCTG ATACCTACAC CCTATGCAGC TCCTAGTGCA GGACCTTGCA	240
GTGACAAGCT CGAG	254

(2) INFORMATION FOR SEQ ID NO:688:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 261 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:688:

GAATTCCGCC TTCATGGCCT AATATTTATT TAGATGCTAT TATTACTGTT TGGACTTTA	60
TTTTGGCAGG CTTTGTTCGA GACTGTAGGG TTTTCCAATG TGACTAATGA CCACCTCTGC	120
CTCTCCCGTG GTGTATTTTG GGCACCCCTCC CACCCGGCTG CATAACCCGC CAGGGCTCCC	180
ACAGAGACAA GGAGGGCACA GGTCCTGCC CCCTCTTGA AATCGATATA CACACATCCA	240
CGCACATGCG GCCCACTCGA G	261

(2) INFORMATION FOR SEQ ID NO:689:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 214 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:689:

GAATTCTAGA CCTGCCTCGA GCTTCTGGCT GTTGTCTTTC CTGGGCATCC TTTTACAAG	60
TGGAAGAACT AGGATGGCTT TCCAAAGTCT TCTAGAAATG AAGTTCTTTC TCTGTGCAGC	120
TTTCCCCCTT GGAGCAGGAG TGAAGATGTT TCATTATCTT GGGCCTGGGA AACCACTTCC	180
CCAGGCTTCT CCCTCCCCCC ACCCCCGACT CGAG	214

(2) INFORMATION FOR SEQ ID NO:690:

(ii) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 307 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:690:

GAATTCGGCC TTCATGCCCTA CAAACTAAA AGTAATCTT TGGAAATCG ATAGTAGTCT	60
TGAAACTATG GAAAACACAG GAGTGATGGA TAAGGTTCA GCAGAGTCG ATGGGGACAT	120
GTCTTCAGAT AATGACTCAT ACCACTCTGA TGAATTCTT ACAAAATTCTA AGTCTGATGA	180
AGACAGGCAG CTAGCTAACT CATTAGAGAG TGTAGGCCA ATAGATTACG TTCTTCCTAG	240
TTGTGGTATT ATTGCCTCAG CGCCTCGATT GGGCAGTCGG TCCCAGTCTC TTAGCAGCAC	300
ACTCGAG	307

(2) INFORMATION FOR SEQ ID NO:691:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 493 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:691:

GAATTCGGCC TTCATGGCCT ACTCCATATT TATTTAGATG CTATTATTAC TGTTTGGACT	60
TTTATTTGG CAGGCTTTTT TCCAGACTCT AGGGTTTTCC AATGTGACTA ATGACCACAC	120
CTGCCCTCTCC CGTCGTCTCT TCTGGCACC CTCCCCACCG GCTGCATACC CGGCCAGGGC	180
TCCCCACAGAG ACAAGGAGGG CACAGGTGTC TGCCCCCTCT TTAAAATCGA TCTACACACA	240
TCCACGCACA TGCACCCCG AGGAAACGAA ACCCACTCTA GAAAACGCGA CCTTGGCCGC	300
ACCTAAAGCA GCCAGCCGTG AGTGCAGACC CCTTGGCCAG CGTGGCGCAG TGGCCCTGAG	360
CAGTAGTGGC GTGTGTGTAG ATCAAGTCGG ATCTAGTCCA GCTCGTTCA TTAGCGATCC	420
ATGTAATCTG ACGTCACTT CTCTCGAAGT CTCTTTTTT GGCCCAGGCC TTGAAGAATA	480
CACTGGACTC GAG	493

(2) INFORMATION FOR SEQ ID NO:692:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 225 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:692:

GAATTCTAGA CCTGCCCCCTG CCTCCTGCAT CCAGCCCCCA ACATGGTGCC AAAGCTTCCA	60
GAAGCCAAAA AGCTTCTGAT TTTTAAGGTA GTGGGCATCT CTCTCCTAAT GACGAAGCTG	120
CTCAGCAACT CCACCTGCC GCGCAGGAA GGAGCAGTCC CCTGCTATCC CTGCAGCCAC	180
TCCCAGCACA CCCGCACACA GCCAGCACCA CCGCCCACTC TCGAG	225

(2) INFORMATION FOR SEQ ID NO:693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:693:

GAATTCGGCC TTCATGGCCT ACTGGCTCAT ACAATACATC AATAAGTATG CAACTTTCA	60
TTTGTATTCT CGTTGCTGGA AGTGGAAAT ACCCCATCTT CCCAGGAGTG AAATGTTCT	120
ACTTTCTCTC CGTGGTCCCC TGTATCCTTA CTCAGCTCTG CTGCTGCTCT CCCAGCCCC	180
TAAAAGTAGC ATGGATCGGG GAAGAAGGAA GGACGGCAGG AAGGCAGGCA GAGATCCTCA	240
GGCAGGTCGA G	251

(2) INFORMATION FOR SEQ ID NO:694:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:694:

GAATTCGGCC TTCATGGCCT AGTGTGTGTG TGC GTGTGTG TGT GTTTACA TATAAGTTT	60
TTTGGTAACA AATAAATTTT GTTAGAGCTA GTCAGATTTC TGTTTCCTTA ATCTGCTAGT	120
TTTGGTAGGT TATATTTTC AAGGAATTG TCCATTCACTC CTATGTTGTT GAATTTGGG	180
TGTAACGTTT TTCAATTACTC TTTCTTTTAAATCTGTG GGATCTGTAA TGATGCC	240
TCTTTCATTC CTGATATGAG TAATTCTTAT TCTCTTTTG TCTATCAGCT CGAG	294

(2) INFORMATION FOR SEQ ID NO:695:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 246 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:695:

GAATTGGCCT TCATGGCCTA ATTGGGACCA AATAGAGGCT CACAGATATT TGGATTATT	60
TATGTGTCTTA TTATTAATA AGGAAAGCAT TTTGTGATAT GTGGAAGACG CTATGTGAAG	120
TTTTACCTAT CTTCTCAAAG ACCTTTCTT TTGTATTTTC TTTGGTGTGTT TCTTAAAGCC	180
AAACAAAGAA ATGTTCTTAA GGAGACAGGG TGGGTTTTTC TGTGGGCCCTA GGCCATGAAG	240
GTCGAG	246

(2) INFORMATION FOR SEQ ID NO:696:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 349 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:696:

GAATTCCGCC	TTCATGGCCT	ACCTAATAT	AAAAAGCATT	GTCACCAGTGT	TGATGCTGAT	60
GCTATTGATG	ATGTTTGCTG	TCCACTGTAC	CTGGGTACA	AGCAATGCCT	ACTCTAGTCC	120
AAGTGTAGTC	CTGGCCTCAT	ACAATCATGA	TGGCACCA	AATATCTTAG	ATGATTTAG	180
AGAAGCTTAC	TTTGGCTAA	GGCAAATAC	AGATGAACAT	GCACGAGTAA	TGTCTTGGTG	240
GGATTATGGC	TATCAGATAG	CTGGAAATGGC	TAATAGAACT	ACGTTGGTGG	ATAATAACAC	300
CTGGAATAAC	AGCCACATAG	CACTGGTGGG	AAAAGCTATG	TCTCTCGAG		349

(2) INFORMATION FOR SEQ ID NO:697:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:697:

GAATTAATA	AGTTACTGAC	TTTGTGACTT	ATTTAATTCA	TATTAATATA	TTAGGCTTCC	60
CAACTGACGG	TGTTGCAGTT	GAGCTAGCTT	CCAGTTTG	AGAAACACAT	AGTTGATTAG	120
TTCTGTCAGT	AATTTTCAGG	GATATTAATA	TAACTTGAT	ATTAGTGAGA	AATTTTCTTT	180
CAGTAGAAA	ATGTTTTCTA	ACTTAGGAGC	TGTTCTCGAG			220

(2) INFORMATION FOR SEQ ID NO:698:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:698:

GAATTCCGCC	AAAGAGGCCT	AGCAGAGCTT	TCATATCCAC	GATGCGTTTT	CTGGCCGCCA	60
CGATCCTGCT	GCTGGCGCTG	GTCGCTGCCA	GCCAGGCCA	GCCCCCTGCAC	TTCAAGGACT	120
GCGGCTCTAA	GGTGGGAGTT	ATAAAGGAGG	TGAATGTGAG	CCCAGTGTCCC	ACCGATCCCT	180
GTCAGCTGCA	CAAAGGCCAG	TCCTACAGTG	TCAACATCAC	CTTTACCAGC	GGCACTCAGT	240
CCCAGAACAG	CACGGCCTTG	GTCCACGGCA	TCCTGGAAGG	GATCCGGTGC	CCCTTCCCTA	300
TTCCTGAGCC	TGACGGTTGT	AAGAGTGGAA	TCAACTGCC	CAGTACAGTC	GAG	353

(2) INFORMATION FOR SEQ ID NO:699:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:699:

GGGATTGAAT TCTAGACCTG CCTCGCTTCC CCACCCCTAC TAACATTAAC GAAAATAACC	60
CCACCCCTACT AAACCCCCATT AAACGCCTGG CAGCCGGAAG CCTATTGCA GGATTTCTCA	120
TTACTAACAA CATTTCCCCCC GCATCCCCCT TCCAAACAAAC AATCCCCCTC TACCTAAAC	180
TCACAGCCCT CGCTGTCACT TTCCTAGGAC TTCTAACAGC CCTAGACCTC AACTACCTAA	240
CCAACAAACT TAAAATAAAA TCCCCACTAT GCACATTTA TTTCCCCAAC TCCTCGAG	298

(2) INFORMATION FOR SEQ ID NO:700:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:700:

GAATTGGCC TTCATGCTTA GCCTCAGCTC TTTCTCTGG GTTGTGTA TTTCTTTTC	60
TGTCCCAAAC AGTTTCCCCC AAAAAAGAA CTTTATGTCT TTCTCTGTCT TCCCTCAGTC	120
CTTCAGTCA GCAGCCTGTG ATTGGGTTT TCCCCTCAGA AACGAACAAT CCAGAACCCA	180
CTGTTAAAAA CAACTGTATT TTGCTTGGG AAGTCCATT GCCTCCCTG AAAACATTAA	240
ACATTCTCC GATCCCCAGC CTGAGTCCTCT CTGTCCTCTGG GCCCCATCCT GCTCCACAGC	300
AGGGCTGGTG TGTCAGCAC AGAGTGACCC TCCGATGCC TTTCCCACCC GCCGCCCTGC	360
CTCCCTCGAG	370

(2) INFORMATION FOR SEQ ID NO:701:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:701:

GAATTGGCC TTCATGGCCT AGGAAAGATC TAATTATCAT GGACCTGCGA CAGTTTCTTA	60
TGTGCTGTC CCTGTGCACA GCCTTTGCCT TGAGCAAACC CACAGAAAAG AAGGACCGTG	120
TNCATCATGA GCCTCAGCTC AGTGACAAGG TTCACAATGA TGCTCAGAGT TTGATTATG	180
ACCATGATGC CTTCCTGGT GCTGAAGAAG CAAAGACCTT TGATCAGCTG ACACCAGAAG	240
AGACCAAGGA AAGGCTTGGG AAGATTGTA GTAAATAGA TGGCGACAAG GACGGGTTTG	300
TCACTGTGGA TGAGCTCAA GACTGGATTA AATTTCGACA AAAGCGCTGG ATTTACGAGG	360
ATGTAGAGCG ACAGTGGAGG GGGCATGACC TCAATGAGGA CGGCTCTGTT TCTGGGAGG	420
AGTATAAAAA TGCCACCTAC GGCTACGTT TAGATGATCC AGATCCTGAT GATGGATTAA	480
ACTATAAACAA GATGATGGTT AGAGACGTT TCGAG	515

(2) INFORMATION FOR SEQ ID NO:702:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:702:

GAATTGGCC TTCATGGCCT AGGGGACCTG ACCTTCACTG TGGCCCAAAA GATGGCTGAG	60
CCAGAGAAGG CCCAGCCCT CAGCATCCTG CTGTACGTGC AGCCCTTCCA GGTGGGCATG	120
CCACCCCCCTG GGTGCTGCAG GGGCCCCCTG CGCCCCAAGA CACTCCTGCT CACCAGCTCC	180
GAGATCTTCC TCCTGGATGA GGACTGTGTC CACTACCCAC TGCCCGAGTT TCCCAAAGAG	240
CGGCCGAGA GAGACAGTA CGGGCTGGAC SATGGCCGCC GCGTCCGGGA CCTGGACCGA	300
GTGCTCATGG GCTACCAAGAC CTACCCGCAG GCGCTCACCC TCGTCTTCGA TGACGTGCAA	360
GGTCATGACC TCAAGCTCGA G	381

(2) INFORMATION FOR SEQ ID NO:703:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:703:

GAATTGGCC TTCATGGCCT AGCTCCACTT TCTCTGAAAA TTTATTCTATA TTGTTAATTA	60
AATTGTTTT TATTATAGAA ATAATATATT GCATGATTG TAAAAATGCA GAGAACAGA	120
ATGCCACAAA ATTATGTAAC CCTTTCTATC TCCCCTGGT GTACCTCCCTT AATCATACTT	180
CTCAGAACCA TTGCAATAA TTTGCTGGGA GTTCTCTGA TGGTTACCAT CGTGACTGAT	240
AGATTATTTT CCCAGGTTCA AGCCGTTCCC CTGCCTCAGC CTCCCGAGTA TCTGGACTA	300
CAGGCATGCA CCACCACTCA GCTCGAG	327

(2) INFORMATION FOR SEQ ID NO:704:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:704:

GAATTGGCC TTCATGGCCT TGCCTTTTTT CTTTCACAC TTTACTACAC ACAATTACTG	60
GATTAATCTC TTTAATGCCG AGATCTTTTT TCCTTAGTGA CACCTTAATC ACTCTTAGCT	120
TAACATATAT GGTCATCCAT TACTGGGTG CCTCTGCCTT TCCAGGATTG GCTGCCACTG	180
CTCCTCCACA TACCCCTGTAT TCTAGCCAAA TGGAACTACT GCTGTGTCCC AACAGAGATTC	240
TTTATTCTCTC TTGGCTGTG TGCTCTATTCTAATGCTAC CTGCCCTCA AAATCGAG	299

(2) INFORMATION FOR SEQ ID NO:705:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:705:

GAATTGGCC TTCATGGCCT ACTTGATTTG TGGCTTATCT CAAGTTACCA TTTTCAGTC	60
AAGTCTGTTT GTTGCTTCT TCAGAAATGT TTTTACAAT CTCAGAAAAA AATATGTCCC	120

GAATTCCGCC TTCATGGCCT AGGGGACCTG ACGTTCACTG TGGCCCAAA GATGGCTGAG	60
CCAGAGAAGG CCCCAGCCCT CAGCATCCTG CTGTACGTGC AGGCCTTCCA GGTGGGCATG	120
CCACCCCCCTG GGTGCTGCAG GGGCCCCCTG CGCCCCAAGA CACTCCTGCT CACCAAGCTCC	180
GAGATCTTC GCTCTGGATGA GGACTGTGTC CACTACCCAC TGCCCCAGTT TGCCAAAGAG	240
CCGCCGCAGA GAGACAGGTA CCGGCTGGAC SATGGCCGCC GCGTCCGGGA CCTGGACCGA	300
GTGCTCATSG GCTACCCAGAC CTACCCCGAG CCCCTCACCC TCGTCTTCGA TGACGTGCAA	360
GGTCATGACC TCAAGCTCGA G	381

(2) INFORMATION FOR SEQ ID NO:703:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:703:

GAATTCCGCC TTCATGGCCT AGCTCCACTT TCTCTGAAAA TTTATTTCATA TTGTTAATT	60
AATTGTTTT TATTATAGAA ATAATATATT GCATGATTG TAAAAATGCA GAGGAACAGA	120
ATGGCACAAA ATTATGTAAC CTTTCTATC TCCCTTGTT GTACCTCCTT AACATACATT	180
CTCAGAACCA TTGCAATAA TTGCTGGGA GTTCTTCTGA TGGTACCAT CGTACTGAT	240
AGATTATTT CCCAGGTTCA AGCGGTTCCC CTGCCTCAGC CTCCCGAGTA TCTGGGACTA	300
CAGGCATGCA CCACCACTCA GCTCGAG	327

(2) INFORMATION FOR SEQ ID NO:704:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:704:

GAATTCCGCC TTCATGGCCT TGCCTTTTTT CTTTCACCAC TTTACTACAC ACAATTACTG	60
GATTAATCTC TTTAATGCCG AGATCTTTTT TCCTTAGTGA CACCTTAATC ACTCTTAGCT	120
TAACATATAT GGTATCCAT TACTGGGTTG CCTCTGCCTT TCCAGGATTG GCTGCCACTG	180
CTCCTCCACA TACCCCTGTAT TCTAGCCAA TGGAATCACT GCTGTGTCCC AAGCAGATTC	240
TTTATTCTC TTGGCTGTTG CTCTCTATTCTAATGCTAC CTGCCCTCA AAACCTCGAG	299

(2) INFORMATION FOR SEQ ID NO:705:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:705:

GAATTCCGCC TTCATGGCCT ACTTGATTG TGGCTTATCT CAAGTACCA TTTTCAGTC	60
AAGTCTGTTT GTTGCTTCT TCAGAAATGT TTTTACAAT CTCAAGAAAA AATATGTCCC	120

AGAAATTGAG	TTTACTGTTC	CTTGTATTTG	GACTCATTG	GGGATTGATG	TACTGCAC	180
ATACTTTCA	ACAACCAAGA	CATCAAAGCA	GTGTCAAGTT	ACGTGAGCAA	ATACTAGACT	240
TAAGCAGAAAG	ATATGTTAAA	GCTCTAGCAG	AGGAAAATAA	GAACACAGTG	GATGTCGAGA	300
ACGGTGCTTC	TATGGCAGGA	TATGCGGATC	TGAAAAGAAC	AATTGCTGTC	CTTCTGGATG	360
ACATTTGCA	ACGATTGGTG	AACCTGGAGA	ACAAAGTTGA	CTATATTGTT	GTGAATGGCT	420
CAGCAGCCAA	CACCACCAAT	GGTACTAGTG	GGAATTGGT	GCCAGTAACC	ACAAATAAAA	480
GAACTAGTCT	CGAG					494

(2) INFORMATION FOR SEQ ID NO:706:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 491 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:706:

GAATTCCGGCC	CTTCATGGCC	TACTCCCGAG	CTCTACTGAC	TCCCAAAAGA	GCGCCCAAGA	60
AGAAAATGGC	CATAAGTGG	GTCCCTGTG	TAGGATTTT	CATCATAGCT	GTGCTGATGA	120
GCGCTCAGGA	ATCATGGGCT	ATCAAAAGAAG	AACATGTGAT	CATCCAGGCC	GAGTTCTATC	180
TGAATCCTGA	CCAATCAGGC	GAGTTTATGT	TTGACTTGA	TGGTGTATGAG	ATTTTCCATG	240
TGGATATGGC	AAAGAAGGGAG	ACGGTCTGGC	GGCTTGAAGA	ATTGGACGA	TTGCCAGCT	300
TTGAGGCTCA	AGGTGCATTG	GCCAACATAG	CTGTGGACAA	AGCCAACCTG	GAAATCATGA	360
CAAAGCGCTC	CAACTATACT	CCGATCACCA	ATGTACCTCC	AGAGGTAAC	GTGCTCACGA	420
ACAGCCCTGT	GGAAGTGGAGA	GAGCCCACG	TCCTCATCTG	TTTCATCGAC	AAGTTCACCC	480
CACCACTCGA	G					491

(2) INFORMATION FOR SEQ ID NO:707:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 242 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:707:

GAATTCCGGCC	TTCATGGCCT	ACCTTATCTT	CTTAACCTTT	CAAATACTTG	CAGATATTTT	60
GCTTGGTCT	TCCCATCTAT	TGCAATACCC	CTTTAGATAA	AGTCAATTCT	TATCTAAAAT	120
CAAATTCTATT	TTATTTGACA	ATGTTTACAA	ACAACCCAG	GACGATAACA	ATTACACTCT	180
CAATACTGGC	ATCACACCTT	CACAATTACA	CTAACCCCAA	CCTAGGCCAT	GAAGGCCTCG	240
AG						242

(2) INFORMATION FOR SEQ ID NO:708:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 285 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:708:

GAATTCCGGCC TTCATGGCCT AGACAGAAATT ACTGGGAACC ATTTTCCAAG TAGCCCACCA	60
CAAAGGTTGT ATTTTGTCAA ATTGAAGGAG TCATCTGACT TTCCCTTAATC ATAAGCTACA	120
AATAATAAA GCTACATCAA TAGATTTCT AATATTATT TAACCTTGAA TTTCTGGAAA	180
AAACCCAAC TGGTAATGAT TTATCATCTG AGCTTTGTTT TTGGCTTG TGATGCTAATT	240
TTTGGCTTAG GATTTTATA TCTATTCAT GAGTGGCACC TCGAC	285

(2) INFORMATION FOR SEQ ID NO:709:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 319 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:709:

GCACGCCATG GGAGAAAAAG AAGAACCAA AAAACAGAA GACAAGTCTT TGGCAAAGCC	60
TGAAACTGAT AAAGAACAGG ACAGTGAAAT GGAGAAGGGT GGAAGAGAAC ATATGGATAT	120
AAGTAAATCT GCAGAGGAGC CACAGGAAAA AGTTGACTTG ACTCTAGATT GTTAACTGA	180
AACCTCTGAA GAGGCAGGAG GAGGAGCACG ACCAGAAGGA CCGAATGAAG CTGAGGTCAC	240
TTCTGGAAAG CCAGAACAGG AAGTACAGA TGCTGAGGAA GAAAATCAG TTTCTGGAAC	300
TGATGTCCAA GATCTCGAG	319

(2) INFORMATION FOR SEQ ID NO:710:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 190 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:710:

GAATTCCGGCC TTCATGGCCT AGACACATAC AAAGATAAGG CTTTGATAAA ATTCAAGAGT	60
TATTTGTATT TTGAGGAAAA AGACTTTGTG GATAAAGCAG AGAAGAGCCT GAAGCAGACT	120
CCCCATAGTG AGATAATATT TTATAAAAAT GGTGTCAATC AAGGTGTGGC TTACAAAGAC	180
ATTCTCGAG	190

(2) INFORMATION FOR SEQ ID NO:711:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 199 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:711:

GGATTGAATT CTAGACCTGC CTCGAGTAAG ACCCTTTTT AAAATGACTC CCACTGTCTA	60
TTCCACAGCC GGTGTGCGGC ATGCTGATTC AATCCCCACA ACAGCCCAGG AGGTAGGCGC	120
CGTCCCACCC TCCCTTACAG GAGGGAAAC TGAGGTTCAAG TGCGTCAGAT GGTCAGCTGC	180
CTCCAAGACC ACGCTCGAG	199

(2) INFORMATION FOR SEQ ID NO:712:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 304 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:712:

GAATTCTGGCC TTCATGGCCT ACCCTGTACCT GTTTTAACT TGCTTTGCT TCAGCGTTCT	60
GTGGTTGTCA ACAGATGCCA GTGAGAGCAG GTGCCAGCAG GGGAAAGACAC AATTTGGAGT	120
TGGCCTGAGA TCTGGGGGAG AAAATCACCT CTGGCTCTT GAAGGAACCC CCTCTCTCCA	180
GTCATGTTGG GCTGCCTGCT GCCAGGACTC TGCCGCCAT GTCTTTGGT GGCTAGAAGG	240
GATGTGCATT CAGGCAGACT GCAGCAGGCC CCAGAGCTGC CGGGCTTTA AACACTCCT	300
CGAG	304

(2) INFORMATION FOR SEQ ID NO:713:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 361 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:713:

GAATTCTGGCCC TTCATGGCCT ACCCAATTCA GTTTCCAGAG GAGGTGGAAC CTTCTGCAAC	60
CCAACAGGAG GCCCCAAATTG AGCCTCCAGT TTCTCTTAGT GAGCATGAAAC TTTCCATCAG	120
TGACCCAGCAG CAGCCAGTTC AGCCTTCAGA GTCTCTTAGG GAGGTGAAAT CTTCTCTGAC	180
CCACCCAGGAG ACCCCAGGTC AGCCTCCAGA ACATCATGAA GTCACAGTTT CACCTCCAGG	240
TCACCATCAA ACTCATCATT TAGATTCAACC CAGTGTCTCT GTGAAGCCTC CAGACGTGCA	300
GCTCACCATATA GCAGCAGAGC CTAGTGCAGA GGTGGAACT TCTCTAGTCC GACCCCTCGA	360
G	361

(2) INFORMATION FOR SEQ ID NO:714:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 316 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:714:

GAATTCTGGCC TTCATGGCCT ACCGAGATGG AAATAACCTA AGAAAAAGAG GGCATCCAGC	60
TCCATCTCCC ATTGGCGTC ATGCTGCTCT GGGTCTGGTA ACTCTTGCC TGATGTTGCT	120
GATTGGCTG GTGACGTTGG GGATGATGTT TTTGCAGATA TCTAATGACA TTAACTCAGA	180
TTCAGAGAAA TTGAGTCAAC TTCAGAAAAC CATCCAACAG CAGCAGGATA ACTTATCCCA	240
GCAACTGGGC AACTCCAACA ACTTGTCCAT GGAGGAGGAA TTTCTCAAGT CACAGATCTC	300
CAGTCTAAC CTCGAG	316

(2) INFORMATION FOR SEQ ID NO:715:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:715:

GAATTGGCC	TTCATGGCCT	AGGCAATATC	AAGGTTTAA	ATCTCGGAGA	AATGGCTTC	60
GTTTGCTTGG	CTATCGGATG	CTTATATACC	TTTCTGATAA	GCACAAACATT	TGGCTGTACT	120
TCATCTTCAG	ACACCCGAGAT	AAAAGTTAAC	CCTCCTCAGG	ATTTTGAGAT	AGTGGATCCC	180
GGATACTTAG	GTTATCTCTA	TTTGAATGG	CAACCCCCAC	TGTCTCTGGA	TCATTTTAAG	240
GAATGCACAG	TGGAATATGA	ACTAAAATAC	CGAAACATTG	GTAGTCAAAC	ATGGAAGACC	300
ATCATTACTA	AGAATCTACA	TTACAAAGAT	GGGTTTGATC	TTAACAAAGG	CATTGAAGCG	360
AAGATACACA	CGTTTTTACCC	ATGGCAATGC	ACAAATGGAT	CAGAAGTTCA	AAGTTCTGG	420
GCAGAAACTA	CTTATTGGAT	ATCACCACTAT	CTCGAG			456

(2) INFORMATION FOR SEQ ID NO:716:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:716:

GAATTGGCC	TTCATGGCCT	AGATCATTCA	GTGGCTCACC	TAATATCACA	GAACAAGTGG	60
TGGAGTCAGA	ATCTTTTATC	TAAAGGAGAT	ATTTTCATCC	TTAGATTAAT	GTCCCTTTCA	120
CAGTCTCATG	CTACTTTCT	TTAAAATGAA	ATTGCTGTT	TTTTTTAAAT	TGATTTGGCC	180
AACTTCATTT	GTAACGGAAG	AATCAAATT	AGAGCCCCGG	TCTCATCCTA	CGGTATCTCG	240
TCCTGAACCT	CTGGTCTCCC	TCAAGAATGA	CTCAGAAGGA	CGGACTCGAG		290

(2) INFORMATION FOR SEQ ID NO:717:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:717:

GAATTGGCC	TTCATGGCCT	AAAAAAAAAAA	GCCTTTAAA	CTTGTAGGAA	TTAAGAAATA	60
AGAATAACCT	ACAAAATGCT	AGCAAAATT	ATCTCATTT	TTTTCATTGT	ATTTTCAGGT	120
TTAACTGAAC	TGAATGACAG	TCCAGTTCCC	CTAGAACTTG	AGCGCTGCAA	GTCTCCTACC	180
TCAGACCATG	TAAATGGACA	CTGCACAAAGT	CCAACCTCTC	AGAGTTGCAG	TTCTGGAAAA	240
CGTCTTTCTA	GTGCCGATGT	TTCAAAAGTA	AATCGCTGGG	GTCCTGGAAG	ACCACCAAGTT	300
CTCGAG						306

(2) INFORMATION FOR SEQ ID NO:718:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:718:

GAATTCCGCC TTCATGGCCT AATATTTATT AAATGACTTG GTAGATAGAG CAACTGACTG	60
AATATATTAT TTTTAGGAA GAAGAAGAAC ATTTTGTCTT AAATTAATT TCTTATTTTA	120
TTTCTTTTC CCCTTTATC CACGGTAGGT CCAGGTAAAG CCAAAGGCCT TATCCTTATC	180
TACACTGCTG GGGGACACAA ACAAGAATT TCAAGTTCAA GTATTATTC TCATTTGAG	240
TAATTTGTT CTCATTTGT TCCAGTTCTC ACTCTCAGAA AAAGATTACT CGAG	294

(2) INFORMATION FOR SEQ ID NO:719:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 263 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:719:

GAAACAATAG AAACACTGAG AGAAAATTCA GAGAGACAGA TAAAGATACT GGAACAGGAA	60
AATGAACATC TGAATCAAAC AGTGTCTTCC TTAAGGCAGC GGTCCCAGAT AAGTGCAGAA	120
GCAAGAGTGA AAGACATTGA AAAAGAAAAC AAAATTCTTC ATGAATCTAT CAAAGAAACA	180
AGTAGCAAGC TAAGCAAGAT TGAATTGAA AAAAGACAAA TTAAAAAAGA ATTGGAACAT	240
TATAAAGAAA AAGGAAGCTC GAG	263

(2) INFORMATION FOR SEQ ID NO:720:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 320 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:720:

GAATTCCGCC TTCATGGCCT ACCTGCCCTT CTGCGGTAC AGCTGCCCTGC TGGGTGGGAG	60
TCCGGGGAA TGGTATGTGT GGTACCAGA GGGCACTGAG TGGGCTTCAG TGGCATGTGA	120
ATCCTGGCAG AGTCTCGGAT CCCCGATGGG GAGAGGAGAA AGCACAAGCC AAGACAACGA	180
GTGGGGGAAG GAGGCAGGGG CTAAGTGACG GGTGGGGGT GGGGGTGGGA ACTCCAGTGT	240
ACACATTGAC AGTCTCTATG TTGGCTTCAC CAGCGCTTCT CTGTTGTCT CGTCCCTGGA	300
TTTCTAACAG TTGCGCTCGAG	320

(2) INFORMATION FOR SEQ ID NO:721:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 292 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 721:

GAATTGGCC TTCATGGCCT AGTCGGGAGT GTCTTAAGCT TTTCATTTAA CCTAAAGTAC	60
AGAGTCTGCT CTGTAGAAAT ATGTCATTAA GAAAATATTT GAGTCCCGAGC TCCTCCCTGT	120
TGTGTAATGT CTGATAATTT CACTCATTAA ATTACCCAGA CAGACCATAA AGTCCCTCTCA	180
GTTCGCATCA CCTGAAAGTC AGTCAGCCTG GGCTGTGAGG ATTGTGAGGT AGAACTCACT	240
GTGGAAGGAC GGCAATTAGGG AAGACTTTAG GAAAATGGAG CGGAACCTCG AG	292

(2) INFORMATION FOR SEQ ID NO: 722:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 722:

CTCGAGACCT GTGTGCGCAG GCAACGGGAA AACTGGAAAT GCGTTGACAA ACTGACGCAA	60
AACTGGGCC AACAGCCACA AGGCACGTGGT CGTTTCCAC TGGGCAAAGT TCAGTCGCAT	120
TTCTTTCTGT TCTCTTTCTT CTCTTCTTT CTCTTCTCTC TTCTTCTTCTT TTCTTCTTTC	180
TTTCTTTCTT CTCTCTCTGT CTCTTCTCTC TTCTTCTTCC TTCTTCTTCTT	240
CCTTCCTCTC TTCTTCTTCTT CTCTTCTTCTT TTCTTCTTCTT TTCTTCTTCTT AAGAGACGGA	300
GTCTCGCTCT GTTACCCAGG CGGGAGTGCA ATGGCACAAAT CTCGGCTCAC TAGGCCATGA	360
AGGCCGAATT C	371

(2) INFORMATION FOR SEQ ID NO: 723:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 723:

GAATTGGCC TTCATGGCCT AGTCCTTGG TGGTTGAAA GTTAGAGAGA TCCTGATAAG	60
CATAATGACC AACATAGAAAG AGATTAAGTA CCTTACTCA TAAATGTGAG TTCACAGACT	120
TCAGGTCTAA ATTGTAACA ATATTTAAGA TGTATATGGC TTAAAGTGCT GGTAGTTTG	180
ATTAGAACATCC ATAGGTTCT AGTCAGTGT CTCTTCTTAA TTGAGTTTT TATGTATTTT	240
TTAACCTAGAA ATAAGAGGGT CTCGAG	266

(2) INFORMATION FOR SEQ ID NO: 724:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 724:

GAATTCCGCT	TCATGGCCTA	GAAAGTTTTT	CAAAAATCT	TCAATTGTCT	CTGGTTGATG	60
CAACTTAATT	TTTGCTGAG	AGAGACCTTA	AATGTAATT	GTATTGTATA	ATTASCCTGA	120
TTAATCTGAC	CTGTACATCA	CGAGTCACCT	GTCTTAGCC	CAAGAGGAAT	GCTTCCTTTC	180
TGATTTGAGG	CAGTGGCCCA	TCATTGCTTC	TAGCAACCTT	CCTACTTACT	AGATGACCTT	240
GAGTCAGGT	TTCTGTATAT	ATGATTCAG	ATTTGTCCCC	TAGAACTGAA	AAAGGGTAGG	300
AGAGGCAAAG	ATAGGAAAAA	TATTTTTAA	AAATTTTAA	GTATTTTATT	TTTATTGGGA	360
AAATATTAT	TGTAAGTCTT	CCATTGTTA	TCCTTCTGCC	ACTAGCATTA	CGTAAAAAGT	420
AAAAAGAGCT	TTACATCAAA	AAGCACAATG	AAACTTTGTA	TCCTTAAGTC	CGTACTCGAG	480

(2) INFORMATION FOR SEQ ID NO:725:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:725:

GAATTCCGCC	TTCATGGCCT	AGTCGGAGGT	GTAGGAGGGG	CCGTGGAGGT	CCAGGTGACT	60
GCTTAGAAAA	CTGCACAGCA	TCTGATGAAA	TTAGCGAATA	AGAACATCAA	CCATGTCTTA	120
CACTCCAGGA	GTGGTGGTG	ACCCCGCCCA	GTGGGCCAG	AGGATCTCTT	CTAACATCCA	180
GAAGATCACA	CAGTGTCTG	TGGAAATACA	AAGAACTCTG	AATCAACTTG	GAACACCTCA	240
AGATTCACCT	GAATTGAGCC	ACAGTTGCA	ACAGAACAG	CAGTACTACTA	ACCAAGCTTGC	300
CAAAGAACAA	GATAAGTACA	TTAAAGAGTT	TGGATCTCTG	CCCACCCACCC	CCAGTGAACA	360
GCGTCAAAGG	AAAATACAGA	AGGATCGTT	AGTGGCAGAG	TTCACAAACAT	CACTGACAAA	420
CTTCCGCAAG	GACTCGAG					438

(2) INFORMATION FOR SEQ ID NO:726:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:726:

GAATTCCGCC	TTCATGGCCT	AGCTACCTAT	CTACAAAAC	TCCTGGATCC	TTTATTACGA	60
ATTGTGATCA	CATCCTCTGA	TTGGCAACAT	GTTAGCTTG	AAAGGGATCC	TACCAGGTTT	120
GTCATTTTT	CACATAGAAC	CGCTGTTTT	TGTTTTTTT	TTTTGTTGT	TTGTTTTACT	180
AAACACTGCAT	GAAGCAAGGC	ACCTTCTCCC	CTTGATCATT	AAAATTAGTT	TTTAATTATA	240
AAAGTTATAT	ACAAATACAC	GTGTTTTAA	TGATATCTGT	AATTTTTTT	TAAGGTATCC	300
TTTATTGTC	CTTAGATCCA	GGGACAAACT	AGAGAAAGGT	GTCTTTGACT	TCCACCTCCA	360
GAGACTGTTA	CTAGTTAAGT	CTGTTCCCT	GTCCCTTTTC	CATGCACCGC	CTCGAG	416

(2) INFORMATION FOR SEQ ID NO:727:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:727:

GAATTGGCC TTCATGGCCT AAGGAGGTCC ATGAGGAAGT CTCCCAGCCT GTCAGTGCAT	60
CTCATGAGTT CGCTGAGTGA TCAGCAGACA GTTCCAGGAA GTGAACAAAGT CCAAGAGGAC	120
TTCTGATTAG TCCACAGTCT CCTCTATAGG CTCAGTAGAT GAAGGGCTT CTGAGGGCTT	180
GCCTACACTT CAAAGCACGT CTAGCACTAA TGCTCCTCCG GATGATGATG ATCGATTGGA	240
AAATGTCAG TATCCCTACC AACTCTACAT TGCTCCTCC ACCAGCAGTA CAGAGCGACC	300
AAGTCCAAAT GGTCCCGACA GACCTTTCA GTGTCCAACC TGCGGGTGC GATTCAACCG	360
TATTCAGAAC CTAAGCAGC ACATGCTCAT CCACTCAGGA ATTAAACCAT TTCACTGTGA	420
CCGCTGTGGG TCTCGAG	437

(2) INFORMATION FOR SEQ ID NO:728:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:728:

GAATTGGCC TTCATGGCCT AGATCACTGC CTTTCAATA ACACCTCTGC CTCTAGAAC	60
ATATGTCAA AGATGAATA CACACCTAGC ACATAGTAGG TGCTCAAATA TTAATTCCT	120
CCTTGCCTTC CTTATCTACC CTGTGTCTC CATTCCCCG TATGATTCCA ACCCAATATA	180
GCAAATGACA TTTACATGTT ATGAAAACAT CTATTGGTA AAATCAGATC TTGGATAAAG	240
AAATTCTGAC TTTTATATAA GCTTTGGTA GACAGAAAAA ACAGAAAGGT ATTCTGTTGGT	300
AGAACATTTT TAAGTTCAAGG AAAGAAAGCT GGAATAATAC TACGTAACCT TGTCAGGGTT	360
ACTTTGACTG AAACACGTTT TTGGTGGATT TCTTTCTC AAAGAACTCT CTAATGCAA	420
CTCCTTGCTG GATTCCCTCAC CCGATCTCGA G	451

(2) INFORMATION FOR SEQ ID NO:729:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:729:

GAATTCAACC ATAAAGATA ATTTATATTA GTGTTCTAT AACTCTAAA ACATCTTTG	60
ATAAGGATAA TAACTCTATT GTCATTCTGT ACTGATATT GGATATAATC CTAGCAGGGC	120
ATAGCTCTGA TTAAAGAACAA TTGAAACCATT CAATTTTTA TTAGCCTCTA TTTTCACTAG	180
CCAGGATATT TTCACTGAAAC TTTTTAGTTT CAAAGCAAGT TTTTCTTTC CAATAGAAAG	240
TGTTATATTA GTAAACAATT TTGCTTCTG CCAAGACCGAG CTCAGTCGGG AAGATCCTAA	300
CCCAGTGGCA AAACCTCGAG	319

(2) INFORMATION FOR SEQ ID NO:730:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:730:

GAATTGGCC TTCATGGCCT AGGGAAGAAT AAAGAACAAA ACCCAAAACT TTGGACCTTA	60
AAAAACCCAG GCTGCATTT TAGTAGCAAT TGGGTGTGTT CGGTTTGAA TATATTTGTA	120
TATACATGCC TCCATGTGCT TTGGCCTTCT GGTATCTCA CCAGATGCTG CCTTTTTTTT	180
TTTTTTAAC AAGTCCCTGT TTCACTTTC CAGCTAGCTG CTGGGTATCT CCAACAAAAT	240
ATCTCATAGA TCTCCAACT GTAAATGTATT CAAGCCAAAAT ATCAGCTCTG CCCATTCTCC	300
ATCCCAAAGC CCCTCCTCTT GGTTACCAGA CAACCTAAC CAAACCACTC GAG	353

(2) INFORMATION FOR SEQ ID NO:731:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:731:

GAATTGGCC TTCATGGCCT AGAGGAGGAA GCCCTTCGTA AAGGTTGCAT CTCCGTCCCT	60
TCGCTCCCGG GGACCCGCGG GAAAAAAAAT AATCCAACAC CCAGGCCCCG CGGCTAGCCC	120
CTTCCACAG GCTCTCTCCG CTCGATTTTG TCACCGTTAT GTGGGAAGCG AATCCATGTA	180
TTTCATGCC CGAGTCTTTG AGCCGTGCTA TACCAAGTTTG TCCAGATTGT TTATACTAGC	240
AATGCACTTT ACGGTGAAGA CCTGCCCTTC CTCTGGAAT CTGGAGCTTC AGTAACAGGA	300
GATGTTTCAC AAAGCAGAAG AATTATTTTC TAAAACAACA ACAATGAAG TGGATGACAT	360
GGACACGTCA GATAACCCAGC TCGAG	385

(2) INFORMATION FOR SEQ ID NO:732:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:732:

GAATTGGCC TTCATGGCCT ACTCCGTCTC CAAAAAAAATAGT GTTCAGCAAG	60
GTTGAAGCAT AAAAGGTTAA TAGCCAGAAT CATTATCAA TTGTATTTCT ATACATCTAC	120
AAGACACAAT CTGAAAATGA AATTAGAGAA ACAATTTCAC TGGCAACAA GAGCAAAACT	180
TCATCTCAAA ATAATAATAA TAATAATAAT AATCATCATC ATCATCATCA TCTACAATGT	240
CATTTCCCAT CCAAGTCTCG AG	262

(2) INFORMATION FOR SEQ ID NO:733:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 503 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:733:

GAATTCCGCC	TTCATGGCCT	AGACCTGCCT	CGAGCTCCGTG	GCCTCGGGCA	CTCTACCCGC	60
TTCAGCCTCC	CAAAGTGCTG	CGACTGATTA	CAAGTATGAG	CCACTACGCC	TGACCATAAC	120
ATGTAAAATT	ATGGCAAATG	GTAATTACA	GCTCAATTCT	AAAATGTGAT	GAAATTAAA	180
TCAGAAAGG	CAAATGAGTC	ACTTTTCTT	AAACACTAAGA	ATTATAAAC	TTTAAATTTC	240
TTTTGTACTG	TAATTTTTA	TGTGACATGT	ATATGTTT	TAATATGTGT	GATAGGATGA	300
GGGGCAGGAG	AGGGGGCTCT	AGACATGAGG	GTGCCTGGGG	CCTCTGTAGA	CCTTCAGATG	360
GCCCTGGGTG	TTATAGCAAG	AGCTGGTCTA	CATCTAATAC	TACTGCAGGT	GCTGTCATGA	420
ATTCTTGTG	TAATTTTTG	TATATTAAAT	GACATTATTC	TATGTATAAT	GTCATTAAAT	480
ACTTATAACC	TACTTCCCTC	GAG				503

(2) INFORMATION FOR SEQ ID NO:734:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:734:

GAATTCCGCC	TTCATGGCNT	AATGGATTCA	TTTTTTTCA	GCAGCATGGC	ATAGTGGATT	60
ATGAAATCAA	AATTAAC	ATGTGGAGTC	NTACATTGAA	ATCCCCCTTC	AACAAAATAG	120
TATACTATGA	GTATTTTAA	ATTATTTAAC	CCCTCCGAAC	ACCAATTGT	ACACGAATAA	180
AACTTGACAC	AACAGGATT	TGTGGGGCGT	GAGTAACACA	ACATATACAA	AAGCACCTTA	240
TAAAGTGTTC	TATATAGCAA	CTCTCTCTC	AGTTGAAACG	GGTCTCAGGA	AAAATTAGCA	300
AATATGAATT	CTAACCTTTG	TACTTACATT	TTAATTCTGC	TAAGTGTGTG	AACCCCAATT	360
TAGCAATTAA	AATATTTATT	TCCAGAATGT	TTTGACCCCTG	AGCATATTT	AAAAAGCAC	420
AGTAGCTCGA	G					431

(2) INFORMATION FOR SEQ ID NO:735:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:735:

AAAAGTGACT	GAAAGTTTG	TAGTGT	TTT	AGTACCGATA	TTTACTGGTA	GTAATATAT	60
ACTAAATCCA	GTGAAATATG	ACTTCTCTAA	CTGAGCTGA	CATATCCTGG	TTATATCTCA	120	
TGGCAGCTGA	AAACTAGAAA	TGACTTATTT	TTACCTTGTA	GCCACAGCAC	ACTTGAGGTT	180	
ATTCTTAGGT	TTTTGTTAGA	GACAAAGCTG	GTTAGTGA	CCTGGATTAA	GAATTATGAG	240	
TGATCCCATA	ACCCCTCGAG					259	

(2) INFORMATION FOR SEQ ID NO:736:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:736:

GAATTGGCC	TTCATGGCCT	AAAGGATATT	GGCATGTTCC	TCTTCTCATC	AATATCCTAA	60
AAGACATTTA	TTTTTACAC	ACTCCTTGGG	AAAATTAAC	TTTTTTCAC	TGAAAATATT	120
TCCTTTTTG	GTTATCTTGA	TCTCAGATTA	TTTTGTGAAA	GAATTTTACT	GTACTTAGTT	180
CAAAGAGTA	GAAAGAATGA	TTTACTATTG	CAGACATATG	TAGGGTAAAA	TCATAATTAA	240
TTTAAACTGA	CTGTACAACA	CCATTTAGAG	TTGATATTGA	CATAAATGTT	ATTAGCCTAC	300
TAATTTGGAA	CTGCATTTCT	CAACAATGCT	GGCAAGCATC	TTCCGTACTT	AGCATACCAA	360
GTTGTAGGGG	AGAGACTGTG	TATATATTAA	TTAAAAGCAA	TCCAAATGGAT	TTGTTTTGT	420
TCATATTTG	GAAACAACTC	GAG				443

(2) INFORMATION FOR SEQ ID NO:737:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:737:

GAATTGGCCT	TCATGGCCTA	CAAAAGATGG	CCCTAACGCT	GGCCTCTAGC	TTTCACTCGT	60
GGTGAATATT	TCAGACCTAA	AGATCCAGAT	AGTATCTCTG	TTCATATGTG	ATAAAGTTGA	120
AGATTGTGGG	GCTACTTTTT	CTCATAGCAC	TTTATTGGA	ATGTTGTTAG	TTTGTGCTGA	180
GAATGGTCGT	CCGTATTTGA	ACCAATTATT	TATTTAAAAA	TATATTTAAG	CTACATTTT	240
GTTTGAAAA	ATTGCCATAA	ATTGGTGCC	ACTTTCTTT	ATTATTTGA	CTGAGTTAAT	300
ATTATTGTAT	TAACATTTA	ACTATATGGT	GTTTACATTC	TTATTTCTTT	TGACATTTG	360
GAAATAATCA	TAACATTGTCT	TTCCAAAATA	ACCATTCT	TGATGGAAC	CTTCCTAGAG	420
TTTTTACCAA	ATAGCTAACT	TTAGTAGTAA	AACCTCATTG	TGTATCCATT	CCCCACTCG	480
AG						482

(2) INFORMATION FOR SEQ ID NO:738:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:738:

GAATTGGCC	TTCATGGCCT	AGATTGTCAG	TTTATCTTAG	ATGATGAGGA	AGCAGTACCA	60
AGAAAACACT	TGGGGGTTGA	TACAAACAGGC	ACATGAGCCC	TTAAAACCTCC	TTCCTGTTTT	120
TTTTCTTTT	TTTTCTCTT	AGGTAGATTA	GTGCATTTAA	AGCCTGAAGT	TAATTTGACC	180
TAAAATTTT	ATAAGTCTTT	GCAGAAAGTT	CACTGTTTC	CTGAAATCAT	CTCCTTGATA	240
ATTTTTATG	TAACAGTTGT	TCATATTGTA	GGAATGATAT	ATATGTCATC	CTGTTACACG	300
TGTCAGGCAC	TCAAAAAAGA	CTCCAAGAGA	ACATGCCCTGA	GAAAGATAAC	TCCCATTAA	360
AAATGATTCA	GTCCTCACT	TGCAATATTG	AGGATAATG	TGTTGAAACA	TTAGGCTACC	420
AGATAAATAA	AAGGTAGTTA	TTTCCTAGGG	TGACTCAGCA	AGATATTCT	CGAG	474

(2) INFORMATION FOR SEQ ID NO:739:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:739:

GAATTGGGCC TTCATGGCCT AGCCTTGAG ATCAATACCT GTGAAAAGTA GGGAAAGAAA	60
GCAGATGAGG CATAGGGAAA AGGTGGACTG CCACAGGAA CCCAGCGAAC CTCACCAGCA	120
GCTCTGGAGC TAAAATAGCT CTTTCAAATT GTCCAGAGTT GGGCTGAGGA GGCCAGAATT	180
TTATTGTGT TCCCCACGATG ACGACTTCGA G	211

(2) INFORMATION FOR SEQ ID NO:740:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:740:

GAATTGGGCC TTCATGGCCT AAATACCTTA ATGGTGGTAG AGCCTTTACC TGTTAGCTTGA	60
AAGGGAAAG ATTGGAGGTA AGAGAGAAAA TGAAAGAACCA CCTCTGGGTC CTTCTGTCCA	120
GTTCAGCA CTAGTCTTAC TCAGCTATCC ATTATAGTT TGCCCTTAAG AAGTCATGAT	180
TAACCTATGA AAAATTATT TGGGGACAGG AGTGTGATAC CTTCCCTTGGT TTTTTTTTGC	240
AGCCCTAAA TCCTATCTTC CTGCCCCACA ATGTGAGCAG CTACCCCTGA TACTCCTTTT	300
CTTTAATGAT TTAACTATCA ACTTGATAAA TAACCTATAG GTGATAGTGA TAATTCCCTGA	360
TTCCAAGAAT GCTCGAG	377

(2) INFORMATION FOR SEQ ID NO:741:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 343 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:741:

GAATTGGGCC TTCATGGCCT AAGGCCTTGTG GGGTTCCCTA GTTGTGCTGC TGCTCTTGCC	60
TAGGAAATCT CCTCTTGCTT TGGCCTCTTT CCTTGGGGCA AGACTGAGGG GGACAGGGAG	120
CTTCAAGTCA CCCCTCCATG TTGAAGTTTG GTAGAAGCTC TGCCCAACACC TTGGACTGGA	180
ACCCAGCCAT GCCAATCCCC ATGATCACCA ATCCGAACCC CTTGAAGTAG AATTTTCATA	240
CCCTACTGAC TAACCACCTT CTTAGCCAGG CCATAGCCAT TCAGCAGTGC CTCCCTCCTC	300
TGGGTAGACA AACAGCCTTG AACAGAAAGG TGGAAACACTC GAG	343

(2) INFORMATION FOR SEQ ID NO:742:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 259 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:742:

GAATTCTGGCC TTCTGGCCTA GAGTCCTTGT TGTCCCTTGC AAAGGTTGCT CATCACCTCT	60
CCCCCTCCCTC TGGCTCTTT CCGTGGTGAT GCATAGTTCA ATGCGCCCG GAAGCTTCAT	120
GATGAGGCCG TCAACCCAAAC TAGCAGCCCT CCTTTCCCTC TTTCTTTGCC AAGTGTCCCTG	180
GACATCAGCT CTTCCTCAGT CTTTGACTCT AAATAAAGAA CTTGAATTTC ACCATTCAAC	240
TGAAATCCCT CTAACCTCG	259

(2) INFORMATION FOR SEQ ID NO:743:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:743:

GAATTCTGGCC TTCATGGCCT ACACCGTCGC CATTGCCAGA AAGAGCGATT TATGGCTTTG	60
TTCTTTCTT AAGCTCCAA TTTGGCTTCA TACTTACCT CGTGTGGGCC TTTATTCCCTG	120
AATCTTGCT AAACCTTTA GGTTTAACCT ATTGGCCTCA AAAATATTGG GCAGTTGCAT	180
TACCTGTCTA CCTCCTTATT GCTATAGTAA TTGGCTACGT GCTCTTGTGTT GGGATTAACA	240
TGATGAGTAC CTCTCCACTC GACTCCATCC ATACAATCAC AGATAACTAT GCAAAAAATC	300
AACAGCAGAA GAAATACCAA GAGGAGGCCA TTCCAGCCTT AAGAGATATT TCTATTAGTG	360
AAGTAAACCA AATGTTCTTT CTTGCAGCCA AAGAACCTTA CACCAAAAAC TGAACGTGT	420
GTAACCATAG TAACACCAAG CACACTCGAG	450

(2) INFORMATION FOR SEQ ID NO:744:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:744:

GAATTCTGGCC TTCATGGCCT AAATCTTCAG GGTCTTAAC TAGTTTTGTA TCCCTAAAAT	60
TAGTGCTGCA TATGTAGACT CAGAAACCTC ACGTAAAAT TAAATTGGC CTCAGGTTGG	120
CAATGTTCCA AGGCAATGGT TAGAAGCAA TTCAGATTCT CCAAGGCCTC AAATAATTCC	180
TACAGATAAA ATCCCAAGGA AATTCAAGCAG TGCTTAGTCA AAAATCCACA AATCAGGCTC	240
GAG	243

(2) INFORMATION FOR SEQ ID NO:745:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:745:

AAGCGAGGCC	CTGGGGACA	ACGTAAAC	ATACTGGCT	AACTAAAGC	TGTGTTCAA	60
GCAGAAGATC	AGCAAGAGG	AGTTTGACCT	TGAAGCTCAT	AGACTTCTCA	CACAGGATAA	120
TGTCCATTCT	CACAATGATT	TCCTCCTGGC	CATTCTCACG	CGTTGTCAGA	TTTTGGTTTC	180
TACACCAGAT	GGTGTGGAT	CTTTGCCTTG	GCCAGGGGT	TCCCGAGCTT	CTCGAG	236

(2) INFORMATION FOR SEQ ID NO:745:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:746:

GAATTCTAGA	CCTGCCTCGA	GCCTGCAGAC	ATCTCCCT	TCTTTGTGGT	TCTGGGAGCC	60
ATTCTGTGCC	TCTAAAGGTCC	TCTTTCTTTT	TTCTCACCAA	TACACATATT	TTCTGTCCCT	120
CGCAATTCTA	TTAACACCTCA	CATTTGATGG	TTGTTTCTT	AAAATTCCCTT	TACTGGTTC	180
CTGCATTCT	CATTCCCTCC	CAGCACAATC	TCGAG			215

(2) INFORMATION FOR SEQ ID NO:746:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:747:

GAATTGGGCC	TTCATGGCCT	AGAAGAAAAC	CCATCAGATA	TTATAATAAG	ACAATAACTC	60
AATTTCAGAC	TTGAAACAA	AGGTGACATT	AATCTATTGA	AATGTGGAA	AATAGTCAAC	120
CTGTATCCTT	CTCATACCAT	AAATCAGCAT	TTTGATCAC	TGGAAGCTTC	ATTTGATGA	180
TTAGCAGTCA	TGTATTGAGG	CTAAATGATA	TGTTTGTGCG	ACAGCATCTC	GAG	233

(2) INFORMATION FOR SEQ ID NO:747:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:748:

GAATTGCCT	TCATGGCCTA	CACAGGAGAA	AAACCCATG	AATGTAGTGA	ATGTGGAAA	60
ACTTTTGTTC	AGAAGTCCAC	CCTCAGAGAT	CATCACAGAA	TTCACACAGG	GGAGAAATCC	120
TTTCAATGCA	ATCAATGTGG	AAAAACATTT	GGCCAGAAGT	CAAACCTAG	AATACATCAG	180

AGAACTCACA CTGGGGAGAA AACTTACCAAG TGTAAATGAAT GTGAAAAATC CTTCTGGCGA	240
AAACATCATC TCATTCAACA TCAACTCGAG	270

(2) INFORMATION FOR SEQ ID NO:749:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 309 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:749:

GAATTCTAGT TTAATTACAT ATACCTCTCT GTTGGCTTAG TAGTAATAAA AATATTTCT	60
GTAGGTGAG AATATCCTTA CAGTCCAAA GGAGAGTACA TGTCACAAT TAAAGTTGA	120
AATTGTGCT TTGATAACAG CATGTTTAT TCATTCAATT TTATAATAAT ATTACTGAGC	180
CTGTATCATA TAGTGATGAA CTTTCAGCT GTTTGAGGG TTTGTGTTAG CCACATTCAC	240
ATTTGTATAA CCTGTGTTTC TTTTTTATTTC TTCTTTATTTC TCATTTAGA TTCAGGGGGT	300
CGGCTCGAG	309

(2) INFORMATION FOR SEQ ID NO:750:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 328 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:750:

GAATTGGCC TTCATGGCCT AAGCTCTTT AGTGAAGGAT TGTTTAAAT AAGAGCTCTC	60
AGTTCAAGAC AACTACTGTT AGGAGCTAA ATCGGAACCA CAATCAGCAT ATAAAGGTCC	120
TAATCCTGAC CTTAACCCCT TTGGAATATT GCTTTATAA ATCATCAATC AACAGTGTTC	180
CACTATGAAA GCATATTCTG TCTTCTTCTT TTCATGTATT CCTTCACTGC TGGTGCTTAA	240
TGTCTTCCCT TCCCTCTCTG CCATTTCTCT TTCCATGAAT TATAATTGCC TTTGAATTG	300
AGAAATTAAA ACCACTCCAC AGCTCGAG	328

(2) INFORMATION FOR SEQ ID NO:751:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 239 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:751:

GAATTGGCC TTCATGGCCT AATAAGGAAG AAATTGTCTC ACTTTATTGA ATAGTTGATT	60
AAAAATTTCT GTTATTTAGA GGTAATATAG TATAAGTTT TTGTATATT ATCTAAGATT	120
TTCCCTTCTGA AAATTTCTT CCCCTTCAT ATTATTTCA TTAAACGATT TTCCATTAAA	180
ATTGTTACT ACAAGAACT ATCTAATATG CAATGAGATT TTTGCAGGGC ATTCTCGAG	239

(2) INFORMATION FOR SEQ ID NO:752:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:752:

GAATTCCGCC TTCATGGCCT AAGGAAAGTA CTTTAGACAA AAAAAAAA AAAAGTGA	60
TTAACCTCTG GGGCAATGAA AGGAAATGTC ATTGGCAGTT TTACCTTAT TCTGCTAATG	120
GCTATTGTGT GTCTGTTAC CTGGAGGCAC TTGGAACTTG TGGCACAGAA TGCTGTATGT	180
ACAGGATATC ATCTACATGG GAATAATTGT TGAAACACC CCAAACTCGA G	231

(2) INFORMATION FOR SEQ ID NO:753:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:753:

GAATTCCGCC TTCATGGCCT ACAATAGAGC TCTTAAACTT ATTTAACTGA AATTTGTAT	60
CTTTTCACCA ACATTTCCCC AACTCCCCCTT TACCCCAACT ACTCCAGCCA CTGATAACCA	120
CCATCTCTGTT CTCTATTTCT TTTTCTTTT TTTTTTTTTT TTTTTAAGAG ATGGCGTCTT	180
GCTGTGTCGC CCAGGCTGAA GGGCAGTGGC ATGATCTCGG CTTACTGCAA CCTCTGCCTC	240
CCCGGTTTAA GCAATTCTCT ACCTCAGCCT CCCGAGTAGC TGGGATTACA AGCACCCATC	300
CACTCGAG	308

(2) INFORMATION FOR SEQ ID NO:754:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:754:

GAATTCTAGA CCTGCCCTGA GCCCTTTGTG GTTTTTAAGA AAAAAATTCT GTGCAGATCT	60
GTTCCCTCTC CTGCTCCTTC CCTTTCTCT ACATACAGTG CTCATTGGAG GCTCCCCACT	120
CGAG	124

(2) INFORMATION FOR SEQ ID NO:755:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:755:

GAATTCTGGCC	TTCATGGCCT	AATCGGTGTC	TTTGGTAAAA	ATTCTATGAG	GATGACATAT	60
TCCATCATGT	TATTCGTTTC	ACATTTCTT	TTGCTCAGTC	TCCAATGCAA	GCACAGCTTG	120
TGGTATAACC	TATTGTTTTC	CCATTCTAA	AACTTCTCAA	TCGATCTTCG	TGTTCTTTA	180
CTGAGGCCAA	TAACTGGCCA	CATACTGCAA	CCTAATGTGC	AGCAGCAACA	AAGGCAGCCA	240
CAAAGTAGCC	AACGTACATT	AACAGGAAGG	TTCTTCTTAA	GACAATGTGTT	AACTCTGTTG	300
ATGCTGGCTT	AAATTCTTC	AGGAGCTACT	TTTCAAGTTA	ATGAAGAAGG	GAATTCAAGAT	360
TCAAATTG						369

(2) INFORMATION FOR SEQ ID NO:756:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:756:

GAATTCTGGCC	TTCATGGCCT	ACCGGCGAGG	AATAGGAATC	ATGGCGGCTG	CGCTGTTCTG	60
GCTGCTGGGA	TTCGCGCTGC	TGGGCACCCA	CGGAGCCTCC	GGGGCTGCCG	GCACAGTCTT	120
CACTACCGTA	GAAGACCTTG	GCTCCAAGAT	ACTCCTCACC	TGCTCCTTGA	ATGACAGCGC	180
CACAGAGGTC	ACAGGGCACC	GCTGGCTGAA	GGGGGGCGTG	GTGCTGAAGG	AGGATGCGCT	240
GCCCCGCCAG	AAAACGGAGT	TCAAGGTGGA	CTCGGACGAC	CAGTGGGGAG	AGTACTCCTG	300
CGTCTCCTC	CCCGAGGCCA	TGGGCACGGC	CAACATCCAG	CTCCACGGGC	CTCCCAGAGT	360
GAAGGCTGTG	AAGTCGTCAG	AACGCATCT	CGAG			394

(2) INFORMATION FOR SEQ ID NO:757:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:757:

GAATTCTGGCC	TTCATGGCCT	ACTGATGTTG	AAGACGACAC	CACGGCTTTG	ATGGAATATC	60
AGATATTGAA	AATGTCTCTC	TGCTGTTC	TCCTTCTGTT	TCTCACACCT	GGTATTTTAT	120
GCATTGTCC	TCTCCAATGT	ATATGCACAG	AGAGGCACAG	GCATGTGGAC	TGTTCAAGGCA	180
GAAACTTGTC	TACATTACCA	TCTGGACTGC	AAGAGAATAT	TATACATTTA	AACCTGTCTT	240
ATAACCACTT	TACTGATCTG	CATAACCACTG	TAACCCATA	TACCAATCTG	AGGACCCCTGG	300
ACATTTCAAA	CAACAGGCTT	GAAAGCCTGC	CTGCTCACTT	ACCTCGGTCT	CTGTGGAACA	360
TGTCTGCTGC	TAACAACAAC	ATTAACACTTC	TTGACAAATC	TGATACTGCT	TATCAGTGGA	420
ATCTTAAATA	TCTGGATGTT	TCTAAGAAC	TGCTGGAAAA	GGTTGTCCTC	ATTTAAATA	480
CACTAAGAAG	TCTCGAG					497

(2) INFORMATION FOR SEQ ID NO:758:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 758:

GAATTCCGCC TTCATGGCCT AACCAAATCA ACAACAAACCT ATTTAGCTGT TCCCCAACCT	60
TTTCCTCCGA CCCCCCTAACCA ACCCCCCCTCC TAATACTAAC TACCTGACTC CTACCCCTCA	120
CAATCATGGC AAGCCAACGC CACTTATCCA GTGAACCCT ATCACGAAAA AAACCTCTACC	180
TCTCTATACT AATCTCCCTA CAAATCTCT TAATTATAAC ATTACACAGCC ACAAAACTCG	240
AG	242

(2) INFORMATION FOR SEQ ID NO: 759:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 759:

GAATTCCGCC TTCATAGCCT ACCTAAATTA ATAATAATGT ATAGTTAGA ATTGCTAAGA	60
GTACTTTTTT TTTTTTTTTT TNGAGACAGG TTCTCGCTCT GCCCTCCAGC CTGGTGACAG	120
AGCAAGATTG CATCTAAAAA AAGAAAAAAA ACACACAGCT AATAGAATTG CCATTGTTTT	180
TCATAATAGA ATCTAGCTGC TTACTCCAAAC CTCACCTCGA G	221

(2) INFORMATION FOR SEQ ID NO: 760:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 760:

GAATTCCGCC TTCATGGCCT AAAATCAAAG ACTTTGCCAA TACCATTCCCT GGCCATGGAG	60
GCATCATGGA TCGTTTGAC TGCCAGTATC TGATGGCCAC CTTGTCAAT GTATACATCG	120
CCAGTTTTAT CAGAGGCCCT AACCCAAGCA AACTGATTCA GCAGTTCCCTG ACTTTACGGC	180
CAGATCAGCA GCTCCACATC TTCAACACGC TGCGGTCTCA TCTGATCGAC AAAGGGATGC	240
TGACATCCAC CACAGAGGAC GAGTAGGGGC CACCCAGGGC CAGGAGAACA GGAACAGAAC	300
TGAGCAGGGG CAGGTCTCCA AGGCAAGCCC AGCTGGTGTG ACTTAGACAA TGACGAGGCT	360
TCAACTCACT GTCTTTTTTTT TTTTTTTTTG GAGGGTATTT TTTATTTGTG GGTTCAAAAA	420
ATCTGTATAT ACAGTCTATG TGTTAGAAT TTGTGTTGTA AGTAAACTAC AGCTTTGAGT	480
TGGAAAGAAG TCACGGGTTG TAAACCAATT TGGATTTTTT TAAACAAAAA GTATTAATAA	540
TCTGGAAGAC TCGAG	555

(2) INFORMATION FOR SEQ ID NO: 761:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:761:

GGCCGATCG	GTTATTTTT	GAAAGTTTA	CTTACAGAGC	ATATAAATT	CCCTGGTTA	60
TTCTCAGCTG	TGATTGAGTT	CTGTGAAAGC	ATAGTACCT	AGTACCCCTG	GATATCTCA	120
CATGTGAAAT	TATTCAAATG	TCTCCCTTAC	TTTTTTTTT	TTTTTTTTG	AGACAGGCTC	180
TGTTGCCCAT	GCTGCAGTGC	AGTGGCACAA	CTATGGCTCA	TCTCAGCCTC	GACCTCCTGG	240
GCTCAAGCGA	TCCTCCCACC	TCAGCCCCC	AGGCAGCTGG	GACCACAGGC	ACACACCACC	300
ATGTCCAGCC	AATTCCGTGA	TTTT				324

(2) INFORMATION FOR SEQ ID NO:762:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:762:

GAATTCCGCC	TTCATGGCCT	AGTGCCTGGG	AGAAAGGGCT	TCCTCCCCA	CACATCAGAC	60
AGGGCACCAA	TGAGTGGGGC	ACTAAAAAA	GAGAGCAGGC	CCTGGAGAGG	AAACCAAAGC	120
AAAGGTTAGT	TTTATAATCT	GATCCCTAA	TTACCTGTAA	TTCATATTTT	CTAAATGCAT	180
TAGCTCTAAT	TCATTGTACT	CCCCCCAAA	CAGAATAATA	CTTTGAAACA	TTAAATACAA	240
ACTACAACTA	AAAAAATAAA	ATTAGGCCCTG	CGGTGGTGGC	TCATGCCTGT	AATCCCAGCA	300
CTTTGGAAGG	CCGAGGCCGG	TGGATCACTC	GAG			333

(2) INFORMATION FOR SEQ ID NO:763:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:763:

GAATTCCGCC	TTCATGGCCT	AATTGAATC	AACACAACCA	CCCACAGCCT	AATTATTAGC	60
ATCATCCCTC	TACTATTTT	TAACCAAATC	AACAACAACC	TATTTAGCTG	TTCCCCAACCC	120
TTTCCCTCG	ACCCCTAAC	AACCCCCCTC	CTAATACTAA	CTACCTGACT	CCTACCCCTC	180
ACAATCATGG	CAAGCCAACG	CCACTTATCC	AGTGAACCCAC	TATCAGAAA	AAAACCTCTAC	240
CTCTCTATAC	TAATCTCCCT	ACAAATCTCC	TTAATTATAA	CATTACAAC	CACAGAACTC	300
GAG						303

(2) INFORMATION FOR SEQ ID NO:764:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:764:

GAATTGGCC TTCATGGCCT AGGGATTTAA AGAGTTTTC TTGGGTGTT GTCAAACCTT	59
TATTCCTGT CTGTGTGCAG AGGGGATTCA ACTTCATTT TTCTGCAGTG GCTCTGGGT	120
CAGCCCCCTTA CTTAAAGATC TGAAAGCAT GAAGACTGGG CTTTTTTTCC TATGTCTCTT	180
GGGAACGTCA GCTGCAATCC CGACAAATGC AAGATTATTA TCTGATCATT CCAAACCAAC	240
TGCTGAAACG GTAGCACCTC TCGAG	265

(2) INFORMATION FOR SEQ ID NO:765:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:765:

GAATTGGCC TTCATGGCCT ACCAACAGCA AGCTCCAATA TCACACATCC AGACTCCTAT	60
GCTTTCCCAA GAACAGGCAC AACCCCCGCA GCAGGGTTTA TTTCAGCCTC AGGTGGCCCT	120
GGGCTCCCTT CCACCTAATC CAATGCCCTA AAGCCAACAA GGAACCATGT TCCAGTCACA	180
GCACCTAATA GTTGCCATGC AGAGTAACTC TCCATCCCAG GAACAGCAGC AGCAGCAGCA	240
ACAGCAGCAG CAACAGCAGC AGCAACAACA ACAGAGCATT TTATTTCAGTA ATCAGAATAC	300
CATGGCTACA ATGGCGTCTC CAAAGCAACC ACCACCAAAC ATGATATTCA ACCCAAATCA	360
AAATCCAATG GCTAATCAGG AGCAACAGAA CCAGTCATT TTTACCAAC AAAGTAACAG	420
TCTCGAG	427

(2) INFORMATION FOR SEQ ID NO:766:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:766:

CGATTGAATT CTTGTCTGTT CTGCTCACT CCCGAGCTCT ACTGACTCCC AACAGAGCGC	60
CCAAGAAGAA AATGGCCATA AGTGGAGTCCT CTGTGCTAGG ATTTCATC ATAGCTGTGC	120
TGATGAGCGC TCAGGAATCA TGGGCTATCA AAGAAGAACAA TGTGATCATC CAGGCCGAGT	180
TCTATCTGAA TCCTGACCAA TCAGGGAGT TTATGTTGA CTTTGATGGT GATGAGATTT	240
TCCATGTGGA TATGGCAAAG AAGGAGGGTC TCGAG	275

(2) INFORMATION FOR SEQ ID NO:767:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:767:

GAATTGGCC TTCATGGCCT ACGTAATTCT GGAAAAGTGA ATACTTGTGA AGAGTCGTCT	60
TGAATGATTT GTAAAAAAATC CTGTTCTTAT ATTCAACGAG TTTCGAATCT TTGTCAGAGG	120

AGTATTACCA TTAGATGAA AAAAAGAAA ATAAATAATA AACACTTTA AAAAAACTCC	180
CCATTCTCTT ATTCTCACTT TTAGGAAAAG AGACTGACTA ATATCTTCTG CCACAAATAC	240
CGATGTTCTT AAAAATATT ATGGGACTGC TTTTGGCAAC CAGCCCTATT TGTGTTTCAT	300
ATCCCTTTT GCTCCCATCT TTCCAAACTC ATAAACTCGA G	341

(2) INFORMATION FOR SEQ ID NO: 768:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 281 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 768:

GAATTGGCC TTCATGGCCT ACAGAAAGAG TTTGAGACCT GAATAGCTCC CAGATTCAG	60
TCTTTCTG TTTTGTTAA CTTTGGGTTA AAAAAAAA AAGTCTGATT GTTTTAATT	120
GAAGGAAAGA TTGTAATAC AGTTCTTTG TTGAAAGAG TTGTGTTGTT CTTTCCCCC	180
AAAGTGGTTT CAGCAATATT TAAGGAGATG TAAGAGCTT ACAAAAAGAC ACTTGATACT	240
TGTTTCAAA CCAGTATACA AGATAAGCTT CCAGGCTCGA G	281

(2) INFORMATION FOR SEQ ID NO: 769:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 352 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 769:

GAATTGGCC TTCATGGCCT ACTAACGAGG AAAGGGATT AAAGAGTTTT TCTTGGGTGT	60
TTGTCAAAC TTTATTCCCT GTCTGTGTC AGAGGGATT CAACTCAAT TTTCTGCAG	120
TGGCTCTGGG TCCAGCCCT TACTTAAAGA TCTGAAAGC ATGAAGACTG GGCTTTTTT	180
CCTATGCTC TTGGGAACTG CAGCTGCAAT CCCGACAAAT GCAAGATTAT TATCTGATCA	240
TTCCAACCA ACTGCTGAAA CGGTAGCAC TGACAAACACT GCAATCCCA GTTTAAGGGC	300
TGAAGCTGAA GAAAATGAAA AAGAAACAGC AGTATCCACA GAGAGACTCG AG	352

(2) INFORMATION FOR SEQ ID NO: 770:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 316 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 770:

GAGCGTGGTG GATATAAAAC AGGTAAGAGA CTTTCATGGT ATACCTTTAT ATTGTTGGAT	60
TAAAGGCACT GCCAACTCAA AAAACTTAAAC CGAAAATTTC TTTTAATCAG TTAAATATT	120
ACTGATATGA AAATGACATG AAACTAACCTT TTGTTGTTT ACTTAAAGGG TGCTCTGTTT	180
GAAACTTCCT CAGACAACAG AATGGGAGAA CCAGATGAAT TTACTAAAAG TATTAACGTC	240
AAATATTAT ACTGCTTTTT TTTGTTGTT TGTTTTGAG ACAGAATCTT GCTCTGTTGC	300

CCAGGCTGGT CTCGAG

316

(2) INFORMATION FOR SEQ ID NO:771:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:771:

GAATTCGGCC TTCATGGCCT ACTTTGATGG AATATCAGAT ATTGAAAATG TCTCTCTGCC	60
TGTTCATCCT TCTGTTCTC ACACCTGGTA TTTTATGCAT TTGCTCTCTC CAATGTATAT	120
GCACAGAGAG GCACAGGGCAT GTGGACTGTT CAGGCAGAAA CTTGCTACA TTACCATCTG	180
GACTGCAAGA GAATATTATA CATTAAACC TGTCTTATAA CCACCTTACT GATCTGCATA	240
ACCAGTTAAC CCAATATACC AATCTGAGGA CCCTGGACAT TTCAAACAAAC AGGCTTGAAA	300
GCCTGCTCTGC TCACTTACCT CGGTCTCTGT GGAACATGTC TGCTGCTAAC AACACATTA	360
AACTTCTTGAT CAAATCTGAT ACTGCTTATC AGTGGAAATCT TAAATATCTG GATGTTTCTA	420
AGAACATGCT GGAAAAGGTT GTCTCATTA AAAATACACT AAGAAGTCTC GAG	473

(2) INFORMATION FOR SEQ ID NO:772:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:772:

ATACAGTAAT CAAAGTAAGT AATATTTCAA TCCAATATTT TAAAAAATCA GAATTAATGC	60
AAAAAAAAACC ATGATGAACA AAATATTAAA ATTTAAAATA AAGACAGGGAT TAGTATTACT	120
GAGTTTCCT TTTGTCAG GCTCTAATAT GGCTGGCAT GGGCGAGAAC ATTACAACAT	180
ACCAGTCGTG TCATGGTGCC CAAGGCTCCA CAGACCTCAG TGGCTCCCTG CTGCCTGCCA	240
CAGCAATCTC GAG	253

(2) INFORMATION FOR SEQ ID NO:773:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:773:

GAATTGGCC TTCATGGCCT AGTGAGAATT GACTGTTGCT TTTGTTTGCC TGCTTACTGTT	60
TTTCCTTAT TTATTTGTT TTGGACCTGT GGCACAAAGG ATCTGTTAC TGACCATCCT	120
TATTTGAGG CACACAGTCAC CCATGGCACC CTGCGCGTA CTCTGTTCC ACTTGTTAT	180
TCTCTGTATC CCCATACTAG TTATTATCGA AACCATCAGC CTACTCATTC AACCAATAGC	240
CCTGGCCGTA CGCCTAACCG CTAACATTAC TACAGGCCAC CTCGAG	286

(2) INFORMATION FOR SEQ ID NO:774:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:774:

GAGGCTGACA AAATACTCAC CTTTACCTTT ATTTTGAT TTTATACTCA CAACCATATT	60
TTTTTGGCC CCCTTCCCTT TATTTTAACT CATAACTGAT ACTTAAAGGT GCTCTGCCTT	120
ATTAATTCAG CTCCCTAGGCT GCAAGTGCAT AATATTTAAA AATTGCAAC TTGACTTTT	180
TAAAAATCTG GTCTTGGTAT GGAGCAACT TGCCCTTTTT TTTTTTTTTT TTGAGACAGA	240
GTCTCGTTT NTGCCCCAGG CTGGAGTGCA GTGGTCCCAT CTCAGCTCAC TGCAACCTCC	300
TCCTCCCCGGG TTCAAGAGAT TCTCCTGCCT CAGCCTCCCG AGTAGCTGGG ATTACAGGTG	360
CCTGCCCAA CACCCCTCGAG	380

(2) INFORMATION FOR SEQ ID NO:775:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 347 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:775:

GGCCTGGTAG GATAAGAATA TAAACTTCAG GGTGACCGAA AAATCAGAAT AGGTGTTGGT	60
ATAGAATGGG GTCTCCTCCT CGGGCGGGGT CGAAGAAGGT GGTGTTGAGG TTGCGGTCTG	120
TTAGTAGTAT AGTGATGCCA GCAGCTAGGA CTGGGAGAGA TAGGAGAAAGT AGGACTGCTG	180
TGATTAGGAC GGATCAGACG AAGAGGGGCG TTTGGTATTG GGTTATGGCA GGGGGTTTTA	240
TATTGATAAT TGGTGTGATG AAATTGATGG CCCCTAAGAT AGAGGAGACA CCTGCTAGGT	300
GTAAGGAGAA GATGGTTAGG TCTACGGAGG CTCCAGGGAA GCTCGAG	347

(2) INFORMATION FOR SEQ ID NO:776:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 348 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:776:

GAATTGGCC TTCATGGCCT AAGAGGATAA GGGAGAAAA AGAAGAAAGT ATTCCATTCC	60
CACATCCCTT TAGGTTGGCT TCTTATTTA TGTTTTGTT GGTGTTTA TTTTGCTTTG	120
TTAACATTTT CAACTAGCTA TAGAAACGTT TGAATTCTT ATTACTGATT AGCATTCAA	180
AACTTGTAA TGAACATTTT TCTCTCTTC TTTTTTTTT TTTTTNGAG ACAGGGTCTC	240
GCTCTGTAC CAAGCTGGAG TGCAGTGAGC CAAGATCTA CTGCTGTCCA TTCCAGCCTG	300
GGTGACAGAA CAAGACCTTG TCCGCCCCACC TTCCACCCCCC CCCTCGAG	348

(2) INFORMATION FOR SEQ ID NO:777:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 377 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:777:

GAATTCGGCC TTCATGGCCT ACATGTTAT TGAGCATT A	CTGTTACCC ATCAGTATT C	60
TTGATGCTAA GGATATAGCA GTGAACAAA CAATCCTGT GGACTTACAT C	ATAGTAGGG	120
AAAATAGACA ATAAATAAT GTATGATAAG TCAGTTGATA ATAAGTGCTA CGAAGTAAA	C	180
CAAAGCAGGA ATAAAGTTGG GGAGAAAAGT GGAGGGTGT TGCTATTCA GTTGAGATCA	TG	240
TTGGGATGGT CTTTCTGAG GAGGGACAT TTGCATAGAG AACCAAGGAT GTGAGTTATG	300	
TGTCTGCTGT GTGTAGAAC A TTCTGGAAA GGGCAGAGAA GGGAAACAAGA CTATTCCAGA	360	
AAAAGAGGGC ACTCGAG	377	

(2) INFORMATION FOR SEQ ID NO:778:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 304 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:778:

GAATTCGGCC TTCATGGCCT AGCACAGCTA GACGGTTCCA GCTCAGGGTC TCTCATGAAG	60
TTGCAATCAA AATATTGGCA GGAGAGAAAA ACATATTTTC AGAACGCTGCA GGCATAGGAA	120
GACTTGGCTG GGGTTGAAGG ATCCACTTCC AAGATGGCGC ACTCAGTGGC TCTTGGCTGG	180
AGGCCTCAGT TCCCTGCTGC GTGGAGCTCT CCCTCCAGCT GCTTGAGTGG ACTCATGACA	240
TGCAGCTGGC CTCCCCCTGGA GCAGTCGATC CAACAATGAG CATGGCCATG AACTAGAGCT	300
CGAG	304

(2) INFORMATION FOR SEQ ID NO:779:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 316 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:779:

GAATTCGGCC TTCATGGCCT AGCCAAAACC ACAGAAATATA TAATATAGAT CTTGGGGATA	60
CAGCAGAGAA AAAAGACAAA AATCCCTGTT ACAATCCGTT CTAGAATTGA TGTTCCCTTG	120
TTGGTTAATT CAAGTTTGAA TTTCAGAAAT CTTACCTCTT GGTGACTGCC TAGAGTGGCA	180
TTGGGCTGGA GGGGAGGAAC TGTTCATGTT GGAAATGGGG AATGGGCCAA AAATGCAATT	240
GAGTAGGTTG ATTAACCTGT CTGCTGTCAG AGTGAAGCA GGGTAGTTT CCCTTCCGA	300
CCAGAGGCAT CTCGAG	316

(2) INFORMATION FOR SEQ ID NO:780:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:780:

GAATTGGCC TTCATGGCCT ACAGAACGATT TGGACAATTC CATTGATAAA ACAGAACGCTG	60
GAATTAAGGA GCTTCAGAAC AGTATGGAGC GCTGGAAAAA TATGGAAAAA GAACATATGG	120
ATGCTATAAA TCATGATACT AAAGAACCTGG AAAAGATGAC AAATCGGCAA GGCGATGCTAT	180
TNAAGAAGAA AGAAGAGGTGT ATGAAGAAAA TTCGAGAACT TGGAAGACT CCCAGGAAG	240
CATTTGAAAA GCACCAGGCT CGAG	264

(2) INFORMATION FOR SEQ ID NO:781:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:781:

GAATTGGCC AAAGAGGCCT AGCGATTGGG TCTTGATAT CTGTAAGCCG TTGAATTAGC	60
CCTGCCCTCT GTTCTTAGTT TAGGAGACCA TAGATGTGCC CTTATTATTG AACTGATT	120
TATTCAGTTA CTGAAGTTAT CTTACCTGAT ACATAATTT ACCCATAGAA ATAATATGA	180
AAATAGCAAAT ATCACTCAGG TAAGATAGAT GAGTGCCTGC TGTGTTCAAG AGACTGTTAA	240
TATGAGGCTC TGGGGCTGCA AAAAATCAAG TTGCTAAGAA ATATGAGGTC AGAGCAGCAG	300
AAGTTCTGAG TAACCACTGA TTACTGGACT TGGGGTGTAC AGAAGTGACT GTGTGGGAGA	360
GGTGAAATTG AGCAGACTCT GAAGGAACCT CTGGGTTTTG GTAAATAGGG AGCTGGGAT	420
GAGGATGCC CAGGTTTTAG AAAGAACACA GGCTGTTGAA TCACACCTGG GTTCAAACCC	480
TGGCTTGCTA CTCCCCTAGTT TGTGACCTTG TCAAATTCT TGATTTCTTT TTCTTTTTC	540
TTTTTTAAAT TTGGAGACA ACAGTCTCCG TCTGTCACCC	580

(2) INFORMATION FOR SEQ ID NO:782:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:782:

GAATTGGCC AAAGAGGCCT AGAATGGTAG AGTAAAAAGA ACCCTCTGCT GAGTAACCAA	60
GCCTTTAATT TCCTGTTCCCT GCTGTAGGGC TTTCACAAAT GCATTTTCA GCCGTTGGT	120
GTGTCCTCGA G	131

(2) INFORMATION FOR SEQ ID NO:783:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:783:

GAATTGGCC AAAGAGGCCT AGATTGAGGT TGTGGTAGAT TAGCGTAGG TAGAAGTGA	60
GGTTAAGGAG GGTGATGGTG GCTATGATGG TGCGGCTCGA GGCAGGTCTA GAATTCAATC	120
G	121

(2) INFORMATION FOR SEQ ID NO:784:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 405 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:784:

GAATTGGCC AAAGAGGCCT AAGCAAGATG AAGCCCCAACAA TCATCTTGT ACTTTCCCTG	60
CTCCTCATCT TGGAGAAGCA AGCAGCTGTG ATGGGACAAA AAGGTGGATC AAAAGGCCGA	120
TTACCAAGTG AATTTCCCA ATTTCCACAC GGACAAAAGG GCCAGCACTA TTCTGGACAA	180
AAAGGCAAGC AACAAACTGA ATCCAAGGC AGTTTTCTA TTCATAACAC ATATCATGTA	240
GATGCCAATG ATCATGACCA GACCCGAAAA ACTCAGCAAT ATGATTGAA TGCCCTACAT	300
AAGACGACAA AATCACAACG ACATCTAGGT GGAAGTCAAC AACTGCTCCA TAATAAACAA	360
GAAGGCAGAG ACCATGATAA ATCAAAGGT CATTTCACAA GGGTA	405

(2) INFORMATION FOR SEQ ID NO:785:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 642 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:785:

GAATTGGCC AAAGAGGCCT ACTACTCACC TCTTGCTCTC TCCCAACCCT AGAAACAGCC	60
ACGACTCCTA CCACAAACTT GGAAACACC ACCACTGAGA CCACCTCCCA CAGTACTCCC	120
AGCTTCACCTT CTTCAGCCAT CTACTCCACC GTCAACATAT CCACAACCTAC CATCTCCTCA	180
TTTCCCCCTT CCTCAGGTAC CATGGTGACA TTCACAACCA TGAACCCATC CTCTCTGAGT	240
ACAGACATAT CTACCAACAC ACTGAAAAT ATCACCCAGC CTTCTGTGGG CTCTACTGGT	300
TTCCTGACTG CAGCTACAGA CCTCACCTCA ACATTCACTG TTTCCACTTC CTCAGCAATG	360
TCCACAAGTG TCACTCCATC TGCCCCCAGC ATCCAGAATA AAGAAATCTC AACACTTGTG	420
AGTACAACCA CTACCAACAG TCCCAGTGA AGAATGACTC TCACAAAGTAC AGAGAATACC	480
CCGACAAGTT ACATCCTGAC CACCAAGTCCA GTGACATATT CATTTCCTCC TTCCATGTCT	540
GCCAGCAGTG ACTGGACCCAC TGACACAGAG AGCATCTCCT CAGCTCCAGC CATCACCAGT	600
ACACTCCACA CAACAGCTGA ATCCACCCCTG GCAGGTCTAG AA	642

(2) INFORMATION FOR SEQ ID NO:786:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 469 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:786:

GAATTCCGCC AAAGAGGCCT ATGGCCTTGG AAGGGATGAG CAAACGGAAG AGAAAAGAGAA	60
GTGTCCAGGA GGGAGAGAAT CCTGACGACG GCGTTCCGGG GAGTCGGCCG GAAGACTACA	120
GGCTTGACCA GTGCGCAGT AGCTTATTC GCGGCGAACCA CCATTCCAGA GGTGGCACCG	180
GTCGGCTGGC GTCCCTCTTC AGTTCTCTGG AGCCCCAGAT TCAACCCGTG TACCTGCCGT	240
TGCCTAAACA AACCATCAA AAAACGAAAC CGAACATGAGGA GGAAGAAAAGT ACATCCCAGA	300
TTGAAAGACC ACTTCGCAA GAACCTGCCA AAAAAGTGAA AGCGAAGAAG AAACACACTA	360
ACGCAGAAAA AAAGTTGGCA GACAGGGAAA GCGCTCTAGC GAGTGTGAT TTAGAAGAAG	420
AAATTCAACCA GAAACAAGGG CTTAGCTCGA GCAGGTCTAG AATTCAATG	469

(2) INFORMATION FOR SEQ ID NO:787:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:787:

GAATTCCGCC AAAGAGGCCT AAGAAAAGAT ATAAATCAGA GAAAAAGCAT GAAGCGTATC	60
ATATTGATT TAACAGTATT GCTTGCCATG TTAGGGCAGG TTGCCTATGC GCAGAAAACG	120
TGTGTCTATCG CATCGGCAGA AAATCATGTG CCTATTCTGT AAGCACTTAT TCATACCAAT	180
AAACATCATT GGGCAAGAAC AGATTATCGG GGCTATTGGA CGATGGCTA TCAGTTTGAT	240
TCAGCAACCG TATCGAAACC TGGTTTTATG AAGGCAACTA TCCGGTACAA GGAACTGCCG	300
GATACTCTGT TTCTCTTGCC GGATGCCAAA CAGTTAGCGC AAGTGACAGT TTGGGGCAAG	360
AATCAGGAAG GCATCAAAAA TATGGAAGAG GATATTCAAG AGAAGATAAA CTCTTTGCCA	420
ACTTCATCTG CTGGCATTGG TTTTGATGCT TTCGGATGGA TGGATAAACCA GGGAAAACGT	480
GATAAGAACG ATCTGCAACA G	501

(2) INFORMATION FOR SEQ ID NO:788:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:788:

TGATGATCGA TATCCAGAAA GACACTGCAGG TGGAAGGTGA GGAGAGTTGAA GTCAACTGCA	60
CTGCTATGGC CAGCAAGCCA GCCACGACTA TCAGGTGGTT CAAAGGAAAC GCAGAACTCG	120
AG	122

(2) INFORMATION FOR SEQ ID NO:789:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:789:

GGTGAGCTGA GATCCGACCA CTGCACTGCA AGACCCGTGTC TCAAAACAAA CAAACAAACA	60
ACAACAAACAA CAACAAACCA AACCAAACAA AAAACCTGCA TAGCCAACTA GACCAGCATA	120
GAGGGCGAAA ACCATGCTTT TTGTCAAATG GTACTGTTTA TTCTGTTTTG CTGTCAGCTG	180
GTGTCAGCTG GTTTGCCGCT 'TCTGATAAAG CTAGCCCTG CTGTGTGCAT GCAGGTTATA GTGCCAGGC	240
TCATATTCC TCTTCTGCT GCACCTCACT CGAG	274

(2) INFORMATION FOR SEQ ID NO:790:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:790:

GAATTCCGCC TTCATGGCCT AGGGAAAGGA GGCGGCAGCC AGGCTGTGTC CCCTGACCGT	60
TGGAGCGTCT CGCACCCCCG CATCCCCGCA CCCTCAAGGC ACCTCCAAAG ATGATGATGG	120
GTTGTGGGGA GTCAGAGCTG AAGTCGGCGG ACGGGGAAAGA AGCCGGGGCG GTCCCGGGGC	180
CACCCCCCGGA GCCCCAAGTC CGCGAACCG	209

(2) INFORMATION FOR SEQ ID NO:791:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:791:

GAGAGAATTA AAGAGAACCA CNAAGCTGAA CCTCAAAAG TTAGCCTGGC GAGGGGAGGA	60
TGATGAGATT TCCCCTGTTG TCACATAAAC AAGGAAGTAA AGGGGGCCCC TTGTGCTCTC	120
AGAACTCCAA GCATGAAACG ATAGCAAAGG GAAAAACAGC TAAGTGTTC CTGGCTGAAT	180
TTTATTTGTC TTTCAGTTTC TGCCATTTC GTTCTGTTA TCGTGTGTTG AGGTGCACTG	240
AACTGCAGCA AACCCAGGGG ATCCAAGGCT ACAGTGGAAA GCCTTGACCA ACAGTGCAGG	300
GAGCAGAAGA CATTAAATGAC GTGATGTCGA CACAGCCGC ACTCAGGATC CTCCAGGAAA	360
AGAACACAGA GATAACCCCG GAACTCGAG	389

(2) INFORMATION FOR SEQ ID NO:792:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:792:

GTGCTTTGGA TTTTCATCC AGCTTTTCT CAACACCCC GCTGGAACTC AGCGGCTCCA	60
TCTCTGCC TTCCGAAGCA CCTGCCTCTC TGCTCTGAT GCCGAGTGAC TTGTCCCCCT	120
TCACATCTCA GTCTTTCT CCCTGGTTG AGACATTAC ATTGTTGAC TCTAGTGATC	180
TGCACTCATC TCAGCTGTCT CTTCAGTT CCACAAATCT TGAGTTTCG CAGCTCCAGC	240
CAAGTCCGA GCTGCCCTTA AACACCATCA TGTTGCTACC TANCCGTTCT GAGGTGTCAC	300
CATGGTCAAG CTTCCCTCT GATTCTCTCG AG	332

(2) INFORMATION FOR SEQ ID NO:793:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:793:

GAATTCCGCC TTCATGGCCT ACTGGAATT CTTTCTGCC CTTTCATATT TTAAGATGGC	60
TGGAATAGCA CAGGGAGTAT ATAGCAGATA TCTTCTGGG AAAAATTCAT CTGAGGATAG	120
CTTTTATTT GCCAATATTG TGCAACCTCT GGCAAGAAACT GGACTACAAC TCTCCAAACG	180
AACTTTCAGT ACTGTACTAC CACAGATTGA TACTACTGGA CAGTTGTTG TACAGACTCG	240
GAAAGGTCAAG GAAGTTCTCG AG	262

(2) INFORMATION FOR SEQ ID NO:794:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:794:

GAATTCCGCC TTCATGGCCT ACTATGCCGT CATGATAGAG AAGATGATCC TGAGAGACCT	60
GTGCCGTTTC ATGTTGTCT ACGTCTGTT CTTGTTGGG TTTTCCACAG CGGTGGTGAC	120
GCTGATTGAA GACGGGAAGA ATGACTCCCT GCGCTCTGAG TCCACGTCGC ACAGGTGGCG	180
GGGGCCTGCC TGCAGGGCCC CCGATAGCTC CTACAACAGC CTGTACTCCA CCTGCCCTGGA	240
GCTGTTCAAG TTCACCATCG GCATGGGGA CCTGGAGTTC ACTGAGAACC ATGAACTTCT	300
CGAG	304

(2) INFORMATION FOR SEQ ID NO:795:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:795:

GCGATTGAAT TCTAGACCTG CCTCCAAGCA GCTGCAGTAT CTCGGAAGAA AAAACGAAGA	60
ATGGAACCT ATAGCCTGGT TCCTAAGAAA AAGACCAAG TATTAACACA GAGGACGGTG	120
ATTGAGATGT TAAAGAGCAT AACTCATTCC ACTGTGGGT CCAAGGGGA GAAGGACCTG	180
GGGCCAGCA GCCTGCACGT GAATGGGAG AGCCTGGAGA TGGAACAGA TGAGGACGAC	240
TCAGAGGAGC TCGAG	255

(2) INFORMATION FOR SEQ ID NO:796:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:796:

CTAGTCTTCC AACCCCTCTG GACTTTCTTT GCTCTGTCT TGTGTTGGGT GTACTGGATC	60
ATGACACTTC TTGTTCTTGG CACTACCGGC AGTCCTGTTG AGAATGAGCA AGGCTTTGTG	120
GAGTTCAAAA TTTCTGGGCC TCTGCAGTAC ATGTGGTGGT ACCATGTGGT GGGCCTGATT	180
TGGATCAGTG AATTATTCT AGCATGTCAG CAGATGACAG TGGCAGGAGC TGTGGTAACA	240
TACTATTTTA CTAGGGAAGT ACTCGAG	267

(2) INFORMATION FOR SEQ ID NO:797:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:797:

GAATTCGGCC TTCATGGCCT AGGGGGAGTT TAGCTGAAAC AAGTTTACA GAAGCAGAGC	60
TGGCAAATAG TTAAATATT AATTGGTTAC AATAGCAGTT ACAAAACAAA TAAACAGTTC	120
CAGGTGCAGG GGCTTAAACT ATCACAAAGA GAGAAATGCA GGGGTTTGC GTGACATTCA	180
CCGAG	185

(2) INFORMATION FOR SEQ ID NO:798:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:798:

GGGCGTGTGA CGACTGCTGG GAGAGGAAAG CGAGACATCA TTCCAACCCT CCAGAAGCTA	60
AAGATCCTGG AACTCAAGGG GAAAACAAAC GTAAGTGCAG AAGCGAACAA GCAAACATGT	120
CCTCAACGGG GCAGGCAGGC TGTCGGGT CAGAGCTGGG ATCTGGGAAG GAACAGAGAG	180
GGCCGCTCAG GGAGAGGAAG CACAGTGCCA CCCGAGGCAAC GCACTCAGCA GGCACCTCGCA	240
GGCTGGGCAG AGGTAGAGAA GCAGCGCTGC ACAGGCAGGC AGCTGACCCA GGGCTCTTAG	300

AGCCCCGGCAG GAGAGCTCGT GTGGGACCTG CGAGGAGGAC AGGAGCCCTC AAAGCAGCAC	360
CGCCTGATTG CAGCCAGGAG GGTAGCATCA AGGAAGATGG AACTGCAGGC AGGCCACATC	420
CAGGGGTGCT CGAG	434

(2) INFORMATION FOR SEQ ID NO:799:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:799:

GAAAAGTCGG ATGCTGGCCT CTGAAATCA GCCAGATCAA GATATTACAC ATTTCTTCCA	60
ACAGATCCAG GAGCTCAATT TGAAATGGA AGACCAACAG GAGAACCTAG ATACTCTTGA	120
GCACCTGGTC ACTGAACGTGA GCTCTGTGG CTTTGCCTG GACTTGCC AGCATCAGGA	180
CAGGGTACAG AATCTAAGAA AAGACTTCAC AGAGCTACAG AAGACAGTTA AAGAGAGAGA	240
GAAAGATGCA TCATCTTGCC AGGAACAGTT GGATGAAATTC CGGAAGCTGG TCAGGACCTT	300
CCAGAAATGG TTGAAAGAAA CTGAAGGGAG TATTCCACCT ACGGAAACTT CTATGAGTGC	360
TAAAGAGTTA GAAAAGCAGA TTGAACACCT GAAGAGTCTA CTAGATGACT GGGCAAGTCT	420
CGAG	424

(2) INFORMATION FOR SEQ ID NO:800:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:800:

GAATTGCGCC TTCATGGCCT AGGGGTGCTG TGTGTTTTC AGGGCGCCCT GCGTCCGGCA	60
GAGGAGGCCA GCATCCCGCT CAGGTGATGA GGAACCCCTC GCGCACCCAG CGCAGAAGGC	120
TGCTGCCGCC GGACCCCTCC ATTGTTGAC CACAACAAGG GCCGGATTCT CACCACAGCAG	180
GATCTTAAGG CCTTGTAGT CCTTCAGCCA CTGTGGGCC TGCCCTTGCC TGTTCTTCTG	240
GAATGTCTTG GGGTTTGAA TCCTGTCACT GTGACCTGCA AATCCAAGAG ACAACTCGAG	300

(2) INFORMATION FOR SEQ ID NO:801:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:801:

GAGAAATCAG TGAAGGATTT GCAACGCTGC ACCGTTTCTC TAACTAGATA TCGCGTCATG	60
ATTAAGGAAG AAGTGGATAG TTCCGTGAAG AAGATCAAAG CTGCCTTGC TGAATTACAC	120
AACTGCATCA TTGACAAAGA AGTTTCATTA ATGGCAGAAA TGGATAAAAGT TAAAGAAGAA	180
GCCATGGAAA TCCTGACTGC TCGTCAGAAG AAAGCAGAAG AACTAAAGAG ACTCACTGAC	240

CTTGGCCAGTC AGATGGCAGA GATGCAGCTG CCCGAACCTA GGGCAGAAAT TAAGCACCGT	300
CTCGAG	306

(2) INFORMATION FOR SEQ ID NO:802:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:802:

GCTCGCGGCC CTTCAGAATT ATAAGGCTGT CTGCAGAGAT TTGAAAAATG GCAACAAATG	60
AAAGTGTAG CATCTTTAGT TCAGCATCCT TGGCTGTGGA ATATGTAGAT TCACCTTAC	120
CTGAGAAATCC TCTGCAAGAA CCATTTAAAA ATGCTTGAA CTATATGTTG AATAATTATA	180
CAAAGTTCCA GATTGACAACG TGGGGATCCC TTATAGTTCA TGAAGCCCTT TATTTCTTAT	240
TCTGTTTACG TGGATGTCTC GAG	263

(2) INFORMATION FOR SEQ ID NO:803:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:803:

GAATTCTGGCC TTCATGGCCT AAATAGTTAG TCACCTTCTG ACCTTCTCCT CTTTCTCAA	60
GCCTTCTGTC CCTGGTTTT GCAAGTGTG CATTTCGCC GAGAATCCGC GTTGCCTACT	120
GCTGCCACCT CCTGTCATT TAGAACTATG CAAAGACTCC GCTTCCGTT TCCTGAGCTC	180
CTCGGGCCCC AGAGTCTCTG TTGATTATT TATTTATTAA TTTATTTATT TGCCAAAAT	240
TCTCCTCTTC AACTTATAGA ATGCACCCAA CTCGAG	276

(2) INFORMATION FOR SEQ ID NO:804:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:804:

GAATTCTGGCC TTCATGGCCTA CAGCCATATT AAAACTAAGT AAACCTCGTCC CTGGGAACTA	60
CACTTTCAAG TTGACTGTAG TAGACTCTGA TGGAGCTACC AACTCTACTA CTGCAAACCT	120
GACAGTGAAC AAAGCTGTGG ATTACCCCCC TGTTGGCCAC GCAGGCCCCA ACCAAGTGAT	180
CACCCCTGCC CAAAACCTCA TCACCCCTTT TGGGAACCAAG AGCACTGATG ATCATGGCAT	240
CACCAAGCTAT GAGTGGTCAC TCAGCCCAAG CAGCAAAGGG AAAGTGGTGG AGATGCAGGG	300
TGTTAGAACCA CCAACCTTAC AGCTCTCTGC GATGCAAGAA GGAGACTACA CTTACCAGCT	360
CACAGTGACT GACACAATAG GACAGCAGGC CACTGCTCAA GTGACTGTTA TTGTGCAACC	420
TGAAAACAAT AAGCCTCCTC AGGCAGATGC AGGCCAGAT AAAGAGCTGA CCCTTCTGT	480

GGATAGCACA ACCCTGGATG GCAGCAAGAG CTCAGATGAT CAGAAAATTA TCTCATATCT	540
CTGGGAAAAA ACACAGGGAC CTGATGGGT GCAGCTCGAG	580

(2) INFORMATION FOR SEQ ID NO:805:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:805:

CAAATTGATT TCGGCACAGT TCTGGGAGCT GGGACATTCA AGGTCACCAC GTTGCCACCT	60
GTGAAGGCTT TCTGCTGCAT CCTCATGTTG GGGAAAGATCA GAAGTGAGAA CACATGCTGG	120
CCAGTCCTTT CACAGCAGCA TCAATCCGTG CATGGGGCAG GGCCCTCGGC CTGAGCGCCT	180
CCCCCAGGCC CTAACTCCCA GCACTGCCCT GCTGGGGATG GAATTTCCA CATGAATCTG	240
GGGGATGCTT TCGGACCACA GCCGGGGAGC CTGCCCTGGC TTCCAGCTGC TGGTGGCCA	300
GGGGCTCCCT GGCTTGCCTC GAG	323

(2) INFORMATION FOR SEQ ID NO:806:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:806:

GCGATTGAAT TCTAGACCTG CCATTCTCGC TCTGCCGACG TTGACTCTCT CTCTGAATCC	60
AGTCCCAACT CCAGCCCTGG CCCCTGTCTT GAGAAGGCC CACCACCCA GAAGGCCAGC	120
CATCTCCAG GGGCCCTCA TCGCCATCGT CTGCAACGGT CTCGTGGCT TCTTGCTGCT	180
GCTGCTCTGG GTCACTCTCT GCTGGGCCTG CCATTCTCGC TCTGCCGACG TTGACTCTCT	240
CTCTGAATCC AGTCCCAACT CCAGCCCTGG CCCCTGTCTT GAGAAGGCC CACCACCACT	300
CGAG	304

(2) INFORMATION FOR SEQ ID NO:807:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 556 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:807:

GAATTCCGGCC TTCATGGCCT AGATATGAGA AATGAGTGTT GGACGTCGAA GAATAAAGTT	60
GTTGGGTATC CTGATGATGG CAAATGTCTT CATTATTTT ATTATGGAAG TCTCCAAAAG	120
CACTAGCCAA GAAAAAAATG GAAAAGGGCA AGTAATAATA CCCAAAGAGA AGTTCTGGAA	180
GATATCTACC CCTCCCGAGG CATACTGGAA CCGAGAGCAA GAGAAGCTGA ACCGGCAGTA	240
CAACCCATC CTGAGCATGC TGACCAACCA GACGGGGGAG GCGGGCAGGC TCTCCAATAT	300
AAGCCATCTG AACTACTGCG AACCTGACCT GAGGGTCACG TCGGTGGTTA CGGGTTTAA.	360

CAACTTGGCG GACAGATTTA AAGACTTTCT GCTGTATTG AGATGCCGCA ATTATTCACT	420
GCTTATAGAT CAGCCGGATA AGTGTGCAA GAAACCTTC TTGTTGCTGG CGATTAAGTC	480
CCTCACTCCA CATTGGCCA GAAGGCAAGC AATCCGGAA TCCTGGGCC AAGAAAGCAA	540
CGCAGGGAAC CTCGAG	556

(2) INFORMATION FOR SEQ ID NO:808:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:808:

GGAAACTTCT AAACTATTTT GCTCGCACT TTTACAACAT GAGAATGTTA GCCTTATTTG	60
TGCAATTGCA TATCAATTTC ATCTTGCTCT TTTATAAGGT CTCCACTTCT TCTGTGGTTG	120
AAGGAAAGGA GCTCCCCACG AGAAGTTCAA GTGAAAATGC CAAAGTGACA AGCCTGGACA	180
GCAGCTCCA TAGAATCATC GCAGTTCACT ATGTTACTAGA GGAGAGCAGC GGCTACATGG	240
AGCCCACGTT GCGTATCTTA GCTATTCTGC ACACGGTCAT TTCTTTCTTC TGCAATCATTG	300
GATACTACTG CTTGAAAGTC CCATTGGTTA TTTTAAGCG AGAAAAGGAA GTGCTCGAG	359

(2) INFORMATION FOR SEQ ID NO:809:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:809:

GAGANACGAC AATGTCCAGG AAACAGAACCC AGAAGGATTTC ATCAGGATTTC ATTTTGATT	60
TGCAGTCCAA TACCGTACTG GCCCAGGGAG GAGCTTTGA GAACATGAAA GAGAAAGATAAA	120
ATGCGGTACG TGCAATAGTT CCTAATAAGA GCAACAATGA AATTATCCTG GTTTTGAGC	180
ACTTTGATAA CTGTGTGGAC AAAACAGTAC AAGCATTCTG GGAAGGTAGT GCCAGTGAAG	240
TACTCAAAGA ATGGACAGTA ACAGNCAAGA AAAAGAACAA AAAGAAGAAG AACTCGAG	299

(2) INFORMATION FOR SEQ ID NO:810:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:810:

GAATTCGGCC TTCATGGCCT AGTAGCTGTT CCAGTACAAT TCAATGTTAT CCAGGTTGGG	60
TGCATGTGA ATGATATTTC TGACTTTTG TATCACTCA GAATTCCAG AGAGCTCTTC	120
CTGGCTGAAA AGATCTCAA GGATCATCTC CGGAATGGAA GAGGTGAGGC CTGTTAGCTT	180
GTGGGCTGCC CAATCCATCC AACCTTGGC ATTGGGATCA ATGTTGATGA GGACAAGACC	240
TTCAACAGTG TCCGGGTGGT TAAGAGCATA TCTCGCCAGG ATGTAGGCTC CAGCTCCAAC	300

ACCAACTCCA ATTATTGTAG AGAAATTTAG GTACTGCAGG ACGCAAGGG A TCATGTCTGC	360
AAGCTGGTCC AGAGATGGGT ACTGATATCC CAAAGGAAC ACAGGGGCTC GAG	413

(2) INFORMATION FOR SEQ ID NO:811:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 324 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:811:

TTGGTATTGT CTCTGTACTA GTCTTCAA ATTCTGCTGT GAGCTTTTG CTTAGACTGT	60
AAGCCTAGA GTCACTCATC ACAGTAATCC TAAAGACAGA TGTGTTCTGTT CTATTTGATA	120
AGGCCCTTTT GTGGCTTGTG CGCACTGTCA GTTTCATGTT TGTTTGTTG TTTTGGAACT	180
GCAGTTACAT CCAGGAGACC TGTGGTGGAC ATAATGGGCT GTAGTTTCGTG CAGTTGTCAG	240
TATAGCTTGT TAGGGAGCTC TTCTGGGCA GAGCTTGCA CAGCAGAGCC CAGTGCTGAG	300
CTGAGTTCTT GGCAACCATCT CGAG	324

(2) INFORMATION FOR SEQ ID NO:812:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 352 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:812:

ACATTTCTTT GTAAGTTNNN AAAAGCTAT GAGGGTTTT TCCACGATTC CGTTCCCAGT	60
TTGGCTTTG TTGTTGTTGT GGCTGTTCTT GGCCCCCTG GGCCCTGCAG TGGAGTGGGG	120
GGCTGCACCT GGGAGCCTG AGCTGAGGCC CAGCCCTCC TGCCCTGCAT TTTCCCTGCCA	180
AGCACGACCT GAGACTCTGA AGCCGATGCC TATAACAGGC AAAACCTGCC AATTCAGCT	240
TGAACGACTG GAGGGTCTG AGGATGGGG TCCCTGGGT GCCATCATGG GCAGGGTGCA	300
TCTGTTGGG TATGCTGCC CCCAGCTGGC GGGGCACCCGG GGACAGCTCG AG	352

(2) INFORMATION FOR SEQ ID NO:813:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 329 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:813:

GAATTCCGGCC TTCATGGCCT AGGGAAAGGG AANGTGGGA GGGTCCGAGG GGAAGGGGAC	60
CCCAGCTTCC CTGTGCCCGC TCACCCCACT CCACCACTCC CCGGTCGCCA GCGGGAGTCT	120
CCTCTCTACC GCCACTGTCA CACCGTAGCC CANATGGATA NCACNGTGT CAGACAAGAT	180
TCCCTCAGAT TCCGAGTTGC CTACCGGTTG TTTCGTTGT TGTTGTTGTT GTNTTTNTTT	240
TTNTTTTNNN TNCGGAAGAC AGCAATAACC ACAGTACATA TTACTGTAGT TCTCNATAGT	300
TNCACATACA TTNATACCAT AACCTCGAG	329

(2) INFORMATION FOR SEQ ID NO:814:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:814:

GAATTCCGGCC TTCATGGCCT ATCCATTTCG AAATCCACCA AGGTCCAGTC GACAGACATT	60
TCCAAAAAGA ATCCTGTTCT AGGACCACCT GCGCTGAGAG CACACCCGGG GGTCAAAGGG	120
CAGCCACCCGG GGGTCAAAGG GCAGCCATCA CCTACTCCCC AGGGAAGGGC TTGGCGGCCAC	180
CAGTCACTGC AACCCCGCT CACCTCCGAT GCCTGCTGTG CCCAGGGTGG TCCCGCTCAT	240
AGCGACGGCC TGNGCGTNCA TANGACCTCG AG	272

(2) INFORMATION FOR SEQ ID NO:815:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 584 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:815:

GATTGAATTG AATGTTAACG ACCAATGCTG GATTTGGTGG TGGACTGAAC ACCAGTGCTG	60
GCTTTGGTGG TGGCCTAGGC ACCAGTGCTG GCTTCAGTGG TGGCCTAACG ACAAGTTCTG	120
GCTTTGATGG TGGGCTAGGT ACCAGCGCTG GCTTCAGTGG AGGACCAGGC ACCAGCACTG	180
GTTTTGGTGG TGGACTGGGC ACCAGTGCTG GCTTCAGTGG CGGACTGGGC ACCAGTGCTG	240
GCTTTGGTGG TGGACTGGTC ACTAGTGATG GCTTTGGTGG TGGACTGGGC ACCAATGCTA	300
GTTTCGGCAG CACACTTGGC ACCAGTGCTG GCTTTAGTGG TGGCCTCAGC ACCAGCGATG	360
GCTTTGGCAG TAGGCTTAAT GCCAGCTTCG ACAGAGGACT GAGTACCATC ATTGGCTTTC	420
GCAGTGGTTC CAACACCAAGC ACTGGCTTTA CTGGCGAAC CAGCACCAAGC ACGGGCTTCA	480
GTAGTGGACC CAGTTCTATT GTTGGCTTCA GCGGTGGACC AAGCACTGGT GTTGGCTTCT	540
GCAGTGGACC AAGCACCAAGT GGCTTCAGCG CGGGACCGCT CGAG	584

(2) INFORMATION FOR SEQ ID NO:816:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:816:

GAGAATGTCC AGCAAGGAAG TGAAGACTGC TCTAAAAAGT GCTAGAGATG CAATCAGAAA	60
CAAAGAAATAC AAAGAAGCTT TGAACACACTG TAAGACAGTG TTAAAGCAAG AGAAAATAA	120
CTATAATGCC TGGGTTTTTA TTGGCGTTGC TGCAGCTGAA CTAGAACAAAC CTGATCAGGC	180
CCAGAGTGCC TATAAAAAG CTGCTGAATT AGAGCCAGAC CAATTACTAG CTTGGCAGGG	240
GTTAGCAAC TTGTATGAGA AATATAATCA CATAAAATGCT AAGGATGACT TGCCCTGGTGT	300
TTACCAAAAG CTCCCTGGATC TTTATGAGAG TGTTGACAAG CAGAAGTGGT GTGATGTCTG	360

CAAGAAACTT GTGGATCTAT ATTACCAAGA AAAGAAACAC CTAGAGGTGG CTCGAACATG	420
GCACAAGTG ATAAAAACAC GGCAGGAACA AGGTGCAGAA AATGAAGAGC TTCATCTCGA	480
G	481

(2) INFORMATION FOR SEQ ID NO:817:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:817:

GAATTCCGCC TTCATGGCCT AGGGGGAGTG GTGGGTATTG CTAAGTTATC AGTTATTTAA	60
CCTTATGGAG TTTTATTTAA CGCTTTTTGT TTGACATGTT TTATATATAT GTAATTTTAT	120
TTATTCTTCA CAAAATCCCT GTGAGGGGG TGTTACTATT GTCCCCATTT AAAGATGAGA	180
ACACTGAGGC ATGTCTAGAA TTCATCGAG	209

(2) INFORMATION FOR SEQ ID NO:818:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:818:

GGCTCTGTGG AATTCCATGG CATCTTCCCC GCCCCCCCC ACCCCCCCCT TTCCCCCTTC	60
TTTTTTTTTT TTTCTTTCTT TTCTCCCCCTT CCCCCCCTTT CACCATTCTC CCTCGGAGGC	120
GCTTTCCCCG GGCAGGGCA GAGCCGGTCT CACCCCCCGC CTCTCCCCGG CCCCCGCCGC	180
CCTATGGCGA GAGGGAGCCC CCTCCCAACC CGGGCTCGAG	220

(2) INFORMATION FOR SEQ ID NO:819:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:819:

GAATTCCGCC TTCATGGCCT ACACATTCTT TTAGTCAGAA ACATTTAAAT AGTAGAGTAA	60
GTTGGCTTGA AGTGAATTT TGTGTGAAAT CTTTCTCTG CCCTAGCCTA GTTTGTCCAT	120
GCACATTGCA ACACAGGAAG AACATTTTA GACCTGCCAG AATATGCAAT GACAGGGTAA	180
AAAATGCCCG AGGTGACTG TGTTCATAGA CATTGTGCTA AACACTCAAC ACTCTGATC	240
ACACTGAATG CTTTGACAG TCCTGTGAAT TGAGGGCTAT TATTATCCCC ATTATATA	300
TGAGCGAGCA GAGGCCAGA CAGATTAACA AAGGTGCTCC CTCGAG	346

(2) INFORMATION FOR SEQ ID NO:820:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 355 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:820:

GCTTATACAG TGTCCGATAG ACACCAGGAA GCNACTAGCA GAGAATTTCG TAGTCATAGG	60
TGGCACTCT ATGTTGCCAG GATTTCTCCA CAGATTGCTT CGAGAAATAA GGTATTTGGT	120
AGAAAAACCA AAATATAAAA AAGCACTTGG CACTAAGACA TTTCGAACCC ATACTCCACC	180
TGCAAAAGCT AATTGTGTGG CCTGGTTGGG AGGGGCTATT TTTGGAGCAT TACAAGATAT	240
ACTTGGGAGC CGTTCTGTTT CAAAGGAATA TTATAATCAG ACGGGCCGTA TACCTGATTG	300
GTGTTCTCTC AATAACCCAC CTTTGGAAAT GATGTTGAT GTCGGGGAAC TCGAG	355

(2) INFORMATION FOR SEQ ID NO:821:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 273 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:821:

GCTCGAGGGC GAAGGGGAGC AATGGCATTG GCGTTGGCCA TCCGTGACAC GGCACTCTAT	60
GCTCGCCAGA TGATGTTCAC GACCACCCCTT CTCATTGTGT TCTTCACTGT CTGGATCATT	120
GGAGGAGGCA CGACACCCAT GTTGTATGG CTTAACATCA GAGTTGGCGT CGAGGAGCCC	180
TCCGAAGAGG ACCAGAATGA ACACCACTGG CAGTACTTCA GAGTTGGTGT TGACCCCGAT	240
CAAGACCCAC CACCAACAA CGACAGACTC GAG	273

(2) INFORMATION FOR SEQ ID NO:822:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 286 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:822:

GAGATAAACAA AAATTGATTG CCCCATTCTC TCACCTCCCC ATCTTGCTTT CCTAGACCCC	60
ACAGAGTTAA AACTTGGGAT TCCCCTGGCC CCCCCAGAAC ACTTGATAT TCTTGTGTTG	120
AGGTTCCGTGC CGCAGTAACA GACACAGTAT TTAATTGACAT ATACAGATGT TTGCTGGGTA	180
TATTCACTGT AAATTTTATT TAATCTGTTT TTTTGTGTGTTA TTGGGGGGTA TTGGGGGGGA	240
GGTTGGTTTT GTTTTAAAT ATAAAAAAAGA AAATCTGTCA CTCGAG	286

(2) INFORMATION FOR SEQ ID NO:823:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 297 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:823:

GGTCTGGAGG AGCCCCGGAG GGCGCTGTGGG TGGACCACTG CAGTAATCTG GGTGAAAGAT	60
GATGATAGGC TAGACTAATA TGTTACCAAGA GACAAAGAAG AGGGACTTGA GAGTTATTAA	120
GGAGGAAAAAA AACAAAACAA AACAAAAATC AACCAGACTT ACCTTTGAA ATAGGACAAG	180
TGAGGAAAAG GAGGGTTTCG AGAATAGCTT ATAGTTTCG AGAAGATGAG GTTGACAAG	240
ATGCCACTGC TTTTCTTAGC ACTCTTCCCT CCCCTAAACC ATCCCGTAGT GCTCGAG	297

(2) INFORMATION FOR SEQ ID NO:824:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:824:

GAATTCTGGCC TTCATGGCCT ACCCTCATTA CCCCAAGTGC CTCCCTAATGG ATCTGTCCTT	60
ATTCTTCCTT GTTCTGTCTC CCTCATGCC TGAGCTCCCT CTCTTTGGGA CCTTCCTCTC	120
CCAAGTCACC ACCCTCTCTC CCCCCTCTACC ACTCAGCCAT TCCCCAGTTT CCACAGTTCC	180
TCAAACATTA CCCCCACTCCC CACTCCCCAG TTTCCTCCCC CTCCCCATTT GTCCCCCTCA	240
CCTGGGGGTC CCCGAAGTAG ATCTGCAG	268

(2) INFORMATION FOR SEQ ID NO:825:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:825:

GAATTCTGGCC AAAGAGGCCT AGATGTGAGC TGGGGAAAGGG AGGGTGGCCA GTAATGGTT	60
TGTTATCAAG CAGGTTGTT ATCACTGTGG GTGACAAGCC CCTTCCCATT TGGGCCCTCT	120
GGGATCCAGT GCAGAACATA TCCCTCGCAG GAGATGAGGA ACTGGGTGT TCACAGAGTA	180
ATCCCTCTCC TCACACTAGTT AGGGCTGCCT CTGGGGTGG CTGAACCTACCC TCATGCAGCC	240
AGAGAAAGTC CTCAGCCAAT GAAATACAGA CACTGGCCAG CCAGCACTGA GGTGGCGAGA	300
CCTTACTGGC TGGTCCCCAG AGTGTCTCCA GCATTGTCTG AGATCTAAA CTGGCTAGAA	360
GGACGGTAAC AGCAGCACCT GTTTCATAGG ACGTGAAGAT AGACGGAGACA G	411

(2) INFORMATION FOR SEQ ID NO:826:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:826:

GAATTGGCC	AAAGAGGCCT	ACTAAAACCA	TAATTGCTTG	TTTTGCTG	TATCTGTCTT	60
TTCACGAACA	TTTGAGTTT	A3CTCTGTCT	TACATTCCC	TCCCTAAAGA	TCATCAGGAC	120
TTTGTTTC	GTGACAATGC	TGGGACCAGA	TTGGCCTTC	TCATCTCAT	ACACCCCTAT	180
TTCCTATGGA	AAACTAAAAT	TGAATTATTC	CAGATATGAT	GACTTTAGGA	TATCCTTTTC	240
CCTCTTGAC	ATCC'CTCATT	GTATTGTGT	TTCCCTT	GTCTCCAACG	TCCCCACAC	300
CCCCAATCCC	TCCACGACTT	TTAAGCCCTT	GGAAGCCAAC	TTGATTAGTC	AGG	353

(2) INFORMATION FOR SEQ ID NO:827:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:827:

GAATTGGCC	AAAGAGGCCT	ACCGTGAGTT	CCCAGGGTGG	CCGGGAGGGG	GAGCTGCGGG	60
GTTCACAGCG	GCTCCCTCTCA	ACGTTCTGG	CTCCGCTCCC	GACTTCTCAG	CCCTGCCTGG	120
AGGGGCTCAG	CCACTGCTT	TAGCTGTCTG	CTGGCTTCC	ACCCCTCCAG	CCTGAACCCCT	180
GACTTCCCA	TGAGGCCCTC	CTGTGGCGGG	GACACTCCAG	GTGCGCTGAC	CCCTTCTCTC	240
CTGAATTCT	GTAACGACAT	CTAACCTTTA	TTTAATTAAT	TTATTTATTT	AGAGATGGAG	300
TTTCTCTCTT	GTTGCCCGG	CTGGAGTGCA	ATGGCACCAT	CTTGGCTCAC	TGCAACCTCC	360
GCCTCCAGG	TTCAGTGAT	TCTCCTGCCT	CGGTCTCCTG	AGTGGCTGGG	ATTGCAGGCA	420
CCCATCTG						428

(2) INFORMATION FOR SEQ ID NO:828:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:828:

GAATTGGCC	AAAGAGGCCT	AAGCGGTATT	TCAGCCACAG	AGTTGGTGT	GGTTTACTT	60
ATCTATTTG	AATTAAAAG	GCTTATAAAAT	AAAGCAGTGA	CACTGCTTAC	TGGAAATGC	120
TGTACCAAAA	AATGTTATCT	TGCT				144

(2) INFORMATION FOR SEQ ID NO:829:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:829:

GAATTCTGGCC AAAGAGGCCT AGCGGACTAG GAGTCATAA AGTGATTGGC TTAGTGGCG 60
 AAATGTTATG CTTTGTGTT TGGATATATC TGGAG 95

(2) INFORMATION FOR SEQ ID NO:830:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 610 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:830:

GAATTCTGGCC AAAGAGGCCT AGTGGCTACC TAAATTGAGT ATCTGGCAAG AGTAAGATTA 60
 AGCAGTAATT TGTTCCAAG AAGAATCTTC TACCAAGGAG CAACTTTAAA GAATGAAATT 120
 AACTTTCTTC TTGGGCGCTGT TGGCTTCTAT TTCAATGTTTC ACACCCAGTG AGAGTCAAAG 180
 ATTCTCCAGA AGACCATATC TACCTGGCCA GCTGCCACCA CCTCCACTCT ACAGGCCAAG 240
 ATGGGTTCCA CCAAGTCCCC CACCTCCCTA TGACTCAAGA CTTAACCTCAC CACTTCTCT 300
 TCCCTTTGTC CCAGGGCGAG TTCCACCACAT TTCTTTCTCT CGATTTAGCC AAGCAGTCAT 360
 TCTATCTCAA CTCTTCCAT TGGAATCTAT TAGACAACCT CGACTCTTTC CGGGTTATCC 420
 AACACCTACAT TTCCCACTAA GACCTTACTA TGTAGGACCT ATTAGGATAT TAAAACCCCC 480
 ATTTCCCTCT ATTCCCTTTT TTCTTGCTAT TTACCTTCCT ATCTCTAACCT CTGAGCCCCA 540
 AATAAACATC ACCACCGCAG ATACAACAAT CACCACAAAT CCCCCCACCA CTGCAACAGC 600
 AACACCCAGC 610

(2) INFORMATION FOR SEQ ID NO:831:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:831:

GAATTCTGGCC AAAGAGGCCT AGGAAGAAC AAGAACAAAGA AAAAGATTA TATTGATTTT 60
 AAAATCATGC AAAAACATGCA ACTCTGTGTT TATATTTACC TGTTTATGCT GATTGTTGCT 120
 GGTCCAGTGG ATCTAAATGA GAACAGTGAG CAAAAAGAAA ATGTGGAAAA AGAGGGCTG 180
 TGTAATGCAT GTACTTGGAG ACAAAACACT AAATCTTCAA GAATAGAAGC CATTAAGATA 240
 CAAATCTCA GTAAACTTCG TCTGGAAACA GCTCTAACCA TCAGCAAAGA TGTTATAAGA 300
 CAACTTTAC CCAAAGCTCC TCCACTCCGG GAACGTGATTG ATCAGTATGA TGTCCAGAGG 360
 GATGACAGCA GCGATGGCTC TTGGAAAGAT GACGATTATC ACGCTAACAC GGAAACAATC 420
 ATTACCATGC CTACAGAGTC TGATTTCTA ATGCAAGTGG ATGGAAAACC CAAATGTTGC 480
 TTCTTTAAAT TTAGCTCTAA AATAAACATAC AATAAAAGTAG TAAAGCCCCA ACTATGGATA 540
 TATTGAGAC CCGCCGAGCT CGAG 564

(2) INFORMATION FOR SEQ ID NO:832:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:832:

GAATTCGGCC	AAAGAGGCCT	ACTCTGTTGA	GATTTCCCCC	TTTAGTTCC	AACCTTCTCC	60
CCACCTACTC	ATTTATCCAT	CCCTCCCACC	AACTCATTTA	TCCATCCAC	CCACTCATTT	120
ATCCATCCAT	CCCACCCACT	CATTTATCTG	TCCATCCCAT	CCACTCATTT	ATCCATCTAT	180
CCCACCCACT	CATTTATCTG	TCCAACCCAT	CCACTCACCC	ACCTACTCAT	TTATCCATCC	240
CATTCGCTTA	CCCATCCATC	TATCCACCT	AAACAATACAT	CCAACCATTC	CCTCACCTAT	300
GCATCTGTCT	GTTCAGCTGT	TCATCCATTTC	ATTGATCTTT	CCATCCATTTC	ATCCACTCAT	360
TCACACACCT	ACCTACCTAC	CCACCCGCTC	ATTTATTACAC	CCACCTACCC	TCTCATCCAT	420
CCAG						424

(2) INFORMATION FOR SEQ ID NO:833:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:833:

GAATTGCCA	AAGAGGNCTA	CTCTACATCA	GCTAACCTTC	CTACAAGATT	ATCAAATTTC	60
ACACAGTATT	TTTCTGTATT	TAATGACTGC	CATGGTCTGC	AAAATTATGT	GATTAAGACAA	120
TGAATGACGC	TTAAAGAAATG	ATGACCTATT	TTCTAAAGTA	CACTCAAAAT	ATTTAAACTTT	180
AGAGACAAAG	CAAAATCTAT	CATAAAAGTTG	GCTTCTGTG	ATAGAAAACAG	AGAGGTAGGT	240
TAATAATCAC	TGTCCTAAGA	TAAGCNAGAA	TGCTTAGAAA	TAAAAGTTGA	GACCCGTCTT	300
CAAAAAAGAG	AAAGTTGAACC	TTCCAGCCCT	GAGTTCTAA	TATTACATGA	AAATTATGAA	360
AATGAGCATT	AAGCCAGTCG	CAG				383

(2) INFORMATION FOR SEQ ID NO:834:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:834:

GAATTCGGCC	AAAGAGGCCT	ACTACGTAGT	TGGAGCTNTT	TCTTCCCCCA	GCAAAGCCAG	60
AGAGCTTGT	CCCCGGCCTC	CTGGACACAT	AGGGCATTAT	CCTGTATTC	TTGGCTTGG	120
CATCTTTAG	CTCAGGAAGG	TAGAAGAGAT	CTGTCCTCAT	GGGTCTCCTT	GCTTCATCC	180
CTTCTTGT	CACTGACATA	TGTATTGTT	ATCTGGTTA	GGGATGGGGG	ACAGATAATA	240
GAACGAGCAA	AGTAACCTAT	ACAGGCCAGC	ATGGAACAGC	ATCTCCCTG	GGCTTGCTCC	300
TGGCTTGTGA	CGCTATAAGA	CAGAGCAGGC	CACATGTGCC	CATCTGCTCC	CCATTCTGA	360
AAGCTGCTGG	GGCCCTCTTG	CAGGCTCTG	GATCTCTGGT	CAGAGTGAAC	TCTTGCTTCC	420
TGTATTCAAGG	CACCTCAGAG	CAGAAAGTAA	GGGGCTTACT	CGAG		464

(2) INFORMATION FOR SEQ ID NO:835:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:835:

GAATTCTGGCC	AAAGAGGCCT	ACTGGGAGTT	CGGAGTGATT	GTTTCCTGTT	ACAGGCCAAA	60
AAATTTGTTT	GGTTACTTAG	TGGTAGCATT	TTGAGAGGAA	AGTTTACAGA	AAACTAGGGT	120
TATTTTGTA	TTATGCTTGA	ATTGTCTTTA	TTGTTTCCAA	GGCATCTTTT	TTTTTCCTT	180
CTAGTTATCA	AGATGTTAGG	TTCTGTGCC	TTGTGGGCCT	TCCCCTGCC	CAAAAAAGC	240
ATGGATGAGC	AGAGTAATAT	CATTAATATG	GCAGTCTTG	TTAGTTTTC	TAGAAAAGAT	300
GGTCTCGAG						309

(2) INFORMATION FOR SEQ ID NO:836:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:836:

GAATTCTGGCC	AAAGAGGCCT	AAGGCAGGTT	TTTTTTCTA	TGCTTATGTA	TTTAGCCTAT	60
CTATTTATAA	CAGTATAATT	CAGAATATAA	ATATGGAACA	AGTTTCATAA	GGAAAGTTAT	120
CTTTAACCTCA	GACATTATAT	CATTAATACT	TCAAATCTCA	TTATACCATT	ATGACCTGAA	180
TGCTACATTT	TTCTTCCTGT	ATGGAGAGCT	TAGGGAAAAA	TTGTGGCCTG	ATGTCCTCAT	240
CCATTCACTT	ATCATAGAGT	ACATAATGAT	CTCAAATATC	CAAAATGGT	TATATTCA	300
TGCATATTTC	TAAGAAAACA	GGCAGGACTC	GAG			333

(2) INFORMATION FOR SEQ ID NO:837:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 706 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:837:

GAATTCTGGCC	AAAGAGGCCT	AATTGATTTC	CCATGAGTCT	TGTAATCTT	GCTCTGCTGA	60
TTGCGTTG	CGTCTCTAGA	CCATCTCGCT	TCGAACAAAT	CGAAAAGAG	GTGAATTCCA	120
GAAGAACGAC	CTGGATTGCA	GAAGAACCG	CTCCGTTCCG	TGACTATGCT	CGTTGATCG	180
GTACCCCTCC	AAATACGGTC	CCTCTTCCGA	GTAAGACTG	CGATGTCGTG	AAGAACCTTC	240
CTGAGAGTTT	TAACCGATTG	GAAAAGTGGC	CGGAATGCAA	GTCCATCACG	GAAATCCGTG	300
ATCAAGGAGA	ATGTCTTCA	TGTTGGCAC	TGGGGAGTGG	CGGAGGTGGC	CACGGATCGT	360
CTTGCATTT	CTTCCAACGG	AAAGGATCAA	TCCCGTCT	CTGCCGAGGA	TCTGTTGGGA	420
TGCTGTGACT	CTTCTGGAAT	GAATGCAAG	GGAGGGTACA	CGGGGAATGG	CCTGGGAGTA	480
TGTACGTCAG	GTGGGAATTG	TGACGGGTGG	AGC GAATGGA	AACAAGGAAT	GGTGAATG	540
GTACCGCTTC	CCGAAGTGCA	GTCA CGGTAT	TCAGGGCTCC	TATCCTGAAT	GCTCTTCCAT	600
CCCCCTGAA	GATCCGGAGT	GTTCACGGAC	TTGCATAAAG	GGGTATCCC	TCCCATAATGA	660
TCAGGACCGT	CACAAATGA	AGTCAGCCTT	CCAGCTGGCA	CTCGAG		706

(2) INFORMATION FOR SEQ ID NO:838:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:838:

GAATTCCGGCC	AAAGAGGCCT	ATAAAAGTCT	TATTTTTAC	TTTGTCCACT	GGAATACATC	60
ATCGTTGGCC	TATCATTCCA	AACTCCCTAC	AGTGTGGCTT	CAGCTTATCT	CTCTCTGTTT	120
TTTACAGGAA	TCCTAACTC	TAACCCAGGG	ACCCTCAACA	TCTGTGCTCG	GTGGACTGTG	180
GCCACATTT	CAGCTGGCCA	GTGTAAAGGT	TTTAGAGGCC	CTTACATGAG	AAGAAATACA	240
ATTTTTAAGT	CTCTGAGATG	ATGTGCTTCT	TACATTTTG	GAATTAAAAT	GCCTCTTAC	300
TTATAAAATG	CTGGTAGTAA	TAGATGGTCA	TTATCTCACT	GTCATTTGTG	AAAGAAAAAA	360
CGATTGTAAT	AGAATTCTTG	CTATTTTTT	TCTCTAAGGG	AGGTAAGTTT	TCTCCCTAAG	420
CAAATTTAT	GGAATGCACA	ATGCTTGGCT	TTCACCTTCT	TTTATTCTCA	CTACCACCGG	480

(2) INFORMATION FOR SEQ ID NO:839:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 589 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:839:

GAATTCCGGCC	AAAGAGGCCT	AGAATTAAGG	TGTATTATGA	GCAGTTGAAG	ATATATAGGA	60
AATTTTTCC	CAAACCACTA	TCTCTGCTCG	TTCTATTAT	TCAGTGTGTT	TATGTTATT	120
CTTCATTATCAT	TCATTTATA	GAACAGTGG	GTGCCTACTG	TATGCATCTA	TTGTTCTGGG	180
TCCTGGGAA	AGAAAACAAA	GTTCCTGCTT	TCATGGAAC	TACATTATAT	TGGCGGAGAC	240
AGTAACAGAC	AAACAAATGT	AGCCTGTGA	CATGTGTTAC	ATGAAAAGCA	GGGTAGGGGG	300
CTGGGAGAGA	GTAGTAGGGA	GTGCTATTTT	CGAGGTGGTT	GTCAGGAAAG	GCCTCACTGA	360
GGAGGTGGCA	TTTGAGTAG	ACCTGAGCG	AGCGGGGGCG	TAAGCCCAGG	CAGCATGTGG	420
AGGAAGAGTG	TTCTGGTGA	AAGGAACAAG	GATAGAGGCC	CGAAGCTAGA	GAGCTCAGCA	480
TGATCAAAGGA	ACAGCAAGCC	CCGTGTGGCT	GGAATGGAGT	GAGCAAAGGA	ATGAGCAGTA	540
GAAGGTGAGT	GAGTTGGGAG	GTCACCAAGAG	ACCATGGCAA	AGACTCGAG		589

(2) INFORMATION FOR SEQ ID NO:840:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 430 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:840:

GAATTCCGGCC	AAAGAGGCCT	AGGGACTAAC	TGCAACGGAG	AGACTCAAGA	TGATTCCCTT	60
TTTACCCATG	TTTCTCTAC	TATTGCTGCT	TATTGTTAAC	CCTATAAACG	CCAACAATCA	120
TTATGACAAG	ATCTGGCTC	ATAGCTGTAT	CAGGGGTGG	GACCAAGGCC	CAAATGTCTG	180
TGCCCTCAA	CAGATTTGG	GCACCAAAAA	GAAATACTTC	AGCACTTGTA	AGAACTGGTA	240
TAAAAAGTCC	ATCTGTGGAC	AGAAAACGAC	TGTGTATAT	GAATGTTGCC	CTGGTTATAT	300
GAGAATGGAA	GGAATGAAAG	GCTGCCAGC	AGTTTGGCCC	ATTGACCATG	TTTATGGCAC	360
TCTGGGCATC	GTGGGAGCCA	CCACAAACGCA	GCGCTATTCT	GACGCCCTAA	AACTGAGGG	420

GGAGATCGAG

430

(2) INFORMATION FOR SEQ ID NO:841:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:841:

GAATTTTAC TTGTCTATAG TCTAGTATTG TTATACCATG TGGCTTGTT ATAATCATGG	60
TTTCCATTCT GTGAGTCCTC AGATTATAGG CCTCTTGCG G	101

(2) INFORMATION FOR SEQ ID NO:842:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:842:

GAATTCGGCC AAAGAGGCCT AAATGGCGTC GTGGCATTGA GGGGCATCCC TCCTAGAACCC	60
TCCAGGAAAA GCTCGCGAA GACGAGGTT TCAGGAGAGA GAGGCTCCA GCAGTCTGGG	120
AAGTGTAGTC CAGTTGGCTT AGCAGTAGTT TCGTTGGGG GGAGCCGAGG TTCCGGGAAG	180
GGGCTAGGCC GGCTTGAAA GAGATTATGA CTGTACCTTT TAACTTGTA GCTGGAACAC	240
AAGAAGTGTGTT TGTTAACATGA ATGACGTACA CATTAAAGAT CTGTTGGAC GCGGAGGATA	300
ATCCTGTGAA TTGCTAACATAG TTCACTGGGT TTGGCCCTTA GTGTTGACTT CAGTATGCTG	360
AGACGGAAAC CAACACGCC AGAGCTAAAG CTTGATGACA TTGAAGAGTT TGAGAACATT	420
CGAAAGGACC TGGAGACCCG TAAGAACACAG AAGGAAGATG TGGAAGTTGT AGGAGGCAG	479

(2) INFORMATION FOR SEQ ID NO:843:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:843:

TGGAAGAGCT AACTCGTCTG GCCTTGTAGC TCTTTGCTGA AGAGCAAGCA GAGGGTCCCC	60
ACCGCCTGCT GTACAAAAGAC GGCTTCAGCA CCATCCTGCA CCTGCTGCTG GGTCACCCCC	120
ACCCCTGCTGC CACAGCTTG CATGCTGAGC TGTGCCAGGC AGGATCCAGC CAAGGCCTCT	180
CCCTCTGTCA GTTCCAGAAC TTCTCCCTCC ATGACCCACT CTATGGAAA CTCTTCAGCA	240
CCTACCTGCG CCCCCCACAC GCATCTCGAG	270

(2) INFORMATION FOR SEQ ID NO:844:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:844:

GAATTCTGGCC	TTCATGGCCT	ACACAGCCAG	TATCAGAACCC	TCAAGAAAAC	GAGGACACTG	60
CGGACAGGGA	CCAAAATTCA	CACCACTTTT	TTCTCTTGCC	TTTCATAGG	ATATTCTGTT	120
AATTGAATTTC	ATCTGAAAT	CAAGGTCAATT	GCAGAGAAGT	CAGCATTCTA	GAGCACAGAA	180
CAGGGCAAAA	CAGGACGAAA	GATGGATTG	GAGACCAAAT	GGAGAAGGAA	GAACAGAGAT	240
ACGTGTGCTC	CAAATATGAC	ACCCAACCTTC	TTTACTCAGA	GCAGTTACAT	GTCAGATTAT	300
ATTTTAGTTT	TTCATTCTC	CTATAGGCAT	ACATACTACA	AGTCTATAAT	AGAAAACCTAG	360
TGGCTGGCGC	CGGTGGCTCA	CGCCCTTAAT	CCCAGCACTT	TATGGCGCTC	GAG	413

(2) INFORMATION FOR SEQ ID NO:845:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:845:

GAATTCTGGCC	TTCATGGCCT	AGGCTCTGTC	TACCAAAAAAA	AAAAAAAAAA	GAAAGAAATC	60
TTGCAGTCTG	AATACATGGT	TGTGTTCTTA	AGAAACCTGG	TGATAACAC	GACAAAACTC	120
CTCGAG						126

(2) INFORMATION FOR SEQ ID NO:846:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:846:

GCTTCATGGC	CTAGTTGAAT	AGTCAGTTAG	AAATGGAAAG	AATGAAAGTT	GAACAAGAAA	60
GACAAAGCCT	TAGAACAAAA	GACACAGCCC	TAGAACAGAA	GGACAAGGCC	CTGGAAACCAA	120
AAGACAAAGA	CTTAGAACAGA	AAAGACAAAGG	CCCTGGAAACA	GAAGGATAAG	ATTCAGAAC	180
AGAAAGACAA	AGCTTTAGAA	CAAAGGGCA	GAGACTTAAAG	GCAAAAGAC	ACAGCCCTAG	240
AACAGAAGGA	CAAGGCCCTA	GAACTCGAG				269

(2) INFORMATION FOR SEQ ID NO:847:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:847:

GGCATTGAAT TCTAGACCA CCTTCAGACC ATCTCGGAAG ATCTAAAAAG CCTGACCATG	60
GACCCCTACA AACTGCCCTC CTCAGTGAAG CAGGTGATTC TGGACTTGAA AGGTTCTGAT	120
TACAGCTGGT CGTATCAGAC GCCACCCCTCT TCCCCCAGCA CCACCATGTC CAGAAAGTCC	180
AGTGTCTCCA GCAGCCTGAA CAGTGTCAAC AGCAGTGACT CCCGGTCCAG CGGCTCCCAC	240
TCGCATTCCC CCAGCATTCT CGAG	264

(2) INFORMATION FOR SEQ ID NO:848:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:848:

GAATTCGGCC TTCATGGCCT AGAACATTCC AAATTTCTT GGTTCAATA CCCTTTTT	60
TCTTTTGAGG GGAAAAGAGG GGAGAAAAAC AGGAGTGATG TCATTTCTT TTCAATGTATT	120
CCAATTAAG AAACAAGGGC AGGCGTATA ATGGCATATT AATACATTAG ACTTAATCTA	180
GAACCCCTGT AGCTTTTGAT TGTCTTTAT TTCTTATCTC TTTGAATTCC TGTTGGTTA	240
CTTGGCTTCC AATGGAGGTG AACTTAACAA CCATACTGAA ATATTCCGTC TTGACTTTGT	300
AAACTGTGGC TACTTGAAT GAAGTTATC TGGGGTCTCG AG	342

(2) INFORMATION FOR SEQ ID NO:849:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:849:

GAATTCGGCC TCATGGCCTA GGTTATTCTA TTATTTGTAG CTGAAATAAT TCCTGGCACA	60
AATGACTTTG AAATTTATCT CTGAACATCC CAAATTCAATT ATTAGCAAAT ATCAGAAACT	120
TCACATCACT CCAGTCTGTT ATTTCACATG GTTTCTTAG GGCCTGGAAA GTTTTACAG	180
CTGGCTTTA TTGACTGTGG TGGCTGATAT GCTGAAGAAT GGAGCTCATT GGTTTGAGGC	240
TTCTGCCAG	249

(2) INFORMATION FOR SEQ ID NO:850:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:850:

GAATTCCGGCC	TTCATGGCCT	AGACATGAAT	TCTTTGACTT	GTGCTCATTC	TTTCTGAAC	60
TATTGAGCCT	TATATATATC	AAATAAGGTT	AATTTACACA	ATAATTATTT	TTAATAATTA	120
ATAAA	ACTCAT	TCATGTAGTA	TATTTAAAAA	CATTATTC	TCTCATTTT	180
TTTCTTC	CTA	TATATT	TTA AGGTTCAAG	AGAAAACGGG	CTTCAGTTT	240
TAGACTTGCA	TTTTACTGT	GCTTATTAA	AATAATGGAT	ATAATTATA	TTAAGGTCCA	300
AATTATTTA	TTCACAGGAT	AATCATGGTC	TCTGATAAAA	GATGCCACA	TTTCTGTGTA	360
CTCACAGTTG	TTGTATATT	TCAATTTC	ATTTGAAAG	AACTCAAC	ACTCGAG	417

(2) INFORMATION FOR SEQ ID NO:851:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:851:

GAATTCCGGCC	TTCATGGCCT	AGCTAGCTAT	TGTAATACA	AATAATAAAG	TCTGCATTTC	60
CTGTCTTCTT	TAAGCCTTCA	TTGCCTTATA	AATCATTACA	TTTAGATTA	GATATTATAT	120
TTTGATCATT	TGAGGAACCA	AATTTAAAAT	ATGGAATAAG	TATGGCATTG	AATTATACAT	180
GCCTATTGCT	AATATATTCA	TATTTATAG	GATTTAATGA	AACAGTCTCC	CAGCTCGAG	239

(2) INFORMATION FOR SEQ ID NO:852:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 489 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:852:

GAATTCCGGCC	TTCCCTAGGA	AAGTTCTTCA	CATCAGGAAA	CATTAGATCA	TATACAGAAA	60
CAA	ACTAAAT	TTGATAAAGT	AGTTATGGAG	TTTTGCATG	AGTGTATGGT	120
AAGAAAACAT	CTATTCTGAA	GCAACAGACA	AATAATCAA	CAGAAGTAGT	TAATAATT	180
GAAAAGATC	TTATGGAAGG	TCTTACTGT	GATGATCACA	TGATGAAGGT	AGAGACAGTT	240
CATTGCAGCG	CTTGCACTGT	GTATATCCCT	GCTTACATA	GTTCAGTCA	GCAGCACTTA	300
AAATCTCC	ATCATATCAA	AGGGAAGCAG	GCTTATAAGG	AACAAATAAA	AAGAGAGGT	360
GTCTTGACTG	CTACAAGCAT	TTAAATAAT	CCAATAGTGA	AGGCAGATA	TGAACGTTT	420
GTAAAGGTG	AGAATCCTT	TGAATTCAA	GACCATTCTC	AGGATCAGCA	AATAAAAGGC	480
AGACTCGAG						489

(2) INFORMATION FOR SEQ ID NO:853:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:853:

GAATTCTGGCC	TTCATGGCCT	ACTTCACTAA	CCTTTTTGT	TTTAAAATGA	ACCTGCTACT	60
TAAAAAAAAT	ACACATCACA	CCCATTAAA	AGTGATCTTG	AGAACCTTT	CAAACCAGAT	120
GGAGCATTGC	TTGCAAATT	TTTTCTCTA	TGTTGCATG	CGCTCGTGTG	TGTGTGTCCA	180
GGCAAGAAC	CATTTATAA	AAATAAGAAC	ACTTGGGCTG	GGCATGGTGG	CTCATGCCTG	240
TGATCGCAGC	TCTCTCGAG					259

(2) INFORMATION FOR SEQ ID NO:854:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 217 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:854:

GAATTCTGGCC	TTCATGGCCT	ACACAGCTGC	AGTCAACATC	CACAACCTACC	GGGACCACAG	60
CCCCTACTGC	TGGCTGGTGT	GGCGTCCAAG	CCTTGGCGCC	TTCTACATCC	CTGTGGCTTT	120
GATTCTGCTC	ATCACCTGGA	TCTATTTCT	GTCGCCGGGC	TACGCTTACG	GGGTCCCTTG	180
GCACAGAAC	CCAAGGCGGG	CAACAGCAGG	GCTCGAG			217

(2) INFORMATION FOR SEQ ID NO:855:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 246 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:855:

GAATTCTGGCC	TTCATGGCCT	AGACCTGCTC	CGAAAATAAA	TAAATAACCC	ACAGAGCTGA	60
GCACAGGCTT	CTTCATGCTT	TTCCCTTGGA	AGGTGTCCTA	GATATATGAT	GATTCTTTT	120
TTCTTTCACC	TCCTCTTGAT	TGTACAAGT	AGCTTGCTTG	GCTCAGGAAC	AACAGAAAGAG	180
AATAAAGAAA	ATGACCTCA	ACCTTCCCTA	CCTCAGTCTT	ATGCAGCGAC	CGCAGCCAGA	240
CTCGAG						246

(2) INFORMATION FOR SEQ ID NO:856:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 334 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:856:

GAATTCTGGCC	TTCATGGCCT	ACTGTCTCAA	AAAACAAACA	AACAAAAAGA	AAGAAAGAAA	60
AAGGAAAGGT	AGACTTATAT	AAAATAGACA	GTAAAGCATA	GGGCAGCAGA	AAGGAAAACC	120
TACTCCGCAA	AAAGTCACTTG	TTTTAACCTC	ATCCAGGAGC	TTCCCTCTAAG	TTCACCTTTA	180
TTTTTCACAC	GTCCCTGGTC	CAAATCCCAC	CATGCTCTGC	CGTATTCTTG	CCCTTTGCTC	240
TGTTGTTGAA	AGACTCATGA	GGGAGGGCTC	TCTATGGATG	GTTCCAATGA	GCCACATGAA	300
CAAAGCCATC	GTCAGTAAGC	AGCCACTTCT	CGAG			334

(2) INFORMATION FOR SEQ ID NO:857:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:857:

GAATTCCACT TGATCAACTT AATTCCCTTT CTTTATCTTC CCTGCCCTCAC TTCCCTTTTC	60
TCCCACCCCTC TTTTCCAAGC TGTTTCGCTT TGCAATATAT TACTGGTAAT GAGTTGCAGG	120
ATCCTCGAG	129

(2) INFORMATION FOR SEQ ID NO:858:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:858:

GAATTCAAGC ACCATAATTG GGCCACTCAG CTGTCTCATCAG GAACTAAGCC AACATTCCCTT	60
TTCAGAAAAA GACTTTGGAG AGGGGCAAAC ACTTCTGACA GTCTACTGT GTACTTATTT	120
TAGAAAATAA GCTGCTCTCA GGTTTCAGTA TCCAGTCAAA TATAATATAG AACTCTAGTC	180
TGTTTGAGT CCTACTACAA TAATATTTTC ACAATAGACT ACCAGTTATG AAGTCTCAC	240
ATTTTCCCCG CATGCTCGAG	260

(2) INFORMATION FOR SEQ ID NO:859:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:859:

GAATTCTGT CCCACCTGCT GAATGAGTGC GTGCCAGCTG AACATCAGCG TGGCTTCGTT	60
CTTCAACACA TTTACAAAAG AAGTAAAAAT AAACAGTTT TTCTTCTCAA TTCTCCTCCC	120
TGCTTTTTTC CTTTGAACC ACAATCATGC CCCAGTAAGT GCTTTCTAG GTGAGAGGTG	180
TGTGTCCCAG GTTGAAGGCA AGGCCAGTGG TCTCGAG	217

(2) INFORMATION FOR SEQ ID NO:860:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear,

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:860:

GAATTGGCC TTCATGGCCT AGAATATTT TATCATCCA AAGCTAAAAC ATTAAAAAAAT	60
TTAACGTTA TTCTTAGAGA TTGATGCAAC TTGCATATCT AATCGAG	107

(2) INFORMATION FOR SEQ ID NO:861:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:861:

GAATTCTAGA CCTGCCTCGA GGGCATCCTT TACTTTTTT TTTAATTCAAG CACAAACCAA	60
ACAAAATTTT AAAATTGAT GAGATTGAA GTTGGACAAA AGTGTATGC AGTTTTAAAA	120
ATTTTTTTT TTTTTTTGA GACCAAGATCT CACTCTGTT CCCAGGCTAG AGTGCAGTGG	180
CATGATCTCA GCCCAACCT CTACCTCTTA GGCTCAAGCG ATCCTCCAT TTCAAGCTCC	240
CAGGTAGCTG GGAGGCTGAA ATGGGAGGAT CAACTCGAG	279

(2) INFORMATION FOR SEQ ID NO:862:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:862:

TGTATTTTA CGTGACCTGT TTTCAGAAAT TTATGATATT TCTATGGTTG GTATTCTCAA	60
TTTTGCAAT GTGCTTGGT GTGGAACCTT TTCATTTGTT TTGCTGGGA ATTGATGGAT	120
CCTTTGCATC AAGATGCTTA TATTTATTCT TCAGTTCTGG GAAACTTCCC TGTATTATTT	180
GTTTGATAAT TGCTTTCTCT CGCTTTCTC TTTCCGTTT TTGGAAATTG CTTGTTGTG	240
TGTTGCATTA CTGCAGAGAA CTCGAG	266

(2) INFORMATION FOR SEQ ID NO:863:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:863:

GAATTGGCC TTCATGGCCT AGTGCTGTGG TAGTTGTGC CTTTAGAGGG ATTTGTGTAT	60
CTCATATAAT TTAATTTTTT GACATTCACT TTTTCACAAT ATTCTGTTAG AATTCTTTA	120
ATTTCTGTAA GGTGATATCT ATACTTTCAT TTATGTCTAG TAACTTGAAT CTTCTCTCTT	180

TTGTTCTTTC TCGGTCAAC TAATAATACG TCAATTTCAG TGATATATCA GAAGAACAA	240
CTTCAAGTT TATTAATTTC CTCTATTGTT TTTATTTCA CTACTTATCT CCATGCTAAT	300
CTTTATTATTCT GTTTACTTTG GTTTAAGTCT GCTCTTCAC TCGAG	355

(2) INFORMATION FOR SEQ ID NO:864:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:864:

GAATTCCGCC TTCATGGCCT AGCTTACTTT ACAATTCTGC TGTTTGCTAA GTGTTCTAT	60
AGTTTTTTTT AAAGGTATGT TAACTATTTC TCCCTTTGG TTTATATTG TAGGAATCTT	120
TGCCTTAAG TGTGCCGTG CAGAAGAATT ATTTAACATG TTGCAAGAGA TTATGCAAA	180
TAATAGTATA AATGTGGAGC TCGAG	205

(2) INFORMATION FOR SEQ ID NO:865:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:865:

GAATTCCGCC TTCATGGCCT AGTCACCTGT TCTGTAGAAT ATGTTCAAT CTGATTTGT	60
CTTTTTGTTT TCTTGTGTTA TTACCTTGT CCTCTATCCC CTGTTTTTC TGAAAATGAA	120
AGTTAGCTTA GAAGTTTCAT TCCATTCTGG TTCAAATGC TTAAGTGCCT TATGTCGTGT	180
CATATTAGGA AACACAGTAT CTAGTGGTCC CAATTTAGT GATTCAAAAA TCAGTCTCTA	240
GGTTCAAGAGA TTAATCAGTA GATTCAAGAGA TCTCTCCATT GTAAATTCT TAATTAACCT	300
TTGAATTGCT AATGTTCTGT TCACTGATCG TTGTGGCCCA AATTATTTAT TTCACTAGGG	360
GACTCGAG	368

(2) INFORMATION FOR SEQ ID NO:866:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:866:

GAATTCCGCC TTCATGGCCT AAGGAGCAGC AGGAACATGG TACATAAAAT CATCCTGCTT	60
CTTATAATGG CAGGAATCAG TGGGATATGG TATTTGTGCA GCATGCTGG GCATCCACTA	120
GAAAGGCCCTG AAGGAAGACT CGAG	144

(2) INFORMATION FOR SEQ ID NO:867:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 268 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:867:

GAATTCCGGCC TTCATCGCAT TGAATTCTAG ACCTGCCTTG AGCCCCTCCA CCCCCAAATC	60
CTTCCTCTCC TCCCCAGTCCC ACCCCTTGCC CCACGGAGTC CTGGGGACGC AGTGCCTTCA	120
CTGGGAAGAG GGCGGGATCG GGCACCTGGTT CCTCCTTGTG CCCCCTTCT TGCGGGCTTG	180
CTACTTTTGT TCTTCTATTG TGTGGCTTTC TGAGTATTG AACCCCCAGTC CTGTGTCACC	240
TTCCCTTTTC TTTCGCGTGC CCCTCGAG	268

(2) INFORMATION FOR SEQ ID NO:868:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 384 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:868:

GAATTCCGGCC TTCATGGCCT ACAGAACTAT AATTATCTT AGTTTAAGCC ACTGGTAAGT	60
GTAATTGTA TTGTAATTG TTACATCTGC TATAGTAAA CTAATACTGA AATTAGAAA	120
AGATGGCTAA CTTATTATGT GGTAAGTTT AAAAGATA AGTAACTCGT TGAAGATCAC	180
ATAATTAGAA AAGAACAG TAGAGCTTGG CCTTGAACTC AACCAAGTGTG ACTCCAGAGC	240
TTGTAGAACAA GAATAACCAC CTCCAAGGCC AGCTGAATCT GACCACAGTC TGGTGAATT	300
CTAGTACATC TCGTTGAGAA GTGGGATTGC CGGAGGGAG TTGGTTATTC ATGAAGGTGA	360
TGATGTTTGT CCAATGTCCT CGAG	384

(2) INFORMATION FOR SEQ ID NO:869:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 273 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:869:

GAATTCCGGCC TCATGGCCTA CTTGGAGAGT TTTGTAAGGA GAGTGGCAAA CTTAGCACGG	60
ACTAATGCCA CGAACACAT GAATCTAAGC CGAACAGCA GTGATAACAA CACTAATACT	120
TTGGGGAGGA ATGTGATGAG CACAGCAACT TCTCCTTCA TGGGTGCTCA GAGTTCCCT	180
AATTGACCA CACCTGGTAC TACATCAACA GTGACTATGT CAACATCCAG TGTTACTAGC	240
AGCAGCAATG TAGCTACAGC AACACACACTC GAG	273

(2) INFORMATION FOR SEQ ID NO:870:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 278 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:870:

GAATTGGCC TTCAATGGCCT AGGTCAGGAG CCTTCTTGGA GTCCCAATTG TGCATCCCCA	60
AATGATAAAAG ATGGGGTGAAG GGAACGTGAGA GCCATGAGTT GGAGAGTCCT CTTGCTTGAG	120
GTCCTGAGA ATGTGCTCCC GGAGTATCCG GATCACTGGA AGCCAGGACT TCAACGCATT	180
GGGTAGTGAG GGATGGAGGG AGGGCTGGA CGCAGAACCA GGATGAAGTC TGCTGGGTGT	240
GAGCCTCCAA GGAGGTAGAA CAAAGAGGGC AACTCGAG	278

(2) INFORMATION FOR SEQ ID NO:871:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:871:

GAATTGGCC TTCAATGGCCT ACCAGACTCC CATAATAATA AACCTGGTA ATAAACAAAG	60
GAACCTCTTC CAGTTCAAGT GTATCAACCA CCACGTACCA GATAAAATCT TATTCACCT	120
TTCACAATTT ACCAGTGTGTT GGCTGTGAAT TAATATTTT ATTTCCTGT GCATTCAAA	180
ATTAAGAGTT TTTTATTGTA TTGTAACTGT AATTTGAGA CTAAAGTCTA AAAACAAGAC	240
ATCATGAAAT GGAGCTGGAG GATACTCGAG	270

(2) INFORMATION FOR SEQ ID NO:872:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:872:

GGTTTAGAAA GGGCACAAAC AGTGCAAACC TGTTCATGAA CCTTACATG TCATGAACAG	60
GGCAGAATGC TTCAGGAAAG AATTGTCGAA AGTAAAAAG CAAATAATGG ATGAGCTTA	120
TTCTAGTTAT TGAAGAATCC AACGGGATGG AAGCTAAATG TAGCACATGG CATGGCGAT	180
GTCTCAACAG TGAGTGGGAT ACAAGTCGT TTTAATGGTT CAGGGCCAAT AACCGGGGAG	240
GGTGAGGAAC GGCATCTCTG TTTTGAGTAA ACAAGAGTGA TTCCCTCCC TGACACTGAA	300
AAATGAAACC TTTGGGGAGA TAGAGGAAGC GATCTCGAG	339

(2) INFORMATION FOR SEQ ID NO:873:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:873:

GAATTCCGCC TTCATGGCCT AACCTTTAAA CCCTAAAATC CAGGAAAAGA AAATAAAATAC	60
ATTATCATGG ACCTGAGGGA TTTTTACCTG TTGGCTGCTC TGATTGCCTG TTTAAGGCTG	120
GATTCGCAA TAGCTCAAGA ACTTATTTAC ACTATTAGAG AGGAATTGCC TGAAAATGTG	180
CCCATAGGAA ACATACCAAA GGATCTGAAC ATTTCTCACCA TCAATGCTGC CACAGGGCCA	240
CCTCG	245

(2) INFORMATION FOR SEQ ID NO:874:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:874:

GAATTCCGCC TTCATGGCCT AGTTTCTTC ACTGGCATTG ACAAAATTAA GCCATTGCTG	60
CCTCATTAAGC CTTGTATTTTG GTGTGCATAT CATATATCCA GACCTGTATG TTCACATTAA	120
GCATTCTTAT ATCACACTGT CTCCCTCATCT ACCATATGGT AAATGTTAAA ACTCCACATT	180
TGTCTGCATC AGGGAAAATG CATGGCACA CATCCTCCCC CCCTTCCCTC GAG	233

(2) INFORMATION FOR SEQ ID NO:875:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:875:

GGACAGGAAG TCAACTTCAA GCAGATTGAC TTGAAACGGG ATCTCATTTA GGAAGCATAA	60
GTGTCCAATC AAAAACTGTG TATTTTTTTA AATTTGGAAA ATACTCAAGT TCCAGTTGCT	120
TATCATTCTC CTTCACTTTC TGAAAACCTG GCAATCCAT GTGGACTTCT GGTAGAACATGA	180
GCAATGCAA GAACGGCTT GGACTTGGCA TGTCCTTGTAA CTTCTGGGGG CTGATGGACC	240
TTACGACCCAC CGTTCTCTCG GACACCCAC ACCTCGAG	278

(2) INFORMATION FOR SEQ ID NO:876:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:876:

GAATTCCGCC TTCATGGCCT AGTCCTCAAATTAAGTATTG CATTATTTTC	60
TTATCATTTA TTGATATTGG TAGTGTTCCT AAAACAGGA AATACATAAT TTGGCATCCT	120
TATTCTTAGT TTTATACCTA AAGAACCTAG TAACTCACAG GAGAACGTAG TAACATTATC	180

ACTTGTAAAT CAAGCTTCAGT TTATCAAACC ATTTTTTTA TTTTGATTCA	240
GCAAATTGTA CAACTAAATT TAATTAAAAA GTAGAGGTCC AAAGCTCGAG	290

(2) INFORMATION FOR SEQ ID NO:877:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:877:

GAATTCCGCC TTCATGGCCT ACTCAAATTG GAAAGAAAGA TTCCCTTGAGA CTTACTTTA	60
AAATCTAAAG TGTGAGGNNAC ACANCAGAGT AAAGNCAGA CTCATTNNAC CTTCGATGTC	120
TGCATAGATC CAGNAGTTGT ACATTTTACCC TAACAACATC ACTTTTGTTG AACATTC	180
CTCCAGAAATG ATCCCCAACATC ACCCTTAATCT CAGAATGCTG GAATGATGTC TGTTGGCAA	240
CCCAGGACTC CACACTCGAG	260

(2) INFORMATION FOR SEQ ID NO:878:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:878:

GAAGCGACCA TTCGTCCAAC AGGTATGGCT GGTTTTGTTG CAATGAGAGA ATGTCCACTC	60
GCAATGATGA GCCTGAGAAG GCAAGTCGTC CGTTTGATGT GGATCGCGAT GGTTTTGTTA	120
TGGGTGAAGG TGCCGGGATT CTTATTCTGG AATCACTCGA ACATGCTGAG AAACGTGGAG	180

(2) INFORMATION FOR SEQ ID NO:879:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:879:

GAATTCCGCC AAAGAGGACT ACACAGAGCC CCTGTTGGG AATTTGAGAT TCTGTGTCAT	60
GCTGGTTTC CTTTCAGAAT TGTCTGAAAT CGAGTTCTCT TAGCCACTGG ACACCTAGTT	120
TTCAGGAGAA TGTCCAAGA TTGTTTATAT ATACAAAATG GCAAAACTAC TGTTTTTCGA	180
ATTGATAATT CAAGCAAAGG CTTCTCTTTA CTGTCACTGA TTTTTTTTTG TTTTTATTTT	240
GTTTCCTTGT TTCTATTTC TTGAAGCTTT GAAGGGAGGA GAAGCAGAAA ATTTTGTTTA	300
TGTTTGTAA AAATCAGAAC TACTTAATGC TTTTTGCCAC AGCATATTTC CTTGCCCTGTT	360
GGAGCCGTTA GGAAGATTAC CTATGTCCTA ATCTTCAACC TGAGAAGATT TTTGACTCTT	420
GTGTCTACTG TTGATTTGTTT GCTTGAGTTC TCAAAGACCT GTGGCCAGGT ATTTTAAAAAA	480
GTCGTCTATT TCTCGAG	497

(2) INFORMATION FOR SEQ ID NO:880:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:880:

GAATTCCGGCC	AAAGAGGCCT	AGCAAAATCA	AATTCAACCC	ATGAGTCACA	GTGCTTTCTT	60
CAACAAGAAA	ACATTGAACA	CAGAAAAGCAA	TTGTGAATAT	AAGGACCCCTG	GGAAAATGAT	120
TCGCACGAGG	CCCCCACCTG	CTTCTTCACA	GAAACAAACCT	CAGAAATGTT	GCTTATTTCAC	180
AGAAAGTTG	AAGCTGAACC	TAGAAGTGAA	CGGTCAAGAT	GAAAGCAATG	ACACAGAACAA	240
GCTTGATGAC	GTGGTGGGT	CTGGTCAGCT	ATTCAGCCAT	AGCTCTTCG	ATGCCTGCAG	300
CAAGAATATT	CATAACAGGAG	AG				322

(2) INFORMATION FOR SEQ ID NO:881:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:881:

GGCCCACCTG	TGTCCTGGTT	GAGGGTCTCC	AGGGTTCTTT	GGGGCCCGAG	GCCAATGGTG	60
GCAGAGCTCA	CATAGAACTA	TGCTTCGTGG	TGTTCTGGGG	AAAACCTTTC	GACTTGTGTT	120
CTATACTATT	CAATATGGCT	GTATAGCTCA	TTGTGCTTT	GAATACGTTG	GTGGTGTGTT	180
CATGTGTTCT	GGACCATCAA	TGGAGCCTAC	AATTCAAAAT	TCAGATATTG	TCTTTGCAGA	240
AAATCTTAGT	CGACATTTTT	ATGGTATCCA	AAGAGGTGAC	ATTGTGATTG	CAAAAAGCCC	300
AAGTGTATCCA	AAATCAAATA	TTTGTAAG	AGTAATTGTT	TTGGAAGGAG	ACAAAATCCT	360
CACCACTAGT	CCATCAGATT	TCTTTAAAG	CCATAGTTAT	GTGCCAATGG	GTCATGTTG	420
GTAGAAGGT	GACAATCTAC	AGAATTCTAC	AGATTCCAGG	TGCTAGGCCT	CTTTGGCCGA	480
A						481

(2) INFORMATION FOR SEQ ID NO:882:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:882:

GAATTCCGGCC	AAAGAGGCCT	AGGGAAGAGT	GGAACAAAAG	TCAGTCGTAC	ATTCAGCTAC	60
ATCAAGAATA	AAATGTCTAG	CAGCAAGAAG	AGCAAAGAAA	AGGAAAAAAGA	AAAAGATAAG	120
ATTAAGGAGA	AGGAGAAAGA	TTCTAAAGAC	AAGGAGAAAG	ATAAGAAGAC	TGTCAACGGG	180
CACACTTCA	GTTCCATTCC	TGTTGTGGGT	CCCATCAGCT	GTAGCCAGTG	TATGAAGCCC	240
TTCACCAACA	AAGATGCCTA	TACTTGTGCA	AATTGCAGTG	CTTTTGTCCA	CAAAGGCTGC	300
CGAGAAAGTC	TAGCCTCCCTG	TGCAAAGGTC	AAAATGAAGC	AGCCCCAAAGG	GAGCCTTCAG	360

GCACATGACA CATCATCACT GCCCACG

387

(2) INFORMATION FOR SEQ ID NO:883:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:883:

GAATTCCGCC	AAAGAGGCCT	AACGCAGCCA	TGGCTCGTGG	TCCAAGAACG	CATCTGAAGC	60
GGGTGGCAGC	TCCAAAGCAT	TGGATGCTGG	ATAAATTGAC	CGGTGTGTTT	GCTCCCTCGTC	120
CATCCACCGG	TCCCCACAAG	TTGAGAGAGT	GTCTCCCCCT	CATCATTTTC	CTGAGGAACA	180
GACTTAAGTA	TGCCC	TGACA	GGAGATGAAG	TAAAGAAGAT	TTGCATGCAG	240
AAATCGATGG	CAAGGTCCGA	ACTGATATAA	CCTACCCTGC	TGGATTCATG	GATGTCATCA	300
GCATTGACAA	GACGGGAGAG	AATTCCGTC	TGATCTATGA	CACCAAGGGT	CGCTTGCTG	360
TACATCGTAT	TACACCTGAG	GCGGGCATAA	CACAGCAAGA	CGAGAAGACC	CTATGGAGCT	420
TTAATTATT	AATGCAAACA	GTA				443

(2) INFORMATION FOR SEQ ID NO:884:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:884:

GAATTCCGCC	AAAGAGGCCT	AAACATCATT	TGTACTCTAA	TCCAATCAAA	GAAGAAATGA	60
CTGAGTCTAA	GTTCTCTAAAG	TACTCTGAAA	TGAGTGAGGA	AAAACGAGCC	AAACTTCGTG	120
AAATTGAGCT	CAAAGTTATG	AACTTCAGG	ATGAATTGGA	ATCTGGAAAA	AGACCTAAAA	180
AACCAGGCCA	GAGTTTCAG	GAGCAAGTAG	AAACACTACAG	AGATAAACCT	CTTCAACGAG	240
AGAAAGAGAA	AGAGTTAGAA	AGAGAACGAG	AAAGAGACAA	GAAAGATAAA	GAAAATTGG	300
AATCTCGCTC	CAAAGACAAG	AAGAAAAAAG	ATGAGTGTAC	TCCGACAAGG	AAG	353

(2) INFORMATION FOR SEQ ID NO:885:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:885:

GAATTCCGCC	AAAGAGGCCT	ACAATTTTTT	GCCTTTTAC	CCTTCTGTCC	TTTAATGCCA	60
TCTCTTTCTC	AATTATTTTC	TCTCATTCTT	TTTCTGAGCA	GACTTATACA	AAAAGGAACA	120
TAAATTAAT	TTCGCAAATA	TCAAAGAGA	GGAACTTTTT	ATTTTTTATT	TTTTGGAAC	180
GGAGTCTCAA	TCTGCTCTCC	AGGCTGGAGT	GCAGTGACGC	AATCTCAGCT	CACTGCAACC	240
TCCGCCTCCC	AGTTCAAGAG	ATTCTCTGCC	TCAGCCTCCC	GAGTAGCTGG	GATTACAGGT	300

ACCCCTCTACC ATACTCAGCT AATTTTGTA TTTTAGTAG AGACTGGTTC ACCATGTGGG	360
CCAGGCTGGT CTCGAACCTCC TGACTTCAGG TGTTCTGCCT GCTTTGCCTC TCCAAAGTGC	420
TGGGATTATA GGCGTGAGCC ACCACTCTCC ACTGAACCTT TTAATCTTAG AGCAG	475

(2) INFORMATION FOR SEQ ID NO:886:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:886:

GAATTCCGCC AAAGAGGCCT AGGGGTGTTA ATTAGCTCAG CTGTAGCAAT CATTCTATAA	60
TCTATATCAA AACATCCCAC TGTATACTTT ATATTTTTT ATAAAATAA ATATTCTTAC	120
AAAAGGACAG GCGCTGTGTC TGTCTGGCTC ACCATTGTAC CCAATACCCA ACAGGGTGC	180
AAGTACCCAA TACCCAAACAG GGTGCCAAGG AACACAAAAAG GCACTCAAAA TATGTTGTT	240
GATTGGAGTT TACAAGGAAG AAAGGTATT TCTTATCCCT CTCTTCCCTT CCCACCCAAA	300
CATAGCTTCT TCTAAAGAAA GAAACTGAGG CTGGGCAAGG TTAAAAGCTA GCTCTGGTA	360
CTTTGCATC CACACTCAGT TTAACCTGTGC CTTAAACCGAG ACTTCATCAA ACTTCAGTCT	420
TCACAAGTCA CTTCACCATTT TTGCTCTAC CTACTTACTG CCTGTGAGG CCTCTTGGC	480
CGAG	484

(2) INFORMATION FOR SEQ ID NO:887:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:887:

GAATTCCGCC AAAGAGGCCT AGTGGGACAT AAGGCTGAA GGTAGCACAC ACAGCACCAT	60
ATTCTTTTTT ACTTGCATGC GAGTTACTTT GAGTGCTTTT CTCTTACCA AATATATGAG	120
TTCTATTACT ACATTCCTTT TCTTGTGTTG TTTTAGTGAG ACAGGGTCTC GTTCTGCCTC	180
CCAG	184

(2) INFORMATION FOR SEQ ID NO:888:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:888:

GAATTCCGCC AAAGAGGCCT AGTTTGCAGAC TTACTTTAA TTCAAATCA GCTGCAGATG	60
TTTGGGAGCC TTCTCGAG	78

(2) INFORMATION FOR SEQ ID NO:889:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 546 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:889:

GAATTCTGGCC	AAAGAGGCCT	AATGGAAGAT	ATGCTGAAAG	ACTTTCTCCT	TGGAGAACAC	60
TTATTATTGG	TTGGCAACCA	GGGTGTAGGA	AAAACAAGA	TTGTTGACAC	ATTCCCTCAC	120
CTGCTCAACA	GACCCCGAGA	ATATATTCA	CTACACAGGG	ATACCACAGT	ACAAACTCTT	180
ACGCTTCAGC	CTTCGGTTAA	AGACGGACTT	ATTGTATATG	AAGACTCACC	TTTGGTTAAA	240
GCAGTAAAGT	TGGGTCTAT	TCTGGTAGTA	GATGAGGCTG	ACAAAGCTCC	AACAAATGTC	300
ACGTGTATTT	AAAAAAGTCT	AGTAGAAAAT	GGAGAAATGA	TTCTAGCAGA	TGGAAGACGC	360
ATTGTTGCAA	ATTCTGCTAA	TGTGAATGGA	AGAGAAAATG	TTGTTAGTGAT	TCATCCTGAT	420
TTTAGGATGA	TTGTTCTGGC	AAATAGACCT	GGATTTCCCT	TCCTAGGCCA	TGATTTCTTC	480
GGTACCTTAG	GTGATATTT	TAGCTGCCAT	GCAGTTGATA	ACCCCAAAACC	CCACTCGGAG	540
CTCGAG						546

(2) INFORMATION FOR SEQ ID NO:890:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 427 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:890:

GAATTCTGGCC	AAAGGGCTA	GAGATTTCAT	GTATTTCT	TCACITCCAA	GAGAGTGGAT	60
AGAATGGAGA	AATCTAGATT	GATCTTACA	GCTCCAGATA	AAGGGACTAA	AAATATTGGT	120
TTAAAATATT	AAAGGTTAAA	GAAAGAGACT	GTTGGTTCT	TTCAAAGTGA	TTTAAATTAA	180
AACTAGGTTT	TTTAACTAA	TTTTGGAAA	TGGGTAAC	ATTTTTCT	CATATCAAGG	240
ATATGTACAT	ATTTCCCATT	TCCCCATAAT	AAAAACAAA	CAACTCCCAT	CCACTTTCTTA	300
TAAATAGTTC	TTAACCTGGG	CTTAGTAACA	ATGTATATTG	TGCCAGTAAT	ACAGAAAAGG	360
TGGGAGTATA	AAGACCATCC	TGTCTGTTA	GAATCCTATA	GAACCAAGGT	GCTGGATTAT	420
GGTGGTT						427

(2) INFORMATION FOR SEQ ID NO:891:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 346 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:891:

GAATTCTGGCC	AAAGAGGCCT	AATTTTATTG	AAACTGCTTA	TGTATGTCAA	AGGAGCCAC	60
AACTTCAGCT	ACACAACCTTT	TTGTATTGAA	AGAACTCATA	CTTTTTGTAG	CTTTTATTTC	120
ACATTTAATT	AAAAGTACT	TTTAGCACTA	AAATGCCCTAG	AAGATTTTAC	TCCAGACCTA	180
TAAGGAAATG	TTTAGTTTT	ATGAAAAATG	ACAAGTCGAT	GGTAAACTT	CTCATGTCTT	240
TGGTGCCTTG	GCCCTAATAG	CACTGGACAA	CACCAACGACC	ACATGGAAAC	ATATTTTGG	300

AAGCAAAACT TTAATTAT ATAACGTATG CTATGGAGAA CTCGAG

346

(2) INFORMATION FOR SEQ ID NO:892:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:892:

GAATTCCGCC AAAGAGGCCT AGTGGAGAGT GAAGCTTAAG ACTGCAATTG CAGAAAAAGT	60
CCATGAGGAG AGAAGAAGGA GAAAAGGGGG AAGAG	95

(2) INFORMATION FOR SEQ ID NO:893:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:893:

TTTTTTTTTT TTTTTTTAA ATACTTCGCA TACTCTCCAA TGCCCCAAAAA TAGCAAGGTG	60
GTAAAAAGAG AATTAGATGA TGATGTTACT GAGTCTGTCA AAGACCTCT TTCCCAATGA	120
AGACGCAGCT GATGATGCTT TTAAGACAAG TGAACATAATT GTTGATGGCC AGGAAGAGAA	180
AGATACAGAT GTTGAAGAAG GATCTGAAGT CGAACATGAA AGACCAGCTT GGAACAGTAA	240
ACTACAATAC ATCCCTGGCCC AAGTTGGATT TTCTGTAGGT TTAGGAAATG TGTGGCGATT	300
TCCATACCTA TGTCAAGAAGA ATGGGGCGGG TGCATATCTT TTACCATATT TAATACTACT	360
TATGGTAATA GGTATTCCCC TTTTTTTCTT CGAACCTCTCT GTGGGTCAAA GAACCACTCT	420
CGAG	424

(2) INFORMATION FOR SEQ ID NO:894:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:894:

GCCAAAATCA AGCAAAGTAT GAAGAAAGAT AAAGAAGGG AAGAAAAAGG GAAGCGAAGA	60
GGATTCCCCA GCATCCTGGG ACCCCCACGG AGACCAAGCC GTCATGACAA CAGTGCATT	120
GGCAGAGCCA TGGAACTACA GAAGGCGCGC CACCCCTAAC ACCTTATCCAC ACCCTCATCT	180
GTGAGTCCTG AACCTCAGGA CTCTGCCAGG TTGCGCCAGA GTGGGTTAGC AAATGAAGGA	240
ACAGACGCTG GATACCTGCC TGCCAATTCC ATGCTTCTG TAGCTTCAGG GGCCTCTTTT	300
TCCCAGGAAG GAGGGAAAGA GAATGATACA GGATCAAAGC AAGTTGGAGA AACATCAGCA	360
CCTGGAGACA CCTTAGATGT CACCCCTCGAG	390

(2) INFORMATION FOR SEQ ID NO:895:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 595 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:895:

GAATTCCGCC	TTCATGGCCT	AGTAGCTGGT	ATTTATTCCC	CAAAGTAATA	ATGTTGAAGT	60
ATGGGTCTCA	TCATTCCAT	ACACAGAAAC	ACAAAACACT	TTGATCATAA	ACTTTTTCT	120
TCAGAAGCCA	AACTAACTTG	CAGAATAATA	GAGCCACTGG	TTTAATGTTT	CCTCAAGATA	180
GGTTTTAGTG	TAAGCTAGTA	TTCTGTGTGT	TCGTAGAAAT	GATTCAATAC	CTGCAGCTGG	240
TGAATTAGGA	ATTGTTATTG	TTGCCCTTTT	TATATTAGAT	GAGGTGCAAA	AATTTTAATG	300
CTAGTCAGTA	TGCACCCACCA	CAGGAAAGTT	AGATCCCATT	AGCACTTGAA	ACTACAGCTT	360
TGGAAACTTA	GGCTAAGTTA	ATTGGATT	GTTACTTGAT	TCACCTACTG	ACCTTTCTT	420
TTGTTTGAAG	TGCTTATCG	CATAATGAGC	TAAGTGTGAT	GCATATTGTT	GAAGAAACAC	480
CCTTTTGGT	CCCTTTGGG	ACAGAGAGGT	ACTCCCTGAT	CTTATGAAAT	GACAGGTTAC	540
TGTTTGCCT	TATTGCTTAA	CTTAATGTTAG	TGAAATAAG	CAGACGAGGC	TCGAG	595

(2) INFORMATION FOR SEQ ID NO:896:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 341 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:896:

GGCTGATCCG	CGTGAACATG	GAGGACTTGC	GAGAGCAGAC	TCACACCCGC	CACTATGAAT	60
TGTACCGACG	CTGTAAGCTT	GAAGAGATGG	GGTTCAAGGA	CACTGACCCT	GACAGCAAAC	120
CCTTCAGTCT	TCAGGAGACA	TATGAAGCAA	AAAGGAATGA	ATTCTGGGA	GAACTGCAGA	180
AGAAAGAAGA	AGAAATGAGA	CAAATGTTG	TTATGAGAGT	GAAGGGAGAA	GAAGCTGAAC	240
TTAAGGAGGC	AGAGAAAGAG	CTTCACGAGA	AGTTTGACCT	TCTAAAGCGG	ACACACCAAG	300
AAGAAAAGAA	GAAAGTGGAA	GACAAGGAGA	AGGAGCTCGA	G		341

(2) INFORMATION FOR SEQ ID NO:897:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 382 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:897:

GAATTCCGCC	TTCATGGCCT	ATGCCTTAAT	TTTGCTGTTT	GCCCTGGAT	CTCTGGGTTT	60
GATTTTTGCG	TTGACTTTAA	ACAGACATAA	GTATCCCCTT	AACCTGTACC	TACTTTTGG	120
ATTTACCGCTG	TTGGAAGCTC	TGACTGTGGC	AGTTGTTGTT	ACTTTCTATG	ATGTATATAT	180
TATTCTGCAA	GCTTCATAC	TGACTACTAC	AGTATTTTTT	GGTTTGACTG	TGTATACTCT	240
ACAATCTAAC	AAGGATTTC	GCAAATTG	AGCAGGGCTG	TTTGCTCTTT	TGTGGATATT	300
GTGCCTGTCA	GGATCTTGA	AGTTTTTTTT	TTATAGTGTGAG	ATAATGGAGT	TGGTCTTAGC	360
CGCTGCAGGA	GCAGCACTCG	AG				382

(2) INFORMATION FOR SEQ ID NO:898:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:898:

GAATTCCGCC	TTCATGGCCT	ACGAGCCTCA	CATCACTTGT	ACAAGCCACC	TGGGAGAAAGT	60
GGCCCTCAGG	AAGATCCTAA	AACCAATACA	CAAATACAAAC	TTTTTCATTT	CATTAATACA	120
TCAAGTTCAT	ATAAGAGTCA	AACAGGTAAA	AGCAGCATCC	CAAACGTGTTT	TCTCCCTCGTA	180
CATGTCAGTT	CCACGATCCT	CACTCTCATA	AAAGTCAGGGA	CTAGAGACCA	ATGTAATTAT	240
CAATACGTAC	CTGCCTTGTG	GTGAACCTTC	AATGCCAACT	AGGAAGGGCG	CTTCCAAAAC	300
GACGTTATTT	GTAACTCCTA	GGAAAGACAAA	CACGGGTCAG	AACCCATACT	CTGCGGGCCT	360
TGAAATGGAA	AATCTCTCCT	CTAGACAGAC	TCATCCTGGC	CGTAAATATC	AGGAGACTCG	420
AG						422

(2) INFORMATION FOR SEQ ID NO:899:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:899:

NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	60
NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	120
NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	180
NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	240
NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	300
NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	360
NNNNNNNNNN	NNNCNTGCAN	GNTTTGGTTC	CNTTTNTTCC	TTGTTTNTTT	TTTGCGACAA	420
TATTTCAAGN	TTTACNAGGC	ATACATCAAT	CCAAGTTCGG	AATTITAATT	AAGAATTTCGG	480
CGTTCATGGC	NTAAAAGAAN	TTGATGCTAC	CCCCGGAAT	GCCAGAACAG	GANATACATT	540
GAAATAGAACN	GTGATGAAGA	GCCCAGGGT	GAATTACTTT	TTNTTCCGGG	CANTGAACGC	600
NTTCATAAAA	AGCCAAAGTC	TGACAAAGAG	ACAAGAGTNG	CAANTNCAT	GGNTGGANAG	660
ACAGACCGAA	AAGAATTNT	GAGGAAGAAA	ACCAAAACAA	ATCCATNNTC	CAGNTCGACA	720
AATNAAGAGA	AGNAANACA	GAAGAACATT	ATGATGATGC	GGTATAGCCA	GAATGTCCGG	780
TCAAAAAATA	AGCATTCCCT	CTCGAG				806

(2) INFORMATION FOR SEQ ID NO:900:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:900:

GAATTGGGCC TTCATGGCCT AGGAGGGCCT GTTTCAGAAT TGCTTTAATA GTTCCCTTCC	60
AGTTGAATTT ACCTTTGCA GGAGCCTCAT CGTCTCTGG TTCTCCGCCC TCAGGATGCT	120
CTGGGAGCTT CATCTTTTC TTCTTAGAAT CTGTTCAAC TTCCGAGTGC CTCCGCTTCC	130
TCTTCCCTGC CCCACCGTG CCTCTTCCTC ACTGGCGTG TCCTTGCGCT GCTTCTTCTT	240
CTTGCTCTC TTCCCTGCAAG ACCATTGGC CTCAGGGACT TCCTCCCCAC CAGCCTCAAG	300
GTCAGCCTCC TGCCTCGAG	319

(2) INFORMATION FOR SEQ ID NO:901:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:901:

GAATTGGGCC TTCATGGCCT AAGAAAAGAC AAGGTCCCCA TAAGAGTGGC GAGAGGAACA	60
GAGCCAGGAC ATCGAAAGC AAGCCCTGT GTTCCCAAAC CGCAGAAAGAG GGAGCTCTGA	120
TGTTAGACAA GCCACCCCTC TACAAGCGAA GCGAAAGTAA CTTTGAGCAA AAATGAGCAA	180
CAGAAAATGA GATCAAGGTC AGATCTCAT AAAAGTTGCA AGATGAAAGA ATGAGCAGCA	240
GAATAAACCTC CCTGTGATGT GGAAAGTGTG CCAGGAAAC AGACCCAAAC GCTCGAG	297

(2) INFORMATION FOR SEQ ID NO:902:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:902:

GAATTGGGCC TTCATGGCCT AGGGGTTCTT TCTCCTGCAC GATGCCAGGT GGTACTGGAA	60
TCTGCTGAGT GGGATTGCGT GGTGAGGATC ATAAGGGCAA ATTCAAAAGG CTTCTGGCTC	120
CATGAGAAAT TCTTGAAGCA GGGTATCTCA CTGCTAGACT CTAACGGAAA TCCTCTTGT	180
GGAGAAAGCCC TTTTGTAAAGA AGGATGGAGT TGTCCCTGTC CCAGTTTGG CCCTTGGGAT	240
TCTGTAGGTG ACGGTCTTAA CTTGTGGTCT GTTCTCTAGG ACTGTGAGTG GTGGATTAGA	300
AGAGAGATGA GGAGCTGCCA AAAGCAGCTA CACAGAGAAC AGAGTTAGCA AATGGCACCC	360
GAGACAGAAC TATAGCAGAT GCAAGAGCCA AAAACCCACA GCCGCATTGA ATTCTAGACC	420
TGCCTCGAG	429

(2) INFORMATION FOR SEQ ID NO:903:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:903:

GAATTGGGCC TTCATGCCTT GTAACCATCA GGTAGATACA GCACCAACGG TAGTGGCTCT	60
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TTATGACTAC ACAGCGAATC GATCAGATGA ACTAACCATC CATCGCCGAG ACATTATCCG	120
AGTGTTCATC AAAGATAATG AAGACTGGTG GTATGGCAGC ATAGGAAAGG GACAGGAAGG	180
TTATTTCCA GCTAAATCATG TGGCTAGTGA AACACTGTAT CAAGAACCTGC CTCCCTGAGAT	240
AAAGGAGCGA TCCCCCTCTTA TAAGCCCTGA GGAAAAAAACT AAAATAGAAA AATCTCCAGT	300
CCTCGAG	307

(2) INFORMATION FOR SEQ ID NO:904:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:904:

GAATTCCGCC TTCATGGCCT AGGACCTCGT AGGTCCCTAC AGCACCAACAG TGCTCTTCAT	60
CTCTCAGAGG ACTGAACCAC CAGCCAGCAC CAACAGAGAC ACTGTGGAAA GCACAAGGAC	120
CCGACGGGCA CTGAGTGACG AGCAGTGTGC TGCGTCATC CTTGTGCTGT TTGCTTTCTT	180
TTCCATTTC ATTGCCTTA TCATTCAAGTA CTTTGTAATC AAGTGAATAT ATAACTTTAT	240
TTTTAACTC TATTACATT TATTTGTCA TGTACTAAAA TTATTTCTGT ATTGCTTTNA	300
TAAAAAACAG TGGCACCTCG AG	322

(2) INFORMATION FOR SEQ ID NO:905:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:905:

GAATTCCGCC TTCATGGCCT AAAAAAACAC ATAATTTGAA TCAACACAAC CACCCACAGC	60
CTAATTATTA GCATCATCCC TCTACTATT TTTAACAAA TCAACACAAC CCTATTTAGC	120
TGTTCCCCAA CCTTTTCCTC CGACCCCCCTA ACAACCCCCC TCCTTAATACT AACTACCTGA	180
CTCCTACCCC TCACAATCAT GGAAGCCAA CGCCACTTAT CCAGTGAACC ACTATCACGA	240
AAAAAAACTCT ACCTCTCTAT ACTAATCTCC CTACAAATCT CCTTAATTAT AACATTACACA	300
GCCACAGAAC AACTCGAG	318

(2) INFORMATION FOR SEQ ID NO:906:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 553 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:906:

GAATTCCGCC TTCATGGCCT ACAGGAAACA TACAAAGCTG CTCATAGTGG GAGTCCTTTT	60
GCTCATGTTG CTGTGCGGCC TCTTCTTCAC TCGACCTTCAG GGCAGCTACT TCATCAGACT	120
GCTGAGTGAC TACTGGATAG TCTTCCCCAT CATCGTCGTT GTCGTATTTG AAACCATGGC	180

TGTATCCTGG	GCCTATGGGG	CCAGGAGGTT	CCTTGCAGAC	CTGACGATCC	TGTTGGCCA	240
CCCCATCTCT	CCCATCTTG	GTTGGCTGTG	GCCCCATCTG	TGTCAGTTG	TGCTGCTAAT	300
CATCTTGTG	ACCATGATGG	TTCATCTTG	TATGAAGCCG	ATCACCTACA	TGTCCCTGGGA	360
CTCAAGCACC	TCAAAGAGG	TGCTTCGACC	ATACCCACCG	TGGGACTGTC	TCTTGATGAT	420
CACCCCTTTT	GCCATTGTCA	TCCTCCCCAT	CCCTGCATAC	TTTGTATACT	GCCGCATACA	480
TAGGATTC	TTCAGGCCA	AGAGCGGAGA	CGGGCCTATG	ACAGCCTCCA	CATCCCTACC	540
CCTAAGTCTC	GAG					553

(2) INFORMATION FOR SEQ ID NO:907:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 557 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:907:

GAATTGGCG	TTCATGGCCT	AGTAGAGAAG	ANNNNTATTGC	NGTGACAATG	AGGTTTCTAC	60
GTTCAGTGGC	AAGAGTTTTT	GTATTCTGA	GTGTTGAAAT	GGCTTCATCC	AAAAAGAAAA	120
ACAACCTTAT	TCCACAGCCA	ATTGGAAAAT	GCAAGCGTGT	ATTCCAAGCA	TTGCTACCTT	180
ACGCTGTGGA	AGAATTGTGC	AACGTAGCAG	AGTCACGTGAT	TGTTCCGTGC	AGAATGGGGA	240
TTGCTCGTCC	AACTGCACCA	TTTACCCCTGG	TCTAGTACTAG	CATAGATGCC	ATGCAGGGCA	300
GTGAAGAATT	ATTTTCAGTG	GAACCACTAC	CACCAAGGAC	ATCATCTGAT	CAGTCTAGCA	360
GCTCCAGTCA	GTCTCAGTCA	TCCTACATCA	TCAGGAATCC	ACAGCAGAGG	CGCATCAGCC	420
AGTCACAGCC	CGTTGGGGGC	AGAGATGAAG	AACAGGATGA	TATTTGTTCA	GCAGATGTGG	480
AAGAGGTTGA	GGTGGTGGAG	GGTGTGGCTG	GAGAAGAGGA	TCATCATGAT	GAACACAGGAAG	540
AACACAGGAA	GCTCGAG					557

(2) INFORMATION FOR SEQ ID NO:908:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:908:

GAATTGGGCC	TTCATGGCCT	AAAAAAAGTCA	GCCAGGTGTG	GTGATGTGCG	CCTGTGGTCC	60
CAGGTATTCA	CGAGCTGAGG	TGGGAGGATC	ACCTCAGCCC	GGGAGGTGGA	GGTTGCAGTG	120
AGCCCATATC	CCGCCACTGC	ACTCCAACCT	GGGAGACAGA	GCGAGACCC	GTCTCCAAAA	180
AAAAAAAAAA	AAAATCCGGG	ATCTATTAT	GTAACTACTA	GAATCTTAAG	TTCAGAATTT	240
ACTCCATAAG	AGTATATAAA	AAACTTACTG	TGATTTTATC	CATGTTTTC	CTAATATATA	300
ATAGGTCTAA	GTCTTGTACT	TTTCTGTCT	GTCCACAGAG	CCTTGAAAT	AATTAGAGC	360
TCAGTCATTC	AGTTTGGATT	TATGTATAAA	TTGAAATATA	TTAATTACTT	ATTTATAGTG	420
CAGCTCGAG						429

(2) INFORMATION FOR SEQ ID NO:909:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear